



FEATURES  
source  
Location/Qualifiers  
1..5711  
/organism="unknown"  
BASE COUNT 1953 a 1099 c 1277 g 1382 t  
ORIGIN

Query Match 100.0%; Score 5711; DB 6; Length 5711;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 5711; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGCTGAGACTTCTGAGACCCCGACAGGCTGTGGGTTTCTCAGATACTGGGCC 60  
DB 1 AGCTGCTGAGACTTCTGAGACCCCGACAGGCTGTGGGTTTCTCAGATACTGGGCC 60  
QY 61 CCTGGGCTCAGAGAGGCTTCAACCTCTGCTGGGTAAGTTCATTGGAACGAAAGAA 120  
DB 61 CCTGGGCTCAGAGAGGCTTCAACCTCTGCTGGGTAAGTTCATTGGAACGAAAGAA 120  
QY 121 TGAATTTATCTGCTCTTGGCGTTGAAAGTAAGTAATGCTATTATGCTATGCAAAA 180  
DB 121 TGAATTTATCTGCTCTTGGCGTTGAAAGTAAGTAATGCTATTATGCTATGCAAAA 180  
QY 181 TCTTGAAGTGTCCCATCTGTCTGAGAGTGTGATCAAGAACCTGTCTCCAAAGTGTGACC 240  
DB 181 TCTTGAAGTGTCCCATCTGTCTGAGAGTGTGATCAAGAACCTGTCTCCAAAGTGTGACC 240  
QY 241 ACATATTTTGGCAAAATTTTGGCATGCTGAAACTCTCAACCGAAGAAAGGCGCTTCACAGT 300  
DB 241 ACATATTTTGGCAAAATTTTGGCATGCTGAAACTCTCAACCGAAGAAAGGCGCTTCACAGT 300  
QY 301 GTCTTTATGTAGAATGATATATACCAAAAGAGGCTTCAAGAAAGTACGAGATTATGTC 360  
DB 301 GTCTTTATGTAGAATGATATATACCAAAAGAGGCTTCAAGAAAGTACGAGATTATGTC 360  
QY 361 AACTTGTGAAGACTATTTGAAATCATTTTGTCTTTTACGCTTGAACAGAGTTGGAGT 420  
DB 361 AACTTGTGAAGACTATTTGAAATCATTTTGTCTTTTACGCTTGAACAGAGTTGGAGT 420  
QY 421 ATGCAACAGCTATTAATTTTGGCAAAAAGAAATTAATCTCTCTGAAACATCTAAAGATG 480  
DB 421 ATGCAACAGCTATTAATTTTGGCAAAAAGAAATTAATCTCTCTGAAACATCTAAAGATG 480  
QY 481 AAGTTTCTATCATCCAAAGTATGGGCTACAGAAACCGTGCCTCAAGAGCTTCTACAGAGT 540  
DB 481 AAGTTTCTATCATCCAAAGTATGGGCTACAGAAACCGTGCCTCAAGAGCTTCTACAGAGT 540  
QY 541 AACCAGAAATCCTCTCTTGGCAGAAACCAAGTCTCAGTGTCCAACTCTTAACTTTGAA 600  
DB 541 AACCAGAAATCCTCTCTTGGCAGAAACCAAGTCTCAGTGTCCAACTCTTAACTTTGAA 600  
QY 601 CTGTGAGAACTCTGAGACAAAGCAGCGGATCAACCTCAAAAGAGCTGTCTACATTTG 660  
DB 601 CTGTGAGAACTCTGAGACAAAGCAGCGGATCAACCTCAAAAGAGCTGTCTACATTTG 660  
QY 661 AATTGGATCTGATTTCTTGAAGATCCGTTAATPAAGGCACTTAATTCAGTGTGGAG 720  
DB 661 AATTGGATCTGATTTCTTGAAGATCCGTTAATPAAGGCACTTAATTCAGTGTGGAG 720  
QY 721 ATCAAGATTTGTACAAATCAACCTCAAGAAACCAAGGATGAATCAATTTGGATTCTG 780  
DB 721 ATCAAGATTTGTACAAATCAACCTCAAGAAACCAAGGATGAATCAATTTGGATTCTG 780  
QY 781 CAAAAAGGCTGCTGTGTAATTTTCTGAGACGAGTGAACAATATCTGAACATCTCATAC 840  
DB 781 CAAAAAGGCTGCTGTGTAATTTTCTGAGACGAGTGAACAATATCTGAACATCTCATAC 840  
QY 841 CCACTAATTAATGATTTGAACAACCACTGAGAAACGCTGAGAGGCAATCCAGAAAGT 900  
DB 841 CCACTAATTAATGATTTGAACAACCACTGAGAAACGCTGAGAGGCAATCCAGAAAGT 900  
QY 901 ATCAGGGTGAATGCTGTTCAAACTTGATGAGACCATGTGGCAAAATATCTCATGCCA 960  
DB 901 ATCAGGGTGAATGCTGTTCAAACTTGATGAGACCATGTGGCAAAATATCTCATGCCA 960

QY 961 GCTCATTCAGCATGAGAACAGCAGTTTATTACTCACTAAAGACAGATGATGATGAAA 1020  
DB 961 GCTCATTCAGCATGAGAACAGCAGTTTATTACTCACTAAAGACAGATGATGATGAAA 1020  
QY 1021 AGGCTGAATTTCTGTATTAATAAGCAACAGCTGCTGTAGCAAGGAGCCAAATPAACAGAT 1080  
DB 1021 AGGCTGAATTTCTGTATTAATAAGCAACAGCTGCTGTAGCAAGGAGCCAAATPAACAGAT 1080  
QY 1081 GGGCTGGAAGTAAAGAAACATGTAATGATAGCGGAGCTCCAGACAGAAAGAAAGTAG 1140  
DB 1081 GGGCTGGAAGTAAAGAAACATGTAATGATAGCGGAGCTCCAGACAGAAAGAAAGTAG 1140  
QY 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAGAAATGAATTAACAGAAACCTGCATGCT 1200  
DB 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAGAAATGAATTAACAGAAACCTGCATGCT 1200  
QY 1201 CAGAGATCTTAGAGATCTGAAGATGTTCTTGGATPAACATTAATAGCAGATTGAGA 1260  
DB 1201 CAGAGATCTTAGAGATCTGAAGATGTTCTTGGATPAACATTAATAGCAGATTGAGA 1260  
QY 1261 AAGTTAATGAGTGGTTTCCAGAGTGAATGTAAGTGTAGGTTGATGAGCTCAATGATG 1320  
DB 1261 AAGTTAATGAGTGGTTTCCAGAGTGAATGTAAGTGTAGGTTGATGAGCTCAATGATG 1320  
QY 1321 GGGAGTCTGAATCAAAATGCCAAAGTAGCTGATTTGACGTTCTAAATGAGGTAGATG 1380  
DB 1321 GGGAGTCTGAATCAAAATGCCAAAGTAGCTGATTTGACGTTCTAAATGAGGTAGATG 1380  
QY 1381 AATATCTGCTTCTTACAGAAATTAAGCTTACTGGCCAGTATCTCTCATGAGCTTTAA 1440  
DB 1381 AATATCTGCTTCTTACAGAAATTAAGCTTACTGGCCAGTATCTCTCATGAGCTTTAA 1440  
QY 1441 TATGTAAGTGAAGAGGTTTCTCCAAATGATGAGAGATTAATGAGAACAAATAT 1500  
DB 1441 TATGTAAGTGAAGAGGTTTCTCCAAATGATGAGAGATTAATGAGAACAAATAT 1500  
QY 1501 TTGGGAAACCTATCGGAAGAGCAAGCCCTCCCACTTAAGCATGATGAAATATC 1560  
DB 1501 TTGGGAAACCTATCGGAAGAGCAAGCCCTCCCACTTAAGCATGATGAAATATC 1560  
QY 1561 TAATTATGAGACATTTGTTACTAGACCAAGATTAATCAAGAGCTTCTCAAAATA 1620  
DB 1561 TAATTATGAGACATTTGTTACTAGACCAAGATTAATCAAGAGCTTCTCAAAATA 1620  
QY 1621 AATTAAAGCTTAAGAGAGCTTACATCAGGCTTCACTCTGAGGATTTTATCAAGAAAG 1680  
DB 1621 AATTAAAGCTTAAGAGAGCTTACATCAGGCTTCACTCTGAGGATTTTATCAAGAAAG 1680  
QY 1681 CAGATTTGGCAGTTCAAAAAGACTCCTGAAATGATTAATCAAGGAACTTAACCAAGAGC 1740  
DB 1681 CAGATTTGGCAGTTCAAAAAGACTCCTGAAATGATTAATCAAGGAACTTAACCAAGAGC 1740  
QY 1741 AGAATGCTCAAGTATGATTAATTAATTAATGATGCTCATGAGATTAATAAGAGTAT 1800  
DB 1741 AGAATGCTCAAGTATGATTAATTAATTAATGATGCTCATGAGATTAATAAGAGTAT 1800  
QY 1801 CTATTCAAGTGAAGAAATATCTAACCAATAGAAATCACTCGAAGAAAGAAATGCTTCA 1860  
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QY 1861 AAAGCAAGCTGAACCTTAATAGCAGATTAACCAATATGAACTGAAATTAATATCC 1920  
DB 1861 AAAGCAAGCTGAACCTTAATAGCAGATTAACCAATATGAACTGAAATTAATATCC 1920  
QY 1921 ACAATTTCAAAAGCACTTAATAAGATAGGCTGAGAGAAAGTCTTCAACGAGCATATTC 1980  
DB 1921 ACAATTTCAAAAGCACTTAATAAGATAGGCTGAGAGAAAGTCTTCAACGAGCATATTC 1980  
QY 1981 ATGGCTTGAATCTAGTGTGATGAGAAATCTAAGCCCACTTAATGATGAGAAATGAGAA 2040  
DB 1981 ATGGCTTGAATCTAGTGTGATGAGAAATCTAAGCCCACTTAATGATGAGAAATGAGAA 2040



QY 2041 TTGATAGTTCTTCTACAGTGAAGATATAAGAAAAAGTACAAACCAATGCCAGTCA 2100  
| | | | |  
Db 2041 TTGATAGTTCTTCTACAGTGAAGATATAAGAAAAAGTACAAACCAATGCCAGTCA 2100  
QY 2101 GGCACGCGAAGAACTTACAACTCATGGAAGTAAAGAACTTGCACTGGAGCCAGAGA 2160  
| | | | |  
Db 2101 GGCACGCGAAGAACTTACAACTCATGGAAGTAAAGAACTTGCACTGGAGCCAGAGA 2160  
QY 2161 GTTACAAAGCAATGAAAGACAAAGTAAAGACATGATTACTTTCCAGAGCTGA 2220  
| | | | |  
Db 2161 GTTACAAAGCAATGAAAGACAAAGTAAAGACATGATTACTTTCCAGAGCTGA 2220  
QY 2221 AGTTAAACAATGACACCTGGTTCTTTTACTAAGTGTCAATAACCACTGAATTAAGAAT 2280  
| | | | |  
Db 2221 AGTTAAACAATGACACCTGGTTCTTTTACTAAGTGTCAATAACCACTGAATTAAGAAT 2280  
QY 2281 TTGTCAATCTTACCTTCCAGAGAAAGAAAGAAAGAACTAGAAACAATTAAAGTGT 2340  
| | | | |  
Db 2281 TTGTCAATCTTACCTTCCAGAGAAAGAAAGAAAGAACTAGAAACAATTAAAGTGT 2340  
QY 2341 CTAAATATGCTGAAGCCCCCAAGATCTGATGTTAAGTGAAGAAAGGTTTGGCAACTG 2400  
| | | | |  
Db 2341 CTAAATATGCTGAAGCCCCCAAGATCTGATGTTAAGTGAAGAAAGGTTTGGCAACTG 2400  
QY 2401 AAAAGATCTGAGAGTACAGTATTTCACTGGTACCTGTA CTGATTAAGCACTCAGG 2460  
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Db 2401 AAAAGATCTGAGAGTACAGTATTTCACTGGTACCTGTA CTGATTAAGCACTCAGG 2460  
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| | | | |  
Db 2461 AAAGATCTCTGTTACTGGAAGTTAGCACTCTAGGGAAGCAAAACAGAACCAATTAAT 2520  
QY 2521 GGTGAGTGAAGTGAAGATTTGAAGCCCAAGGACATAATCTGATGTTTCCAAAG 2580  
| | | | |  
Db 2521 GGTGAGTGAAGTGAAGATTTGAAGCCCAAGGACATAATCTGATGTTTCCAAAG 2580  
QY 2581 ATTAATGAATGACACAGAAAGCTTTAAGTATCCATGGAGATGAAGTTAAACCAAGTC 2640  
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Db 2581 ATTAATGAATGACACAGAAAGCTTTAAGTATCCATGGAGATGAAGTTAAACCAAGTC 2640  
QY 2641 GGGAAACAAAGCATAGAAATGGAAGAAAGTGAAGCTTGATCTGATTTTGCAGAAATCAT 2700  
| | | | |  
Db 2641 GGGAAACAAAGCATAGAAATGGAAGAAAGTGAAGCTTGATCTGATTTTGCAGAAATCAT 2700  
QY 2701 TCAAGGTTCAAGAGGCGCAGTATTTGCTGTTTCAATCCAGAAATGAGAGAGG 2760  
| | | | |  
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QY 2761 AATGTCGAACATTTCTGCGCACTGCGGCTCTTAAAGAAACAAAGTCCAAAGTCACTT 2820  
| | | | |  
Db 2761 AATGTCGAACATTTCTGCGCACTGCGGCTCTTAAAGAAACAAAGTCCAAAGTCACTT 2820  
QY 2821 TTGAATGTGAACAAAGAAAGAAATCAAGAAAGATGATCTAATATCAAGCTGTAC 2880  
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Db 2821 TTGAATGTGAACAAAGAAAGAAATCAAGAAAGATGATCTAATATCAAGCTGTAC 2880  
QY 2881 AACAAGTTAATATCACTGAGGCTTCCGTGTTGCTGAGAAAGTAAAGCAAGTTGATA 2940  
| | | | |  
Db 2881 AACAAGTTAATATCACTGAGGCTTCCGTGTTGCTGAGAAAGTAAAGCAAGTTGATA 2940  
QY 2941 ATGCCAAATGTAGTATCAAGAGAGGCTAGGTTTGTCTATCATCTCAGTCAAGAGCA 3000  
| | | | |  
Db 2941 ATGCCAAATGTAGTATCAAGAGAGGCTAGGTTTGTCTATCATCTCAGTCAAGAGCA 3000  
QY 3001 AGGAAACTGAGCTCATTTACTTCCAAATTAACATGAGACTTTTACAAACCAATATCGATAC 3060  
| | | | |  
Db 3001 AGGAAACTGAGCTCATTTACTTCCAAATTAACATGAGACTTTTACAAACCAATATCGATAC 3060  
QY 3061 CACCACTTTTCCATCAAGTCACTTTGTTAAACCTAAAGTAAAGAAATCTGCTAGAGG 3120  
| | | | |  
Db 3061 CACCACTTTTCCATCAAGTCACTTTGTTAAACCTAAAGTAAAGAAATCTGCTAGAGG 3120  
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Db 3121 AAAAATTTGAGAAACATTCATATGTCACTGAAAGAGAAATGGAAATGAGAACTTCCAA 3180  
| | | | |  
QY 3181 GTTACGTGAGCAATTTAGCCGTAAATTAAGTAAAGAAATGTTTAAAGAGCCAGCT 3240  
| | | | |  
Db 3181 GTTACGTGAGCAATTTAGCCGTAAATTAAGTAAAGAAATGTTTAAAGAGCCAGCT 3240  
QY 3241 CAAGCAATTAATGAGAGTTCAGACTTAAGAAAGTGGGCTCAGTATTAATGA 3300  
| | | | |  
Db 3241 CAAGCAATTAATGAGAGTTCAGACTTAAGAAAGTGGGCTCAGTATTAATGA 3300  
QY 3301 TAGGTTCCAGTATGAAACATTTCAAGCAAGAACTAGTGAAGAAAGAGGCCAAATTTGA 3360  
| | | | |  
Db 3301 TAGGTTCCAGTATGAAACATTTCAAGCAAGAACTAGTGAAGAAAGAGGCCAAATTTGA 3360  
QY 3361 ATGCTATGCTTATGATTAAGGAGTTTGGCAACCTGAGGCTATTAACAAAGTCTTCCGGA 3420  
| | | | |  
Db 3361 ATGCTATGCTTATGATTAAGGAGTTTGGCAACCTGAGGCTATTAACAAAGTCTTCCGGA 3420  
QY 3421 GTAAATTTGAGCATCCTGAAATTAAGAAAGCAAGAAATGAGAAAGTTCAGACTGTA 3480  
| | | | |  
Db 3421 GTAAATTTGAGCATCCTGAAATTAAGAAAGCAAGAAATGAGAAAGTTCAGACTGTA 3480  
QY 3481 ATACAGATTTCTCTCATATCTGATTTTCAATTAAGTGAAGAGCCATATGGAGTATGTC 3540  
| | | | |  
Db 3481 ATACAGATTTCTCTCATATCTGATTTTCAATTAAGTGAAGAGCCATATGGAGTATGTC 3540  
QY 3541 ATGATCTCAGGTTGTTCTGAGACACCTGATGACCTGTTAGATGATGTAATTAAGG 3600  
| | | | |  
Db 3541 ATGATCTCAGGTTGTTCTGAGACACCTGATGACCTGTTAGATGATGTAATTAAGG 3600  
QY 3601 AAGATCTAGTATTTGCTGAAATGACATTAAGAAAGTTCGCTGTTTACCAAAAGG 3660  
| | | | |  
Db 3601 AAGATCTAGTATTTGCTGAAATGACATTAAGAAAGTTCGCTGTTTACCAAAAGG 3660  
QY 3661 TCCAGAGAGAGAGCTTAGCAGAGTCTAGCCCTTTTCAACCATACACATTTGGCTCAGG 3720  
| | | | |  
Db 3661 TCCAGAGAGAGAGCTTAGCAGAGTCTAGCCCTTTTCAACCATACACATTTGGCTCAGG 3720  
QY 3721 GTTACCGAAGAGGGGCCAAAGAAATTAAGTCTCAGAAAGAACTTATTAAGTGAAGATG 3780  
| | | | |  
Db 3721 GTTACCGAAGAGGGGCCAAAGAAATTAAGTCTCAGAAAGAACTTATTAAGTGAAGATG 3780  
QY 3781 AAGACCTTCCCTGCTTCCAAACCTGTTATTTGTAAGTAAACAATATACCTTCAGT 3840  
| | | | |  
Db 3781 AAGACCTTCCCTGCTTCCAAACCTGTTATTTGTAAGTAAACAATATACCTTCAGT 3840  
QY 3841 CTACTAGGCATAGCACCGTTGCTACCGAGTGTCTGTCTAAGAAACAGAGAGAAATTAAT 3900  
| | | | |  
Db 3841 CTACTAGGCATAGCACCGTTGCTACCGAGTGTCTGTCTAAGAAACAGAGAGAAATTAAT 3900  
QY 3901 TATCATTTGAAGATGCTTAAATTAAGTCTGAGTAAACAGGTAATTTGGCAAGGATCTC 3960  
| | | | |  
Db 3901 TATCATTTGAAGATGCTTAAATTAAGTCTGAGTAAACAGGTAATTTGGCAAGGATCTC 3960  
QY 3961 AGGAACATCACCTTAGTAGAGAAACAAATGTTCTGAGCTGTTTCTTACAGTGA 4020  
| | | | |  
Db 3961 AGGAACATCACCTTAGTAGAGAAACAAATGTTCTGAGCTGTTTCTTACAGTGA 4020  
QY 4021 GTGAATTTGGAAGACTTGAAGTGAAGTAAATACAAACCCAGAGATCTTCTTGAATGTTCTT 4080  
| | | | |  
Db 4021 GTGAATTTGGAAGACTTGAAGTGAAGTAAATACAAACCCAGAGATCTTCTTGAATGTTCTT 4080  
QY 4081 CCAAAACAATAGGAGTACAGTCTGAAGCCAGGAGTGGTCTGAGTGAAGAAATTTGG 4140  
| | | | |  
Db 4081 CCAAAACAATAGGAGTACAGTCTGAAGCCAGGAGTGGTCTGAGTGAAGAAATTTGG 4140  
QY 4141 TTTGAGATGATGAAGAAAGAGAGAGGCTTGAAGAAATTAATCAAGAAAGCAAGCA 4200  
| | | | |  
Db 4141 TTTGAGATGATGAAGAAAGAGAGAGGCTTGAAGAAATTAATCAAGAAAGCAAGCA 4200  
QY 4201 TGGATTTAACTTAGTGAAGCAGCATCTGGGTGAGAGTGAAGCAAGCGTCTGAG 4260  
| | | | |

|    |      |   |      |
|----|------|---|------|
| Db | 4201 | TGGATTCAAACTTAGGTGAAGACGACATCTGGGTGTGAGATGAAGAAACAAAGGCTCTCTGAG | 4260 |
| Qy | 4261 | ACTGCTCAGGGCTATCTCTCAGATGACATTTTAAACCACTCAGACAGAGGATACCATGC     | 4320 |
| Db | 4261 | ACTGCTCAGGGGCTATCCTCTCAGATGACATTTTAAACCACTCAGACAGAGGATACCATGC   | 4320 |
| Qy | 4321 | AACATTAACCTGATTAAGGCTCAGACAGGAATGCGTGAACATAAGAGCTGTGTTAACAGC    | 4380 |
| Db | 4321 | AACATTAACCTGATTAAGGCTCAGACAGGAATGCGTGAACATAAGAGCTGTGTTAACAGC    | 4380 |
| Qy | 4391 | ATGGAGCAGGCTTCTAAACGCTAACGCTTCCATCATTAAGTACTCTTCGCTTGAG         | 4440 |
| Db | 4391 | ATGGAGGCGAGGCTTCTAAACGCTTCCATCATTAAGTACTCTTCGCTTGAG             | 4440 |
| Qy | 4441 | ACCTGGGAATCCAGAACAAAGACATCAGAAAAAGAGATTAACTTACAGAAAAATA         | 4500 |
| Db | 4441 | ACCTGGGAATCCAGAACAAAGACATCAGAAAAAGAGATTAACTTACAGAAAAATA         | 4500 |
| Qy | 4501 | GTGAATACCCTATTAACCCAGAAATCCAGAAAGCCTTTCTGCTGACAAAGTTGAGGTCGTG   | 4560 |
| Db | 4501 | GTGAATACCCTATTAACCCAGAAATCCAGAAAGCCTTTCTGCTGACAAAGTTGAGGTCGTG   | 4560 |
| Qy | 4561 | CAGATTAAGTCTACCACTAAAAATTAAGAACACAGAGTGGAAAGTCAATCCCTTCTAAT     | 4620 |
| Db | 4561 | CAGATTAAGTCTACCACTAAAAATTAAGAACACAGAGTGGAAAGTCAATCCCTTCTAAT     | 4620 |
| Qy | 4621 | GCCCATCATTAAGTATGATAGGTGTATCATGACAGATTGCTCTGGAGTCTTCAGAAATGAA   | 4680 |
| Db | 4621 | GCCCATCATTAAGTATGATAGGTGTATCATGACAGATTGCTCTGGAGTCTTCAGAAATGAA   | 4680 |
| Qy | 4681 | ACTAACCATTCTCAAGAGAGAGCTCATTAAGTTGTATATGTGGAGAGCACAGCTGGAG      | 4740 |
| Db | 4681 | ACTAACCATTCTCAAGAGAGAGCTCATTAAGTTGTATATGTGGAGAGCACAGCTGGAG      | 4740 |
| Qy | 4741 | AGTCTGGGSCACACGATTTGACGGAAACATCTTAACCTGSCAAAGGCAGATCTAAGGAA     | 4800 |
| Db | 4741 | AGTCTGGGSCACACGATTTGACGGAAACATCTTAACCTGSCAAAGGCAGATTTAAGGAA     | 4800 |
| Qy | 4801 | CCCCTTAACCTGGAATGTGAATCAGGCTCTTCTCTGTATGACCCTGAATCTGATCCTTCTG   | 4860 |
| Db | 4801 | CCCCTTAACCTGGAATGTGAATCAGGCTCTTCTCTGTATGACCCTGAATCTGATCCTTCTG   | 4860 |
| Qy | 4861 | AAGACAGAGCCCCAGAGTACGCTCGTGTGGCAACATCAATCTTCAACCTGTGATTA        | 4920 |
| Db | 4861 | AAGACAGAGCCCCAGAGTACGCTCGTGTGGCAACATCAATCTTCAACCTGTGATTA        | 4920 |
| Qy | 4921 | AAGTTCGCCAATTTGAAGTTGACGAATCTGCCAGGCTCAGCTGCTCATACTACTG         | 4980 |
| Db | 4921 | AAGTTCGCCAATTTGAAGTTGACGAATCTGCCAGGCTCAGCTGCTCATACTACTG         | 4980 |
| Qy | 4981 | ATACGTCTGGGTATATGCAATGGAAGAAAGTGTGACAGAGAAACCGAATTTGACG         | 5040 |
| Db | 4981 | ATACGTCTGGGTATATGCAATGGAAGAAAGTGTGACAGAGAAACCGAATTTGACG         | 5040 |
| Qy | 5041 | CTTCAACAGAAAGGTCACAACAAAGAAATGTCCATGTGTGTCTGGGCTGACCCCAAGAG     | 5100 |
| Db | 5041 | CTTCAACAGAAAGGTCACAACAAAGAAATGTCCATGTGTGTCTGGGCTGACCCCAAGAG     | 5100 |
| Qy | 5101 | AATTTATGCTCGTGTACAAAGTTGCCAGAAAAACACACATCATCTTAATCTTAATTA       | 5160 |
| Db | 5101 | AATTTATGCTCGTGTACAAAGTTGCCAGAAAAACACACATCATCTTAATCTTAATTA       | 5160 |
| Qy | 5161 | CTGAAGAGACTACTCAATGTGTATGAAAAACAGATGCTGAGTTGTGTGTGAACGGACAC     | 5220 |
| Db | 5161 | CTGAAGAGACTACTCAATGTGTATGAAAAACAGATGCTGAGTTGTGTGTGAACGGACAC     | 5220 |
| Qy | 5221 | TGAAAATATTTTCTAGGAATTCGGAGAGAAATGGATAGTTAGCTATTTCTGGGTGACC      | 5280 |
| Db | 5221 | TGAAAATATTTTCTAGGAATTCGGAGAGAAATGGATAGTTAGCTATTTCTGGGTGACC      | 5280 |
| Qy | 5281 | AGCTATATTAAGAAAGAAAAATGCTGAATGACATGATTTTGAAGTCAGAGGACATGTGG     | 5340 |
| Db | 5281 | AGCTATATTAAGAAAGAAAAATGCTGAATGACATGATTTTGAAGTCAGAGGACATGTGG     | 5340 |

|  |   |  |                            |  |  |  |
|--|---|--|----------------------------|--|--|--|
| QY   | 5341  | TCATATGAGAAGAAACCCACCAAGCTGCCAAAGGAGACAGAGATCCGACAGACGAAGAATCT   | 5400                       |  |  |  |
| Db   | 5341  | TCATATGAGAAGAAACCCACCAAGCTGCCAAAGGAGAGATCCGACAGACGAAGAATCT       | 5400                       |  |  |  |
| QY   | 5401  | TCAGAGGGGCTTGGAATCTGTGTCTATGATGGGCCCTTACCAACATGCGCCACAGATCAACTGG | 5460                       |  |  |  |
| Db   | 5401  | TCAGAGGGGCTTGGAATCTGTGTCTATGATGGGCCCTTACCAACATGCGCCACAGATCAACTGG | 5460                       |  |  |  |
| QY   | 5461  | AATGAGTGTACAGCTGTGTGTGCTTCTGTGTGTGAAGAGAGCTTTATCATTTACCCCTTG     | 5520                       |  |  |  |
| Db   | 5461  | AATGAGTGTGTACAGCTGTGTGTGCTTCTGTGTGTGAAGAGAGCTTTATCATTTACCCCTTG   | 5520                       |  |  |  |
| QY   | 5521  | GCACAGGTCACCCCAATGTGTGTGTGTCAGCCAGATGAGCTGTGACAGAGACAAATGAGCT    | 5580                       |  |  |  |
| Db   | 5521  | GCACAGGTCACCCCAATGTGTGTGTGTCAGCCAGATGAGCTGTGACAGAGACAAATGAGCT    | 5580                       |  |  |  |
| QY   | 5581  | TCCATATGCAATTTGGGACAGATGTGTGAGGACCTGTGTGTGACCCGAGAGTGGGTGTGACA   | 5640                       |  |  |  |
| Db   | 5581  | TCCATATGCAATTTGGGACAGATGTGTGAGGACCTGTGTGTGACCCGAGAGTGGGTGTGACA   | 5640                       |  |  |  |
| QY   | 5641  | GTGTAGCACTCTTACCAAGTGCACAGAGCTGTGACACACTTCTGTATACCCCAATCCCCCACA  | 5700                       |  |  |  |
| Db   | 5641  | GTGTAGCACTCTTACCAAGTGCACAGAGCTGTGACACACTTCTGTATACCCCAATCCCCCACA  | 5700                       |  |  |  |
| QY   | 5701  | GCCACTACTGA 5711   |                            |  |  |  |
| Db   | 5701  | GCCACTACTGA 5711   |                            |  |  |  |
| RESULT 2   |   |  |                            |  |  |  |
| LOCUS  | AR112808  | 5711 bp  | DNA linear PAT 16-MAY-2001 |  |  |  |
| DEFINITION   | Sequence 1 from patent US 6130322.                                |  |                            |  |  |  |
| ACCESSION  | AR112808  |  |                            |  |  |  |
| VERSION  | AR112808.1  | GI:14092708  |                            |  |  |  |
| KEYWORDS   | Unknown.  |  |                            |  |  |  |
| SOURCE   | Unknown.  |  |                            |  |  |  |
| ORGANISM   | Unclassified.   |  |                            |  |  |  |
| REFERENCE  | 1 (bases 1 to 5711)   |  |                            |  |  |  |
| AUTHORS  | Murphy,P.D., Allen,A.C.P., Alvarres,C.P., Critz,B.S., Olson,S.J., |  |                            |  |  |  |
|  | Thurber,D. and Zeng,B.  |  |                            |  |  |  |
| TITLE  | Coding sequences of the human BRCA1 gene                          |  |                            |  |  |  |
| JOURNAL  | Patent: US 6130322-A 1 10-OCT-2000;                               |  |                            |  |  |  |
| FEATURES   | Location/Qualifiers   |  |                            |  |  |  |
| source   | 1..5711   |  |                            |  |  |  |
|  | /organism="unknown"   |  |                            |  |  |  |
| BASE COUNT   | 1953 a  | 1099 c   | 1277 g 1382 t              |  |  |  |
| ORIGIN   |   |  |                            |  |  |  |
| Query Match 100.0%; Score 5711; DB 6; Length 5711;                         |   |  |                            |  |  |  |
| Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0; |   |  |                            |  |  |  |
| Matches 5711; Conservative 0; Mismatches 0; Indels 0; Gaps 0;              |   |  |                            |  |  |  |
| QY   | 1   | AGCTCGCTGAGACTCTCTCGAGACCCCGACACGAGCTGTGAGGTTTCTCAGATTAACCTGGCC  | 60                         |  |  |  |
| Db   | 1   | AGCTCGCTGAGACTCTCTCGAGACCCCGACACGAGCTGTGAGGTTTCTCAGATTAACCTGGCC  | 60                         |  |  |  |
| QY   | 61  | CTTGCGCTCAGAGAGCCTTCAACCTCTGTCTTGTGGTTAAAGTTCAATTGGAAACAGAAAGAA  | 120                        |  |  |  |
| Db   | 61  | CTTGCGCTCAGAGAGCCTTCAACCTCTGTCTTGTGGTTAAAGTTCAATTGGAAACAGAAAGAA  | 120                        |  |  |  |
| QY   | 121   | TGAGATTATCTGCTCTTGGGTTGAAGAAGTACAAAATGTCAATTAATGCTATGACAGAAA     | 180                        |  |  |  |
| Db   | 121   | TGAGATTATCTGCTCTTGGGTTGAAGAAGTACAAAATGTCAATTAATGCTATGACAGAAA     | 180                        |  |  |  |
| QY   | 181   | TCTTAGAGTGTCCCATCTGTCTGTGAGTTGATCAAGAAGCTGTCTCCACAAAGTGTACC      | 240                        |  |  |  |
| Db   | 181   | TCTTAGAGTGTCCCATCTGTGTGAGTTGATCAAGAAGCTGTCTCCACAAAGTGTACC        | 240                        |  |  |  |
| QY   | 241   | ACATATTTTGGCAATTTTGCATGCTGAAACTTTCACACGAGAGAAAGGGCTTACAGT        | 300                        |  |  |  |

Dh 241 ACAATATTTGCAAAATTTGCAAGTCGAAACCTTCTCAACCAAGAAAGGAGCCCTTCAAGT 300  
Qy 301 GTTCCTTATGTAAGATGATATATACCAAAAGAGCCTACAGAAAGTACGAGATTTAGTC 360  
Dh 301 GTTCCTTATGTAAGATGATATATACCAAAAGAGCCTACAGAAAGTACGAGATTTAGTC 360  
Qy 361 AACTTGTGAAGAGCTATTGAAATCATTTGTGCTTTTCAAGCTTGAACACAGGTTTGAAT 420  
Dh 361 AACTTGTGAAGAGCTATTGAAATCATTTGTGCTTTTCAAGCTTGAACACAGGTTTGAAT 420  
Qy 421 ATGCAACAGCTATATATTTTGGCAAAAGAAATTAATCTCTCTGAACATCTAAAGATG 480  
Dh 421 ATGCAACAGCTATATATTTTGGCAAAAGAAATTAATCTCTCTGAACATCTAAAGATG 480  
Qy 481 AAGTTCTATCATCCAAAGATGGGTACAGAAACCGTGCAAAAGACTTCTACAGAGTG 540  
Dh 481 AAGTTCTATCATCCAAAGATGGGTACAGAAACCGTGCAAAAGACTTCTACAGAGTG 540  
Qy 541 AACCCGAAATCCTTCTTGCAAGAAACAGTCTCAGTGTCCAACTCTTAACTTTGAA 600  
Dh 541 AACCCGAAATCCTTCTTGCAAGAAACAGTCTCAGTGTCCAACTCTTAACTTTGAA 600  
Qy 601 CTGTGAACTCTGAGGACAAAGCAGCGGATACACCTCAAAAGAGCTGTCTACATTG 660  
Dh 601 CTGTGAACTCTGAGGACAAAGCAGCGGATACACCTCAAAAGAGCTGTCTACATTG 660  
Qy 661 AATGGGATCTGATTTCTTGAAAGATACCGTTATATAAGGCACTTATGCAAGTGGAG 720  
Dh 661 AATGGGATCTGATTTCTTGAAAGATACCGTTATATAAGGCACTTATGCAAGTGGAG 720  
Qy 721 ATCAAGAAATTTGTAACAAATCACCCCTCAAGAAACAGGATGAAATCACTTTGATCTG 780  
Dh 721 ATCAAGAAATTTGTAACAAATCACCCCTCAAGAAACAGGATGAAATCACTTTGATCTG 780  
Qy 781 CAAAAAGGCTCTGTGTAATTTTCTGAGACGAGATGTAAACAAATCTGAACATCATCAC 840  
Dh 781 CAAAAAGGCTCTGTGTAATTTTCTGAGACGAGATGTAAACAAATCTGAACATCATCAC 840  
Qy 841 CCAAGTATATATATTTGAAACACACTGAGAGGCTGAGTGAAGGCTTCCAGAAAGT 900  
Dh 841 CCAAGTATATATATTTGAAACACACTGAGAGGCTGAGTGAAGGCTTCCAGAAAGT 900  
Qy 901 ATCAGGATGTTCTGTTTCAAACTTGATGAGGAGGATGAGCACTTCAATCTGATGCA 960  
Dh 901 ATCAGGATGTTCTGTTTCAAACTTGATGAGGAGGATGAGCACTTCAATCTGATGCA 960  
Qy 961 GCTCATTAAGCACTGAGAACAGAGTTTATCTCACTAAAGACAGAAATGATGAGAA 1020  
Dh 961 GCTCATTAAGCACTGAGAACAGAGTTTATCTCACTAAAGACAGAAATGATGAGAA 1020  
Qy 1021 AGGCTGAATTTCTGTAATAAAGCAACAGCTGGCTTACAGAGGACCAATACAGAT 1080  
Dh 1021 AGGCTGAATTTCTGTAATAAAGCAACAGCTGGCTTACAGAGGACCAATACAGAT 1080  
Qy 1081 GGGCTGGAAGTAAGAAACATGTAATGATAGCGGACCTCCAGACAGAAAAAGGTAG 1140  
Dh 1081 GGGCTGGAAGTAAGAAACATGTAATGATAGCGGACCTCCAGACAGAAAAAGGTAG 1140  
Qy 1141 ATCTGAATCTGATCCCTGCTGTGAGAGAAAAAGATGAAATGAGCAAACTGCCATGCT 1200  
Dh 1141 ATCTGAATCTGATCCCTGCTGTGAGAGAAAAAGATGAAATGAGCAAACTGCCATGCT 1200  
Qy 1201 CAGAGATCTGAGATCTGAAGATGTTCTTGATTAACATTAATAGACATTTGCA 1260  
Dh 1201 CAGAGATCTGAGATCTGAAGATGTTCTTGATTAACATTAATAGACATTTGCA 1260  
Qy 1261 AAGTTAATGATGTTTTCAGAAAGTAACTGTTAGTTCTGATGCTCAGATGATG 1320  
Dh 1261 AAGTTAATGATGTTTTCAGAAAGTAACTGTTAGTTCTGATGCTCAGATGATG 1320  
Qy 1321 GGGAGCTGAATCAAAATGCCAAAGTATGCTGATGATTTGACGTTCTTAATGAGTATG 1380  
Dh 1321 GGGAGCTGAATCAAAATGCCAAAGTATGCTGATGATTTGACGTTCTTAATGAGTATG 1380

Qy 1381 AATATTTGTTCTTCAAGAGAAATAGACTTACTGGCAGATGATCCATGAGGCTTTAA 1440  
Dh 1381 AATATTTGTTCTTCAAGAGAAATAGACTTACTGGCAGATGATCCATGAGGCTTTAA 1440  
Qy 1441 TATGTAAGTAAGTAAGTTCCTCACTCAATCATGTAAGATATATTTGAGACAAATAT 1500  
Dh 1441 TATGTAAGTAAGTAAGTTCCTCACTCAATCATGTAAGATATATTTGAGACAAATAT 1500  
Qy 1501 TTGGGAAAACTATGGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1560  
Dh 1501 TTGGGAAAACTATGGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1560  
Qy 1561 TAAATATGAGGACATTTGTTACTGAGCAAGATATATCAAGAGGCTCCCTCACAAATA 1620  
Dh 1561 TAAATATGAGGACATTTGTTACTGAGCAAGATATATCAAGAGGCTCCCTCACAAATA 1620  
Qy 1621 AATTAAGGTAAGAAAGAGACCTACATCAGGCTTCACTCTGAGAGATTTTATCAAGAA 1680  
Dh 1621 AATTAAGGTAAGAAAGAGACCTACATCAGGCTTCACTCTGAGAGATTTTATCAAGAA 1680  
Qy 1681 CAGATTTGGCAGTTCAAAAGACTCCTGAATGATATATCAAGGAACTAAACCAAGGAG 1740  
Dh 1681 CAGATTTGGCAGTTCAAAAGACTCCTGAATGATATATCAAGGAACTAAACCAAGGAG 1740  
Qy 1741 AGAATGCTCAAGTATGATATATTAATATAGTGTATGAGATATAAACCAAAAGGTATT 1800  
Dh 1741 AGAATGCTCAAGTATGATATATTAATATAGTGTATGAGATATAAACCAAAAGGTATT 1800  
Qy 1801 CTATTCAGATGAGAAAAATCTTAACCAATGAAATCACTGCAAAAGAAATCTGCTTTCA 1860  
Dh 1801 CTATTCAGATGAGAAAAATCTTAACCAATGAAATCACTGCAAAAGAAATCTGCTTTCA 1860  
Qy 1861 AAACGAAAGCTGAACCTTATAGCAGACAGTATAGAAATATGAAATCTGAAATTAATTC 1920  
Dh 1861 AAACGAAAGCTGAACCTTATAGCAGACAGTATAGAAATATGAAATCTGAAATTAATTC 1920  
Qy 1921 ACAATTTCAAAAGCACTTAAAGAAATAGCTGAGAGGAGGAGGAGGAGGAGGAGGAG 1980  
Dh 1921 ACAATTTCAAAAGCACTTAAAGAAATAGCTGAGAGGAGGAGGAGGAGGAGGAGGAG 1980  
Qy 1981 ATGCGCTTGAATAGTATGATAGTAAGATCTAAGCCCACTAATTTGATCTGATTTGCA 2040  
Dh 1981 ATGCGCTTGAATAGTATGATAGTAAGATCTAAGCCCACTAATTTGATCTGATTTGCA 2040  
Qy 2041 TTGATAGTTGTTCTAGCAGTGAAGATTAAGAAAAAGTAAACCAATGCGCAGTCA 2100  
Dh 2041 TTGATAGTTGTTCTAGCAGTGAAGATTAAGAAAAAGTAAACCAATGCGCAGTCA 2100  
Qy 2101 GGCACAGCAGAAACCTAACAATCATGGAAGTAAAGAACTGCACTGAGGCAAGAA 2160  
Dh 2101 GGCACAGCAGAAACCTAACAATCATGGAAGTAAAGAACTGCACTGAGGCAAGAA 2160  
Qy 2161 GTAACAAACCAATGAAAGACAAAGTAAAGACATGACAGTATATCTTTCCAGAGCTGA 2220  
Dh 2161 GTAACAAACCAATGAAAGACAAAGTAAAGACATGACAGTATATCTTTCCAGAGCTGA 2220  
Qy 2221 AGTTAACAATGCACTGCTTTTACTAAGTGTCAATATACAGTGAACCTTAAGAT 2280  
Dh 2221 AGTTAACAATGCACTGCTTTTACTAAGTGTCAATATACAGTGAACCTTAAGAT 2280  
Qy 2281 TTGTCATCTAGCTTCCAGAGAGAAAGAAAGAAAGAAAGAAAGTAAAGTGT 2340  
Dh 2281 TTGTCATCTAGCTTCCAGAGAGAAAGAAAGAAAGAAAGTAAAGTGT 2340  
Qy 2341 CTAATTAATGCTGAAGACCCCAAGATCTCATGTTAAGTGAAGAAAGGTTTTCAGAACTG 2400  
Dh 2341 CTAATTAATGCTGAAGACCCCAAGATCTCATGTTAAGTGAAGAAAGGTTTTCAGAACTG 2400  
Qy 2401 AAAATCTGTAGAGAGTATGAGTATTTCACTGATGATCTGATATGAGCACTGAG 2460  
Dh 2401 AAAATCTGTAGAGAGTATGAGTATTTCACTGATGATCTGATATGAGCACTGAG 2460

|     |      |  |      |
|-----|------|--|------|
| OY  | 2461 | AAAGTATCTCGTACTCTGGAAGTTAGCACTTAGGGAAGCCAAAACGAACTAAAT   | 2520 |
| Db  | 2461 | AAAGTATCTCGTACTCTGGAAGTTAGCACTTAGGGAAGGCCAAAACGAACTAAAT  | 2520 |
| OY  | 2521 | GGTGTAGTGTGTGTGAGCACTTTGAAAACCCCAAGGGAAGTAAATCAAGTGTGTC  | 2580 |
| Db  | 2521 | GTGTGTAGTGTGTGTGAGCACTTTGAAAACCCCAAGGGAAGTAAATCAAGTGTGTC | 2580 |
| OY  | 2591 | ATAATAGAAATGACACAGAAAGGCTTTAAGTATCCATTGGGACATGAAGTTAAC   | 2640 |
| Db  | 2591 | ATAATAGAAATGACACAGAAAGGCTTTAAGTATCCATTGGGACATGAAGTTAAC   | 2640 |
| OY  | 2641 | GGGAAACAAGCATAGAAATGGAAGAAAGTGAATCTGATGCTCAGTATTTGCAAT   | 2700 |
| Db  | 2641 | GGGAAACAAGCATAGAAATGGAAGAAAGTGAATCTGATGCTCAGTATTTGCAAT   | 2700 |
| OY  | 2701 | TCAGGTTTCAAGGCCGCAAGTCAATTGCTGCTGTGTTTCAAAATCCAGAAATC    | 2760 |
| Db  | 2701 | TCAGGTTTCAAGGCCGCAAGTCAATTGCTGCTGTGTTTCAAAATCCAGAAATC    | 2760 |
| OY  | 2761 | AATGTGCAACATTTCTGTGCCACTGTGGGTCTTTAAAGAACAAAGTCCAAAGT    | 2820 |
| Db  | 2761 | AATGTGCAACATTTCTGTGCCACTGTGGGTCTTTAAAGAACAAAGTCCAAAGT    | 2820 |
| OY  | 2821 | TTGAATGTGAACAAAGGAAGAAATCAAGAAAGAAATGAGTCTTAATATCAAGCT   | 2880 |
| Db  | 2821 | TTGAATGTGAACAAAGGAAGAAATCAAGAAAGAAATGAGTCTTAATATCAAGCT   | 2880 |
| OY  | 2881 | AGACAGTTAATATCACTGCGAGGCTTCTGTGGTGTGTCAGAAAGATPAAGCA     | 2940 |
| Db  | 2881 | AGACAGTTAATATCACTGCGAGGCTTCTGTGGTGTGTCAGAAAGATPAAGCA     | 2940 |
| -OY | 2941 | ATGCCAAATGTAGTATCAAGAGAGGCTCTAGGTTTGTCTATCATCTCAGTTC     | 3000 |
| Db  | 2941 | ATGCCAAATGTAGTATCAAGAGAGGCTCTAGGTTTGTCTATCATCTCAGTTC     | 3000 |
| OY  | 3001 | ACGAAACTGGACTCATTTACTCCAAATPAACATGACCTTTTAAACCAATATG     | 3060 |
| Db  | 3001 | ACGAAACTGGACTCATTTACTCCAAATPAACATGACCTTTTAAACCAATATG     | 3060 |
| OY  | 3061 | CACCACTTTTCCCATCAAGTCATTTGTGTAAACTTAATGTAAAGAAATCTG      | 3120 |
| Db  | 3061 | CACCACTTTTCCCATCAAGTCATTTGTGTAAACTTAATGTAAAGAAATCTG      | 3120 |
| OY  | 3121 | AAAACCTTGAGGAACTTCAATCTGACCTGAAAGAGAAATGGAAATGAGAAC      | 3180 |
| Db  | 3121 | AAAACCTTGAGGAACTTCAATCTGACCTGAAAGAGAAATGGAAATGAGAAC      | 3180 |
| OY  | 3181 | GTCAGTGAACCAATTAAGCCGTATPAACATTAAGAGAAATGTTTTAAAGAG      | 3240 |
| Db  | 3181 | GTCAGTGAACCAATTAAGCCGTATPAACATTAAGAGAAATGTTTTAAAGAG      | 3240 |
| OY  | 3241 | CAAGCAATTTTAAATGAAGTGTTCAGTACTAATGAAGGGGCTCCAGTATTA      | 3300 |
| Db  | 3241 | CAAGCAATTTTAAATGAAGTGTTCAGTACTAATGAAGGGGCTCCAGTATTA      | 3300 |
| OY  | 3301 | TAGGTTCCAGTATGAAACATTCAGACAGAACTAGTAGAAACAGAGGCCAAAT     | 3360 |
| Db  | 3301 | TAGGTTCCAGTATGAAACATTCAGACAGAACTAGTAGAAACAGAGGCCAAAT     | 3360 |
| OY  | 3361 | ATGCTATGCTTAGATTAGGGGTTTTGGCACTGAGGCTATTAACAAAGTCTT      | 3420 |
| Db  | 3361 | ATGCTATGCTTAGATTAGGGGTTTTGGCACTGAGGCTATTAACAAAGTCTT      | 3420 |
| OY  | 3421 | GTAATTTGTAAGCATCTCTGAAATTAAGAAAGCAAGATATGAAGAGTAGT       | 3480 |
| Db  | 3421 | GTAATTTGTAAGCATCTCTGAAATTAAGAAAGCAAGATATGAAGAGTAGT       | 3480 |
| OY  | 3481 | ATACAGATTTCTCCATATCTGATTTCAATATCTTAGAACACGCTATGGAAG      | 3540 |
| Db  | 3481 | ATACAGATTTCTCCATATCTGATTTCAATATCTTAGAACACGCTATGGAAG      | 3540 |
| -OY | 3541 | ATGCATCTCAGGTTTGTTCGAGAACCTGATGACCTGTAGATGATGTGAATTA     | 3600 |

|    |      |   |      |
|----|------|---|------|
| Db | 3541 | ATGCATCTCAGGTTTGTTGTCGACACCTGATGACCTTGTATGATGATGTAATAAAGG       | 3600 |
| Oy | 3601 | AAGATACTAGTTTGTGCTGAAAAATGACATTAAGAAAGTTTGTGTTTAAAGCAAAAGCG     | 3660 |
| Db | 3601 | AAGATACTAGTTTGTCTGAAAATGACATTAAGAAAGTTGTGCTGTTTAAAGCAAAAGCG     | 3660 |
| Oy | 3661 | TCACAGAGGAGAGCTTGGACGAGGCTCTAGCCCTTTACCCATTCACATTTGGCTCAGG      | 3720 |
| Db | 3661 | TCACAGAGGAGAGCTTGGACGAGGCTCTAGCCCTTTACCCATTCACATTTGGCTCAGG      | 3720 |
| Oy | 3721 | GTTACCGAAGAGGGGCGCAAGAAATTAGAGTCCCTCAGAAGAGAACTTACTAGTAGATG     | 3780 |
| Db | 3721 | GTTACCGAAGAGGGGCGCAAGAAATTAGAGTCCCTCAGAAGAGAACTTACTAGTAGATG     | 3780 |
| Oy | 3781 | AAGAGCTTCCCTGCTTCCACACCTGTATTGTGTAAGTAACATATACCTTCTCAGT         | 3840 |
| Db | 3781 | AAGAGCTTCCCTGCTTCCACACCTGTATTGTGTAAGTAACATATACCTTCTCAGT         | 3840 |
| Oy | 3841 | CTACTAGGCATAGCACCCGTTGCTACCGAGTGTCTGTCTTAAGACACAGAGAGAAATTTAT   | 3900 |
| Db | 3841 | CTACTAGGCATAGCACCCGTTGCTACCGAGTGTCTGTCTTAAGACACAGAGAGAAATTTAT   | 3900 |
| Oy | 3901 | TATCATTTAAGAAATGCTTAATATGATGCTGACATACCCAGTAATATTGGCAAAAGCATCTC  | 3960 |
| Db | 3901 | TATCATTTAAGAAATGCTTAATATGATGCTGACATACCCAGTAATATTGGCAAAAGCATCTC  | 3960 |
| Oy | 3961 | AGGAACATCACCTTGTAGAGAAACAAATGTCTGTAGCTTGTTTCTTACAGTGCAC         | 4020 |
| Db | 3961 | AGGAACATCACCTTGTAGAGAAACAAATGTCTGTAGCTTGTTTCTTACAGTGCAC         | 4020 |
| Oy | 4021 | GTGAATTTGGAAGACTTGACTGCAAAATACAAACACCAGAGATCTTCTTGAATGGTCTT     | 4080 |
| Db | 4021 | GTGAATTTGGAAGACTTGACTGCAAAATACAAACACCAGAGATCTTCTTGAATGGTCTT     | 4080 |
| Oy | 4081 | CCAAACAANTAGGATCAGTCTGTAACCCAGGGAGTGTGTGATGTACAGGAATTTGG        | 4140 |
| Db | 4081 | CCAAACAANTAGGATCAGTCTGTAACCCAGGGAGTGTGTGATGTACAGGAATTTGG        | 4140 |
| Oy | 4141 | TTTCAGATGATGAGAAAGAGAAAGGGCTTTGAAAGAAATATATCAGAAAGCAAAAGCA      | 4200 |
| Db | 4141 | TTTCAGATGATGAGAAAGAGAAAGGGCTTTGAAAGAAATATATCAGAAAGCAAAAGCA      | 4200 |
| Oy | 4201 | TGGATTTCAAACCTTAGTGAAGCAGCATCTGGGTGTGAGATGAAACAAAGCTCTCTGAAG    | 4260 |
| Db | 4201 | TGGATTTCAAACCTTAGTGAAGCAGCATCTGGGTGTGAGATGAAACAAAGCTCTCTGAAG    | 4260 |
| Oy | 4261 | ACTGCTCAGGGCTATCTCTCTCAGAGTGCATTTTAAACCACTCAGAGAGGGAATCAGATGC   | 4320 |
| Db | 4261 | ACTGCTCAGGGCTATCTCTCTCAGAGTGCATTTTAAACCACTCAGAGAGGGAATCAGATGC   | 4320 |
| Oy | 4321 | AACATPAACCTGATAAAGCTCCAGCAGGAAATGGCTGAACCTAGAAAGCTGTATTAGAACAGC | 4380 |
| Db | 4321 | AACATPAACCTGATAAAGCTCCAGCAGGAAATGGCTGAACCTAGAAAGCTGTATTAGAACAGC | 4380 |
| Oy | 4381 | ATGGAGCCAGGCTTCTTAACAGCTAACCTTCCATCATATAGTACTCTCTGCCCCTTGAGG    | 4440 |
| Db | 4381 | ATGGAGCCAGGCTTCTTAACAGCTAACCTTCCATCATATAGTACTCTCTGCCCCTTGAGG    | 4440 |
| Oy | 4441 | ACCTGCGAAATCCAGACAAAGGCATATAGAAAAGCAGTATTAACTTACAGAAAAGTA       | 4500 |
| Db | 4441 | ACCTGCGAAATCCAGACAAAGGCATATAGAAAAGCAGTATTAACTTACAGAAAAGTA       | 4500 |
| Oy | 4501 | GTGAATACCCTATTAAGCCAGAAATCCAGAAAGGCTTTTCGCTGACAAAGTTTAGGGTGTG   | 4560 |
| Db | 4501 | GTGAATACCCTATTAAGCCAGAAATCCAGAAAGGCTTTTCGCTGACAAAGTTTAGGGTGTG   | 4560 |
| Oy | 4561 | CAGATAGTTCTACAGATAAAATTAAGAACCAAGAGGTGGAAAGGTCAATCCCTCTTAAT     | 4620 |
| Db | 4561 | CAGATAGTTCTACAGATAAAATTAAGAACCAAGAGGTGGAAAGGTCAATCCCTCTTAAT     | 4620 |
| Oy | 4621 | GCCCATCATTAAGATATAGTGTGATCATGACAGTTGCTTGGAGTCTTCAGAAATAGAA      | 4680 |
| Db | 4621 | GCCCATCATTAAGATATAGTGTGATCATGACAGTTGCTTGGAGTCTTCAGAAATAGAA      | 4680 |

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Db      4621 GCCCATCATTAGATGATAGTGTGATGACATGACAGTTGCTCTGGAGCTTTCAGAAATAGAA 4680
Oy      4681 ACTACCATCTCAAGAGAGAGCTCATTAGGTTGTGTGAGAGAGCAACAGCTGAAG 4740
Db      4681 ACTACCATCTCAAGAGAGAGCTCATTAGGTTGTGTGAGAGAGCAACAGCTGAAG 4740
Oy      4741 AGTCTGGGCAACAGATTTGACCGAAACATCTTACTTCTCCAGAGCAAGATCTAGAGGAA 4800
Db      4741 AGTCTGGGCAACAGATTTGACCGAAACATCTTACTTCTCCAGAGCAAGATCTAGAGGAA 4800
Oy      4801 CCCCTTACTGGAATCTGGAATAGCCTCTTCTGTATGACCTGTAATCTGATCCTTCTG 4860
Db      4801 CCCCTTACTGGAATCTGGAATAGCCTCTTCTGTATGACCTGTAATCTGATCCTTCTG 4860
Oy      4861 AAGACAGAGCCCGAGAGTACGCTGCTGTGGCAACATACCATCTTCAACCTCTGATGA 4920
Db      4861 AAGACAGAGCCCGAGAGTACGCTGCTGTGGCAACATACCATCTTCAACCTCTGATGA 4920
Oy      4921 AAGTCCCAATTGAAAGTTGACGAATCTGCCCCAGGGCTCCAGCTGCTCATACTACTG 4980
Db      4921 AAGTCCCAATTGAAAGTTGACGAATCTGCCCCAGGGCTCCAGCTGCTCATACTACTG 4980
Oy      4981 ATRCTGCTGGTATATGCAATGGAAGAAAGTGTGACGAGGAGAAAGCAATTTGACG 5040
Db      4981 ATRCTGCTGGTATATGCAATGGAAGAAAGTGTGACGAGGAGAAAGCAATTTGACG 5040
Oy      5041 CTTCACAGAAAGGCTCAACAAAGATGTCATGCTGTGCTGCTGACCCCAAG 5100
Db      5041 CTTCACAGAAAGGCTCAACAAAGATGTCATGCTGTGCTGCTGACCCCAAG 5100
Oy      5101 AATTATGCTGTGTCAGAGTTTGCAGAAACACCAACATCACTTTAACTAACTAAATTA 5160
Db      5101 AATTATGCTGTGTCAGAGTTTGCAGAAACACCAACATCACTTTAACTAACTAAATTA 5160
Oy      5161 CTGAAGAGACTACTCTGTTGTTATGAAACAGATCTGATGTTGTGTGTAACGAGAC 5220
Db      5161 CTGAAGAGACTACTCTGTTGTTATGAAACAGATCTGATGTTGTGTGTAACGAGAC 5220
Oy      5221 TGAATATTTTCTAGGAATTTGGGGAGGAAATGGGTAGTTAGCTATTTCTGGGTGACCC 5280
Db      5221 TGAATATTTTCTAGGAATTTGGGGAGGAAATGGGTAGTTAGCTATTTCTGGGTGACCC 5280
Oy      5281 AGCTATTTAAAGAAAGAAATATGCTGATAGCATGATTTTGAAGTCAGAGAGATGTGG 5340
Db      5281 AGCTATTTAAAGAAAGAAATATGCTGATAGCATGATTTTGAAGTCAGAGAGATGTGG 5340
Oy      5341 TCAATGGAAGAAACCAACAGGTCACAAAGCGAGCAAGAGATCCCGAGACAGAAAGATCT 5400
Db      5341 TCAATGGAAGAAACCAACAGGTCACAAAGCGAGCAAGAGATCCCGAGACAGAAAGATCT 5400
Oy      5401 TCAGGGGGCTAGAAATCTGTGCTATGGGCCCTTCAACAAATGCCCAAGATCAACTGG 5460
Db      5401 TCAGGGGGCTAGAAATCTGTGCTATGGGCCCTTCAACAAATGCCCAAGATCAACTGG 5460
Oy      5461 AATGATGATGACGCTGTGTGCTTCTGTGTGTAAGAGCTTTTCAATTCACCTTGG 5520
Db      5461 AATGATGATGACGCTGTGTGCTTCTGTGTGTAAGAGCTTTTCAATTCACCTTGG 5520
Oy      5521 GCACAGAGTCTCAACCAATTTGTTGTGTGACGACAGATCTGAGACAGAGCAATGGCT 5580
Db      5521 GCACAGAGTCTCAACCAATTTGTTGTGTGACGACAGATCTGAGACAGAGCAATGGCT 5580
Oy      5581 TCACATGATTTGGGAGATGTGTGAGAGCACTGTGTGACCCGAGAGTGGGTGGAGCA 5640
Db      5581 TCACATGATTTGGGAGATGTGTGAGAGCACTGTGTGACCCGAGAGTGGGTGGAGCA 5640
Oy      5641 GTGTAGACTCTACAGTGTGCAAGAGCTGACACCTACTGATACCCCAAGATCCCCACA 5700
Db      5641 GTGTAGACTCTACAGTGTGCAAGAGCTGACACCTACTGATACCCCAAGATCCCCACA 5700
Oy      5701 GGCACACTGCA 5711
Db      5701 GGCACACTGCA 5711

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RESULT 3
LOCUS 159546 5711 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 1 from patent US 5654155.
ACCESSION 159546
VERSION 159546.1 GI:2478178
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 5711)
AUTHORS Murphy, P.D., Allen, A.C., Alvarez, C.P., Critz, B.S., Olson, S.J.,
Scheller, D.B. and Zeng, B.
TITLE Consensus sequence of the human BRCA1 gene
JOURNAL Patent: US 5654155-A 1 05-AUG-1997;
FEATURES
source location/Qualifiers
BASE COUNT 1953 a 1099 c 1277 g 1382 t
ORIGIN
Query Match 100.0%; Score 5711; DB 6; Length 5711;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5711; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy      1 AGCTGCTGAGACTTCTCTGAGACCCCGACAGAGCTGTGGGTTTCTCAGATTAAGTGGCC 60
Db      1 AGCTGCTGAGACTTCTCTGAGACCCCGACAGAGCTGTGGGTTTCTCAGATTAAGTGGCC 60
Oy      61 CTGCGCTCAGAGAGGCTTTCACCTCTGCTGCTGAGTAAAGTTCAATGGAAGAGAGAA 120
Db      61 CTGCGCTCAGAGAGGCTTTCACCTCTGCTGCTGAGTAAAGTTCAATGGAAGAGAGAA 120
Oy      121 TGGATTTATCTGCTCTTGGCGTTGGAAGAGTACAAATGTCAATTAATGCTATGAGAGAAA 180
Db      121 TGGATTTATCTGCTCTTGGCGTTGGAAGAGTACAAATGTCAATTAATGCTATGAGAGAAA 180
Oy      121 TGGATTTATCTGCTCTTGGCGTTGGAAGAGTACAAATGTCAATTAATGCTATGAGAGAAA 180
Db      121 TGGATTTATCTGCTCTTGGCGTTGGAAGAGTACAAATGTCAATTAATGCTATGAGAGAAA 180
Oy      181 TCTTGAAGTGTCCATCTGTCTGAGTGTATGAGAAAGTCTGCTCCCAAGAGTGTGACC 240
Db      181 TCTTGAAGTGTCCATCTGTCTGAGTGTATGAGAAAGTCTGCTCCCAAGAGTGTGACC 240
Oy      181 TCTTGAAGTGTCCATCTGTCTGAGTGTATGAGAAAGTCTGCTCCCAAGAGTGTGACC 240
Db      181 TCTTGAAGTGTCCATCTGTCTGAGTGTATGAGAAAGTCTGCTCCCAAGAGTGTGACC 240
Oy      241 ACATATTTTGAAGATTTTGAAGTGTGAGAACTTCTCAACAGAGAGAGGCTTCAAGT 300
Db      241 ACATATTTTGAAGATTTTGAAGTGTGAGAACTTCTCAACAGAGAGAGGCTTCAAGT 300
Oy      241 ACATATTTTGAAGATTTTGAAGTGTGAGAACTTCTCAACAGAGAGAGGCTTCAAGT 300
Db      241 ACATATTTTGAAGATTTTGAAGTGTGAGAACTTCTCAACAGAGAGAGGCTTCAAGT 300
Oy      301 GTCTTTATGTAAGATGATATTAACCAAAAGAGCTTCAAGAAAGTACGAGATTTAGTC 360
Db      301 GTCTTTATGTAAGATGATATTAACCAAAAGAGCTTCAAGAAAGTACGAGATTTAGTC 360
Oy      361 AACTTTGGAAGAGCTATTTGAAGATCAATTTGTGCTTTTCACTTGAACACAGTTGGAGT 420
Db      361 AACTTTGGAAGAGCTATTTGAAGATCAATTTGTGCTTTTCACTTGAACACAGTTGGAGT 420
Oy      421 ATGCAACAGAGCTATATTTTGAAGAAAGAGAAATTAATCTCTCTGAACATCTTAAAGATG 480
Db      421 ATGCAACAGAGCTATATTTTGAAGAAAGAGAAATTAATCTCTCTGAACATCTTAAAGATG 480
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KEYWORDS  
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ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 5711)  
AUTHORS Murphy, P.D., Allen, A.C., Alvares, C.P., Critz, B.S., Olson, S.J.,  
Scheller, D.B. and Zeng, B.  
TITLE Coding sequences of the human BRCA1 gene  
JOURNAL Patent: US 5750400-A 5 12-MAY-1998;  
FEATURES Location/Qualifiers  
source 1..5711  
BASE COUNT 1953 a 1098 c 1277 g 1383 t  
ORIGIN

Query Match 100.0%; Score 5709.4; DB 6; Length 5711;  
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VERSION AR112809.1 GI:14092709  
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ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 5711)  
AUTHORS Murphy,P.D., Allen,A.C.P., Alvares,C.P., Critez,B.S., Olson,S.J.,  
Thurber,D. and Zeng,B.  
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JOURNAL Patent: US 6130322-A 3 10-OCT-2000;  
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LOCUS AR007334  
DEFINITION Sequence 3 from patent US 5750400.  
ACCESSION AR007334  
VERSION AR007334.1 GI:3966818  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.



## Unclassified.

1 (bases 1 to 5711)

AUTHORS Murphy, P.D., Allen, A.C., Alvares, C.P., Citz, B.S., Olson, S.J.,

Scheller, D.B. and Zeng, B.

TITLE Coding sequences of the human BRCA1 gene

JOURNAL Patent: US 5750400-A 3 12-MAY-1998;

FEATURES Location/Qualifiers

Source

1..5711

/organism="unknown"

BASE COUNT 1956 a 1098 c 1274 g 1383 t

ORIGIN

Query Match 99.8%; Score 5701.4; DB 6; Length 5711;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 5705; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Qy 3061 CACCACTTTTCCCATCAAGTCAATTTGTTAAATCTAATGTGAAGAAAACTGCTGAGG 3120  
Db 3061 CACCACTTTTCCCATCAAGTCAATTTGTTAAATCTAATGTGAAGAAAACTGCTGAGG 3120  
Qy 3121 AAAACTTTGAGAAACATTCATGATGCTGGAAGAGAAATGGAAATGAGAACATTCGA 3180  
Db 3121 AAAACTTTGAGAAACATTCATGATGCTGGAAGAGAAATGGAAATGAGAACATTCGA 3180  
Qy 3181 GTACAGTGAAGCAATTAAGCCGTAATTAAGTGAAGAAATGTTTAAAGAGCCAGCT 3240  
Db 3181 GTACAGTGAAGCAATTAAGCCGTAATTAAGTGAAGAAATGTTTAAAGAGCCAGCT 3240  
Qy 3241 CAAGCAATATTAATGAAGTGAAGTTCAGTACTAATGAAGTGGCTCAGATTAATGA 3300  
Db 3241 CAAGCAATATTAATGAAGTGAAGTTCAGTACTAATGAAGTGGCTCAGATTAATGA 3300  
Qy 3301 TAGGTTCCAGTGAAGTGAAGTTCAGTACTAATGAAGTGGCTCAGATTAATGA 3360  
Db 3301 TAGGTTCCAGTGAAGTGAAGTTCAGTACTAATGAAGTGGCTCAGATTAATGA 3360  
Qy 3361 ATGCTATGCTTGAAGTGAAGTTCAGTACTAATGAAGTGGCTCAGATTAATGA 3420  
Db 3361 ATGCTATGCTTGAAGTGAAGTTCAGTACTAATGAAGTGGCTCAGATTAATGA 3420  
Qy 3421 GTATATGTAAGCATCTGTAATTAAGAAAGCAAGATGAAGTGAAGTGAAGTGAAGT 3480  
Db 3421 GTATATGTAAGCATCTGTAATTAAGAAAGCAAGATGAAGTGAAGTGAAGTGAAGT 3480  
Qy 3481 ATACAGATTTCTCTCATATCTGATTTCAATTAAGTGAAGTGAAGTGAAGTGAAGT 3540  
Db 3481 ATACAGATTTCTCTCATATCTGATTTCAATTAAGTGAAGTGAAGTGAAGTGAAGT 3540  
Qy 3541 ATGATCTGAGTGTGCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 3600  
Db 3541 ATGATCTGAGTGTGCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 3600  
Qy 3601 AAGATCTGAGTGTGCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 3660  
Db 3601 AAGATCTGAGTGTGCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 3660  
Qy 3661 TCCAGAGAGAGAGCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 3720  
Db 3661 TCCAGAGAGAGAGCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 3720  
Qy 3721 GTTACGAGAGAGAGAGCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 3780  
Db 3721 GTTACGAGAGAGAGAGCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 3780  
Qy 3781 AAGAGCTTCCGCTGCTGCAACCTGTTATTTGGTAAAGTAAACATATACCTTCAGT 3840  
Db 3781 AAGAGCTTCCGCTGCTGCAACCTGTTATTTGGTAAAGTAAACATATATACCTTCAGT 3840  
Qy 3841 CTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 3900  
Db 3841 CTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 3900  
Qy 3901 TATCATGGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 3960  
Db 3901 TATCATGGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 3960  
Qy 3961 AGGAAACATCACTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 4020  
Db 3961 AGGAAACATCACTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 4020  
Qy 4021 GTGAATGGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 4080  
Db 4021 GTGAATGGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 4080  
Qy 4081 CCAACCAATGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 4140  
Db 4081 CCAACCAATGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 4140



QY 181 TCTTAGAGTGTCCCATCTGTCTGAGATTGATCAAGAAACCTGTCTCCACAAAGTGTGACC 240  
Db 181 TCTTAGAGTGTCCCATCTGTCTGAGATTGATCAAGAAACCTGTCTCCACAAAGTGTGACC 240  
QY 241 ACAATTTTSCAAATTTTSGATGCTGAACCTTCTCAACCAAGAAAGGGCCCTTCAAGT 300  
Db 241 ACAATTTTSCAAATTTTSGATGCTGAACCTTCTCAACCAAGAAAGGGCCCTTCAAGT 300  
QY 301 GTCCCTTATGTAAGATATATTAACCAAAAGAGCCCTACAAAGAAAGTATTAAGT 360  
Db 301 GTCCCTTATGTAAGATATTAACCAAAAGAGCCCTACAAAGAAAGTATTAAGT 360  
QY 361 AACTTGTGAAGCTATTTGAAAATCATTTGTCTTTTACGTTGACACAGGTTTGGAGT 420  
Db 361 AACTTGTGAAGCTATTTGAAAATCATTTGTCTTTTACGTTGACACAGGTTTGGAGT 420  
QY 421 ATGCAAAACAGCTATTAATTTTGCAAAAAGAAAATACTCTCTGAACATCTAAAAGATG 480  
Db 421 ATGCAAAACAGCTATTAATTTTGCAAAAAGAAAATACTCTCTGAACATCTAAAAGATG 480  
QY 481 AAGTTTCTATCATCAAAAGATGGGCTACAGAAACCGTCCAAAAGACTTCAAGAGT 540  
Db 481 AAGTTTCTATCATCAAAAGATGGGCTACAGAAACCGTCCAAAAGACTTCAAGAGT 540  
QY 541 AACCCGAAAATCCTTCCCTGACAGAAAACAGTCTCAGTGTCAACTCTCTAACCTTGAA 600  
Db 541 AACCCGAAAATCCTTCCCTGACAGAAAACAGTCTCAGTGTCAACTCTCTAACCTTGAA 600  
QY 601 CTGTGAAACTCTGAGAGCAACAGCGGATTAACAACCTCAAAAGAGTCTGTCTTACATG 660  
Db 601 CTGTGAAACTCTGAGAGCAACAGCGGATTAACAACCTCAAAAGAGTCTGTCTTACATG 660  
QY 661 AATTGGATGTGAATCTTCTGAAGATACCGTTAATAAGGCACTTATTCAGTGTGGAG 720  
Db 661 AATTGGATGTGAATCTTCTGAAGATACCGTTAATAAGGCACTTATTCAGTGTGGAG 720  
QY 721 ATCAAGAAATTTGTTCAAAATCAACCCCTCAAGAAACAGGATGAATCAAGTTGGATTCTG 780  
Db 721 ATCAAGAAATTTGTTCAAAATCAACCCCTCAAGAAACAGGATGAATCAAGTTGGATTCTG 780  
QY 781 CAAAAAAGGCTGCTGTGGAATTTTCTGAGACGATGTAACTGAACATCATCAAC 840  
Db 781 CAAAAAAGGCTGCTGTGGAATTTTCTGAGACGATGTAACTGAACATCATCAAC 840  
QY 841 CCAGTATATATGATTTGAACCACTGAGAAAGGCTGAGTGAAGGCAATCCAGAAAGT 900  
Db 841 CCAGTATATATGATTTGAACCACTGAGAAAGGCTGAGTGAAGGCAATCCAGAAAGT 900  
QY 901 ATCAGGGATGTTCTGTTTCAAACTTGATGTGAGGCAATGTGCAAAATCTCATGCCA 960  
Db 901 ATCAGGGATGTTCTGTTTCAAACTTGATGTGAGGCAATGTGCAAAATCTCATGCCA 960  
QY 961 GCTCATTAACGATGAGAACAGAGTTTATTACTCACTAAAGACAGATGAATGTAGAA 1020  
Db 961 GCTCATTAACGATGAGAACAGAGTTTATTACTCACTAAAGACAGATGAATGTAGAA 1020  
QY 1021 AGGCTGAATTTCTGTAATTAAGCAACAGGCTGGCTTAGCAAGAGCAATTAAGAT 1080  
Db 1021 AGGCTGAATTTCTGTAATTAAGCAACAGGCTGGCTTAGCAAGAGCAATTAAGAT 1080  
QY 1081 GGGCTGGAAGTAAAGAAACATGTATGATAGCGGACTCCAGACACAGAAAAGGTAG 1140  
Db 1081 GGGCTGGAAGTAAAGAAACATGTATGATAGCGGACTCCAGACACAGAAAAGGTAG 1140  
QY 1141 ATCTGAATGCTATCCCTGTGTGAGAGAAAGATGAATTAAGCAAACTGCCATGCT 1200  
Db 1141 ATCTGAATGCTATCCCTGTGTGAGAGAAAGATGAATTAAGCAAACTGCCATGCT 1200  
QY 1201 CAGAGATCTTAGAGTACTGAAGATGTTCTTGAATTAACATTAAGAGATTCAGA 1260  
Db 1201 CAGAGATCTTAGAGTACTGAAGATGTTCTTGAATTAACATTAAGAGATTCAGA 1260  
QY 1261 AAGTTAATGATGTTTCCAGAAAGTATGAATCTGTAGGTTCTGATGACTCATGATG 1320

Db 1261 AAGTTAATGATGTTTCCAGAAAGTATGAATCTGTAGGTTCTGATGACTCATGATG 1320  
QY 1321 GGGAGCTGAATCAAAATGCGCAAGTATGATGATTTGAACGTTCAAAATGAGTATG 1380  
Db 1321 GGGAGCTGAATCAAAATGCGCAAGTATGATGATTTGAACGTTCAAAATGAGTATG 1380  
QY 1381 AATATCTGGTCTTCTAGAGAAATAGACTTCTGAGAGTATCTCTAGAGCTTTAA 1440  
Db 1381 AATATCTGGTCTTCTAGAGAAATAGACTTCTGAGAGTATCTCTAGAGCTTTAA 1440  
QY 1441 TATGTAAAGTAAAGATTTCACTCCAAATCAGTATGAGATATATTAAGACAAATAT 1500  
Db 1441 TATGTAAAGTAAAGATTTCACTCCAAATCAGTATGAGATATATTAAGACAAATAT 1500  
QY 1501 TTGGGAAAACCTATGGAAGAAAGGCAAGGCTCCCACTTAAGCCATGTAATGAAATC 1560  
Db 1501 TTGGGAAAACCTATGGAAGAAAGGCAAGGCTCCCACTTAAGCCATGTAATGAAATC 1560  
QY 1561 TAATTATAGAGCATTTGTTACTGAGCCACAGATATATACAGAGGCTCCCTCACAATTA 1620  
Db 1561 TAATTATAGAGCATTTGTTACTGAGCCACAGATATATACAGAGGCTCCCTCACAATTA 1620  
QY 1621 AATTAAGGCTAAAGAGACCTATACAGGCTTCAATCTGAGATTTTATCAAGAAAG 1680  
Db 1621 AATTAAGGCTAAAGAGACCTATACAGGCTTCAATCTGAGATTTTATCAAGAAAG 1680  
QY 1681 CAGATTTGGCAGTTCAAAAGACTCTCTGAATATATATGAGGAACTAAACAAACGGAGC 1740  
Db 1681 CAGATTTGGCAGTTCAAAAGACTCTCTGAATATATATGAGGAACTAAACAAACGGAGC 1740  
QY 1741 AGAATGCTCAATGATGATTAATTAATGATGATGATGATGATGATGATGATGATGAT 1800  
Db 1741 AGAATGCTCAATGATGATTAATTAATGATGATGATGATGATGATGATGATGATGAT 1800  
QY 1801 CTATTCAGATGAGAAAATCTTAACCAATGAATCACTGCAAAAAGAAATCTGCTTTCA 1860  
Db 1801 CTATTCAGATGAGAAAATCTTAACCAATGAATCACTGCAAAAAGAAATCTGCTTTCA 1860  
QY 1861 AAAAGAAAGTAACTATTAACAGCAGTATTAAGCAATGGAATCTCGAATTAATATCC 1920  
Db 1861 AAAAGAAAGTAACTATTAACAGCAGTATTAAGCAATGGAATCTCGAATTAATATCC 1920  
QY 1921 ACAATTCAAAACCTTAATAAAGATGAGTGAAGGAGGAGTCTTCAAGGCAATATTC 1980  
Db 1921 ACAATTCAAAACCTTAATAAAGATGAGTGAAGGAGGAGTCTTCAAGGCAATATTC 1980  
QY 1981 ATGCGCTTGAATCTAGTATGATGATGATGATGATGATGATGATGATGATGATGAT 2040  
Db 1981 ATGCGCTTGAATCTAGTATGATGATGATGATGATGATGATGATGATGATGATGAT 2040  
QY 2041 TTGATATGTTGTTCTGACAGTGAAGATTAAGAAAAAGTAAACCAATGCCAGTCA 2100  
Db 2041 TTGATATGTTGTTCTGACAGTGAAGATTAAGAAAAAGTAAACCAATGCCAGTCA 2100  
QY 2101 GGCACAGCAGAAACCTAACAATCATGGAAGTAAAGAACTCTCACTGAGGCCAAGAA 2160  
Db 2101 GGCACAGCAGAAACCTAACAATCATGGAAGTAAAGAACTCTCACTGAGGCCAAGAA 2160  
QY 2161 GTTAACAGCAAAATGAACAGACAACTAAAGACATGACAGTATCTTTCCAGAGCTGA 2220  
Db 2161 GTTAACAGCAAAATGAACAGACAACTAAAGACATGACAGTATCTTTCCAGAGCTGA 2220  
QY 2221 AGTTAAACAATGCACTGCTGTTTCTTATCAATGTTCAATCAAGTAAAGAT 2280  
Db 2221 AGTTAAACAATGCACTGCTGTTTCTTATCAATGTTCAATCAAGTAAAGAT 2280  
QY 2281 TTGTCATCTGAGCTTCCAGAGAGAAAGAAAGAGAAATATAGAAACAGTTAAAGT 2340  
Db 2281 TTGTCATCTGAGCTTCCAGAGAGAAAGAAAGAGAAATATAGAAACAGTTAAAGT 2340  
QY 2341 CTAAATATGCTGAGAACCCCAAGATCTCATGTTAAGTGAAGAAAGGTTTTCAGAACTG 2400

|   |      |   |      |
|---|------|---|------|
| D | 2341 | CTAATATGCTGAAGACCCCAAAAGATCTCATGTTAACTGAGAAAGGGTTTGCAAACTG    | 2400 |
| Q | 2401 | AAAGATCTGTAGAAGTAGCAGTAATTTCACTGGTACCTGGTACTGATTAATGCACTCAGG  | 2460 |
| D | 2401 | AAAGATCTGTAGAAGTAGCAGTAATTTCACTGGTACCTGGTACTGATTAATGCACTCAGG  | 2460 |
| Q | 2461 | AAAGTATCTGCTTAACCTGGAAGTTAGCACTCTAGGGAAAGCAAAACGAACCAATTAAT   | 2520 |
| D | 2461 | AAAGTATCTGCTTAACCTGGAAGTTAGCACTCTAGGGAAAGCAAAACGAACCAATTAAT   | 2520 |
| Q | 2521 | GTGTGAGTCAGTGTGCAAGCTTTTGAAAACCCCAAGGGACTAATTCATGGTTGTTCCAAG  | 2580 |
| D | 2521 | GTGTGAGTCAGTGTGCAAGCTTTTGAAAACCCCAAGGGACTAATTCATGGTTGTTCCAAG  | 2580 |
| Q | 2581 | ATTAATGAAATATGACACGAAGGCTTTAAGTATCCATTGGGACATGAAGTTAACCACTC   | 2640 |
| D | 2581 | ATTAATGAAATATGACACGAAGGCTTTAAGTATCCATTGGGACATGAAGTTAACCACTC   | 2640 |
| Q | 2641 | GGGAAACAAGCATAGAAATGGAAGAAAGTGAATCTTAGTGCAGTATTTTGCAAAATCAT   | 2700 |
| D | 2641 | GGGAAACAAGCATAGAAATGGAAGAAAGTGAATCTTAGTGCAGTATTTTGCAAAATCAT   | 2700 |
| Q | 2701 | TCGAAGTTTCAAAAGCCGCACTATTTGCTCTGTTTCAATTCAGAAATGCAAGAAGG      | 2760 |
| D | 2701 | TCGAAGTTTCAAAAGCCGCACTATTTGCTCTGTTTCAATTCAGAAATGCAAGAAGG      | 2760 |
| Q | 2761 | AATGTGCAACATTTCTGCGCCACTCTGGGTCCTTAAGAAACAAAGTCCAAATCCTT      | 2820 |
| D | 2761 | AATGTGCAACATTTCTGCGCCACTCTGGGTCCTTAAGAAACAAAGTCCAAATCCTT      | 2820 |
| Q | 2821 | TTGAATGTGACAAAGGAAGAAATCAGGAAGAAATGAGTCTTAATATCAGGCTGTAC      | 2880 |
| D | 2821 | TTGAATGTGACAAAGGAAGAAATCAGGAAGAAATGAGTCTTAATATCAGGCTGTAC      | 2880 |
| Q | 2881 | AAGCACTTAATATCATCTGCAAGGCTTTCTGTGTTGGTCAGAAAGATTAAGCACTGATA   | 2940 |
| D | 2881 | AAGCACTTAATATCATCTGCAAGGCTTTCTGTGTTGGTCAGAAAGATTAAGCACTGATA   | 2940 |
| Q | 2941 | ATGCCAAATGTAGTATCAGGAAGAGGCTCTAGGTTTGTCTATCATCTCAGTTCAGAGCA   | 3000 |
| D | 2941 | ATGCCAAATGTAGTATCAGGAAGAGGCTCTAGGTTTGTCTATCATCTCAGTTCAGAGCA   | 3000 |
| Q | 3001 | ACGAACCTGGACATCTATTTCTCCAAATTAACATGAGCTTTTACAAACCCATATGCTATAC | 3060 |
| D | 3001 | ACGAACCTGGACATCTATTTCTCCAAATTAACATGAGCTTTTACAAACCCATATGCTATAC | 3060 |
| Q | 3061 | CACCACTTTTCCCATCAAGTCAATTTGTAAACTTAATGTAAAGAAATTCGCTTAGAGG    | 3120 |
| D | 3061 | CACCACTTTTCCCATCAAGTCAATTTGTAAACTTAATGTAAAGAAATTCGCTTAGAGG    | 3120 |
| Q | 3121 | AAAACTTTGAGAACATTCATATGTCACCTGAAAGAGAAATGGAATGAGAACATTTCCA    | 3180 |
| D | 3121 | AAAACTTTGAGAACATTCATATGTCACCTGAAAGAGAAATGGAATGAGAACATTTCCA    | 3180 |
| Q | 3181 | GTACACTGAGCAACAATTAAGCCGTAAATACATTAAGAGAAATGTTTTAAAGAGCCAGCT  | 3240 |
| D | 3181 | GTACACTGAGCAACAATTAAGCCGTAAATACATTAAGAGAAATGTTTTAAAGAGCCAGCT  | 3240 |
| Q | 3241 | CAAGCAATATTAATGAAGTAGTGTCCAGTACTAATGAAGTGGGCTCCAGTATTAATGAAA  | 3300 |
| D | 3241 | CAAGCAATATTAATGAAGTAGTGTCCAGTACTAATGAAGTGGGCTCCAGTATTAATGAAA  | 3300 |
| Q | 3301 | TAGGTTCCAGTGTGAAAACATTCACAGCAAGCTAGGTAGAAACAGAGGCCAAAAATTTGA  | 3360 |
| D | 3301 | TAGGTTCCAGTGTGAAAACATTCACAGCAAGCTAGGTAGAAACAGAGGCCAAAAATTTGA  | 3360 |
| Q | 3361 | ATGCTATGCTTAATTAAGGAGTTTTCGAACCTGAGGCTCTAATACAAAGTCTTCTGGA    | 3420 |
| D | 3361 | ATGCTATGCTTAATTAAGGAGTTTTCGAACCTGAGGCTCTAATACAAAGTCTTCTGGA    | 3420 |
| Q | 3421 | GTATTTGTAGCAATCTGTAATTAAGAAAGCAAGATTAAGAAAGTAGTTCAGACTGTTA    | 3480 |
| D | 3421 | GTATTTGTAGCAATCTGTAATTAAGAAAGCAAGATTAAGAAAGTAGTTCAGACTGTTA    | 3480 |

|    |      |  |      |
|----|------|--|------|
| OY | 3461 | ATACAGATTTTCTTCCATATCTGATTTCACTTAAGAACACCCCTATGGGAATGTC          | 3540 |
| Db | 3481 | ATACAGATTTTCTTCCATATCTGATTTCACTTAAGAACACCCCTATGGGAATGTC          | 3540 |
| OY | 3541 | ATGACATCTCAGGTTTGTCTGAGACACCTGTATGACCTGTATGATATGTCATAATTAAG      | 3600 |
| Db | 3541 | ATGACATCTCAGGTTTGTCTGAGACACCTGTATGACCTGTATGATATGTCATAATTAAG      | 3600 |
| OY | 3601 | AAGATCTAGTTTGTCTGAAAAATGACATTAAGAAAGTTCTGCTGTTTTAGCAAAACCG       | 3660 |
| Db | 3601 | AAGATCTAGTTTGTCTGAAAAATGACATTAAGAAAGTTCTGCTGTTTTAGCAAAACCG       | 3660 |
| OY | 3661 | TCCAGAGGAGAGAGCTTATGACAGAGTCCCTAGCCCTTTCACCCATACATTTGGCTCAGG     | 3720 |
| Db | 3661 | TCCAGAGAGAGAGCTTATGACAGAGTCCCTAGCCCTTTCACCCATACATTTGGCTCAGG      | 3720 |
| OY | 3721 | GTTACCGAAGAGGGGCCAAGAAATTAGAGTCTCAGAAAGAGAACTTATCTAGTGAAGTC      | 3780 |
| Db | 3721 | GTTACCGAAGAGGGGCCAAGAAATTAGAGTCTCAGAAAGAGAACTTATCTAGTGAAGTC      | 3780 |
| OY | 3781 | AAGAGCTTCCCTGCTTCCAACTTGTATTTGGTAAAGTAAACAATATACCTTCTAGT         | 3840 |
| Db | 3781 | AAGAGCTTCCCTGCTTCCAACTTGTATTTGGTAAAGTAAACAATATACCTTCTAGT         | 3840 |
| OY | 3841 | CTACTAGGATAGACCGTGTCTACACAGTGTCTGTCTAAGAACACAGAGAGAAATTTAT       | 3900 |
| Db | 3841 | CTACTAGGATAGACCGTGTCTACACAGTGTCTGTCTAAGAACACAGAGAGAAATTTAT       | 3900 |
| OY | 3901 | TATCATTTAGAGATATGCTTAAATATGATCTGACGTAAACAAGTATATTTGGCAAAAGCATCTC | 3960 |
| Db | 3901 | TATCATTTAGAGATATGCTTAAATATGATCTGACGTAAACAAGTATATTTGGCAAAAGCATCTC | 3960 |
| OY | 3961 | AGGAACATACACTTATAGTGGAGGAAACAAATGTTGTGATGTTTCTTCAAGTGCA          | 4020 |
| Db | 3961 | AGGAACATACACTTATAGTGGAGGAAACAAATGTTGTGATGTTTCTTCAAGTGCA          | 4020 |
| OY | 4021 | GTGAATTGGAAGACTTGACTTGCAAATACAAACACCCAGAGTCTTTCTTGAATGGTCTT      | 4080 |
| Db | 4021 | GTGAATTGGAAGACTTGACTTGCAAATACAAACACCCAGAGTCTTTCTTGAATGGTCTT      | 4080 |
| OY | 4081 | CCAAACCAATAGAGCATACGTCCTGAAAGCCAGGGAGTTGCTCTGAGTACACAAGAAATTTG   | 4140 |
| Db | 4081 | CCAAACCAATAGAGCATACGTCCTGAAAGCCAGGGAGTTGCTCTGAGTACACAAGAAATTTG   | 4140 |
| OY | 4141 | TTTCAGATGATGAAAGAAAGAGGAAACGGGCTTTGGAAGAAATATCAAGAGAGCAAAACA     | 4200 |
| Db | 4141 | TTTCAGATGATGAAAGAAAGAGGAAACGGGCTTTGGAAGAAATATCAAGAGAGCAAAACA     | 4200 |
| OY | 4201 | TGGAATTCAACTTAGTGTGAGACAGCATCTGGGTGTGAGAGTGAAGAAACAAGTCTCTTAAG   | 4260 |
| Db | 4201 | TGGAATTCAACTTAGTGTGAGACAGCATCTGGGTGTGAGAGTGAAGAAACAAGTCTCTTAAG   | 4260 |
| OY | 4261 | ACTGCTCAGGGCTTATTCCTCTCAGAGTACATTTTAACCACTCAGACAGAGGATTCACATGC   | 4320 |
| Db | 4261 | ACTGCTCAGGGCTTATTCCTCTCAGAGTACATTTTAACCACTCAGACAGAGGATTCACATGC   | 4320 |
| OY | 4321 | AACATTAACCTGATTAAGCTCCAGCAGAGAAATGCGTGAATAGAAAGCTGTGTTAGAACAGC   | 4380 |
| Db | 4321 | AACATTAACCTGATTAAGCTCCAGCAGAGAAATGCGTGAATAGAAAGCTGTGTTAGAACAGC   | 4380 |
| OY | 4381 | ATGGGAGCCAGCCTTCTTACACAGCTACCCCTTTCATCAATAGTACTCCTCTGCCCCTTAGG   | 4440 |
| Db | 4381 | ATGGGAGCCAGCCTTCTTACACAGCTACCCCTTTCATCAATAGTACTCCTCTGCCCCTTAGG   | 4440 |
| OY | 4441 | ACCTGCGAAATCCAGAACAAAGACATCTCAGAAAAAGCAGATTTACTTCCAGAAAAAGTA     | 4500 |
| Db | 4441 | ACCTGCGAAATCCAGAACAAAGACATCTCAGAAAAAGCAGATTTACTTCCAGAAAAAGTA     | 4500 |
| OY | 4501 | GTGAATACCTTATTAAGCCAGAAATCCAGAGGCTTTCTGCTGACAAAGTTGAAGTGTCTG     | 4560 |
| Db | 4501 | GTGAATACCTTATTAAGCCAGAAATCCAGAGGCTTTCTGCTGACAAAGTTGAAGTGTCTG     | 4560 |

QY 4561 CAGATAGTCTTACAGTAAATAAAGAACAGAGTGAAGAGTCAATCCCTCTTAAT 4620  
DB 4561 CAGATAGTCTTACAGTAAATAAAGAACAGAGTGAAGAGTCAATCCCTCTTAAT 4620  
QY 4621 GCCCATATATAGTATAGTGTGACATGACAGTGTCTGTGGAGTCTTCAAGATGAA 4680  
DB 4621 GCCCATATATAGTATAGTGTGACATGACAGTGTCTGTGGAGTCTTCAAGATGAA 4680  
QY 4681 ACTACCATCTCAAGAGAGAGTCAATTAAGTGTGATGAGAGAGCAACAGCTGGAAG 4740  
DB 4681 ACTACCATCTCAAGAGAGAGTCAATTAAGTGTGATGAGAGAGCAACAGCTGGAAG 4740  
QY 4741 AGTCTGGGCCACAGATTTGACGGAACATCTTATCCAGAGCAAGATCTAGAGGAA 4800  
DB 4741 AGTCTGGGCCACAGATTTGACGGAACATCTTATCCAGAGCAAGATCTAGAGGAA 4800  
QY 4801 CCCCTTACTGGAATCTGGAATCAAGCTCTTCTGTGATGACCTGAACTGATCTTCTG 4860  
DB 4801 CCCCTTACTGGAATCTGGAATCAAGCTCTTCTGTGATGACCTGAACTGATCTTCTG 4860  
QY 4861 AAGCAGAGGCCACAGAGTCAAGTGTGGAACAATACATCTTCAACCTCTGACATTA 4920  
DB 4861 AAGCAGAGGCCACAGAGTCAAGTGTGGAACAATACATCTTCAACCTCTGACATTA 4920  
QY 4921 AAGTCTCCCAATGAAAGTTGACAAATCTGCCAGAGGTCCAGCTGTGCTCATACTAG 4980  
DB 4921 AAGTCTCCCAATGAAAGTTGACAAATCTGCCAGAGGTCCAGCTGTGCTCATACTAG 4980  
QY 4981 ATACTGTGGGTATATGCAATGGAAGAAAGTGTGACAGAGGAAAGCCAGATTTGAC 5040  
DB 4981 ATACTGTGGGTATATGCAATGGAAGAAAGTGTGACAGAGGAAAGCCAGATTTGAC 5040  
QY 5041 CTTCACAGAAAGAGTCAACAAAGATGTCATGAGTGTGCTGAGCTGACCCAGAG 5100  
DB 5041 CTTCACAGAAAGAGTCAACAAAGATGTCATGAGTGTGCTGAGCTGACCCAGAG 5100  
QY 5101 AATTTATGCTGTGTAACAAGTTTGCAGAAACACCAATCACTTAACTAATCTAATTA 5160  
DB 5101 AATTTATGCTGTGTAACAAGTTTGCAGAAACACCAATCACTTAACTAATCTAATTA 5160  
QY 5161 CTGAAGAGTACTCATGTTGTTATGAAAAGATGTGAGTGTGTGTGAACGAGAC 5220  
DB 5161 CTGAAGAGTACTCATGTTGTTATGAAAAGATGTGAGTGTGTGTGAACGAGAC 5220  
QY 5221 TGAATATTTTCTAGGAATGGGGAGAGAAATGGGATGATTAATTTCTGGGTGACCC 5280  
DB 5221 TGAATATTTTCTAGGAATGGGGAGAGAAATGGGATGATTAATTTCTGGGTGACCC 5280  
QY 5281 AGTCTATTAAGAAAGAAATCTGAATGAGCATGATTTTGAAGTCAGAGAGATGTG 5340  
DB 5281 AGTCTATTAAGAAAGAAATCTGAATGAGCATGATTTTGAAGTCAGAGAGATGTG 5340  
QY 5341 TCATGGAAGAAACCAAGGTCACAAAGGACCAAGAGAAATCCAGAGCAGAAAGATCT 5400  
DB 5341 TCATGGAAGAAACCAAGGTCACAAAGGACCAAGAGAAATCCAGAGCAGAAAGATCT 5400  
QY 5401 TCAGGGGGCTAGAAATCTGTGATGAGGCTTCAACCAATGAGCCCAAGATCACTG 5460  
DB 5401 TCAGGGGGCTAGAAATCTGTGATGAGGCTTCAACCAATGAGCCCAAGATCACTG 5460  
QY 5461 AATGATGATGACAGTGTGTGTGCTTGTGTGTGGAAGAGCTTTGATCAATCACTG 5520  
DB 5461 AATGATGATGACAGTGTGTGTGCTTGTGTGTGGAAGAGCTTTGATCAATCACTG 5520  
QY 5521 GGCACAGTGTCCCAATTTGTGTGTGTGACCAATGCTTGAACAGAGACATGGCT 5580  
DB 5521 GGCACAGTGTCCCAATTTGTGTGTGTGACCAATGCTTGAACAGAGACATGGCT 5580  
QY 5581 TCCATCAATTTGGGAGATGTGAGACACTGTGGTGAACCGAGAGTGGGTGTTGAGA 5640  
DB 5581 TCCATCAATTTGGGAGATGTGAGACACTGTGGTGAACCGAGAGTGGGTGTTGAGA 5640  
QY 5641 GTGTAGACCTTACAGTGCAGAGAGTGAACCTGATGATACCCAGATCCCCACA 5700

DB 5641 GTGTAGACCTTACAGTGCAGAGAGTGAACCTGATGATACCCAGATCCCCACA 5700  
QY 5701 GCCACTACTGA 5711  
DB 5701 GCCACTACTGA 5711  
RESULT 8  
AR033056 5711 bp DNA linear PAT 29-SEP-1999  
LOCUS AR033056 Sequence 1 from patent US 5869245.  
DEFINITION AR033056  
ACCESSION AR033056  
VERSION AR033056.1 GI:5948661  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE Unclassified.  
AUTHORS 1 (bases 1 to 5711)  
TITLE Yeung, A.T.  
JOURNAL Mismatch endonuclease and its use in identifying mutations in  
FEATURES Targeted polynucleotide strands  
PATENT: US 5869245-A 1 09-FEB-1999;  
LOCATION/Qualifiers  
SOURCE 1. 5711  
BASE COUNT 1956 a 1099 c 1274 g 1382 t  
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DB 541 AACCCGAAATCTCTTCTTGGCAGAAACCAAGTCTCAAGTCTCAACTCTTCACTTTGAA 600

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| QY | 601  | CTGTGGAAC   | CTCTGAGGACAAGCAGCGGATACAACTCCAAAGACGTCTGTCTACATTTG | 660 |
| Db | 601  | CTGTGGAAC   | CTCTGAGGACAAGCAGCGGATACAACTCCAAAGACGTCTGTCTACATTTG | 660 |
| QY | 661  | AATTTGGAGTCTGATTTCTTCTGGAAGATTCGGTAAATAAGGCAACTTATTTGGAGTTGGGAG | 720  |     |
| Db | 661  | AATTTGGAGTCTGATTTCTTCTGGAAGATTCGGTAAATAAGGCAACTTATTTGGAGTTGGGAG | 720  |     |
| QY | 721  | ATCAAGAAATTTGTTACAAATCACCCTCAAGAAACAGGAGTGAATCAGTTTGGATTTCTG    | 780  |     |
| Db | 721  | ATCAAGAAATTTGTTACAAATCACCCTCAAGAAACAGGAGTGAATCAGTTTGGATTTCTG    | 780  |     |
| QY | 781  | CAAAAAAGCGTCTGTTGGAATTTTCTGAGACGGATGTAACTGAACATCATCAAC          | 840  |     |
| Db | 781  | CAAAAAAGCGTCTGTTGGAATTTTCTGAGACGGATGTAACTGAACATCATCAAC          | 840  |     |
| QY | 841  | CCAGTAATATATGATTTTGAAACCACTGAGAAAGGTGAGCGTGAAGGCAATCAGAAAAGT    | 900  |     |
| Db | 841  | CCAGTAATATATGATTTTGAAACCACTGAGAAAGGTGAGCGTGAAGGCAATCAGAAAAGT    | 900  |     |
| QY | 901  | ATCAGGGTAGTTCTGTTTCAAACTTGCAATGTGAGCCATGTGCGCAAAATACATCCCA      | 960  |     |
| Db | 901  | ATCAGGGTAGTTCTGTTTCAAACTTGCAATGTGAGCCATGTGCGCAAAATACATCCCA      | 960  |     |
| QY | 961  | GCTCATTTACAGCATGTGAGAACAGCATTTATTACTCACTAAAGACAAATGATATAGAAA    | 1020   |     |
| Db | 961  | GCTCATTTACAGCATGTGAGAACAGCATTTATTACTCACTAAAGACAAATGATATAGAAA    | 1020   |     |
| QY | 1021 | AGGCTGAATTTCTGTAAATAAAGCAAAACAGCGTGGCTTAGCAAGAGGCAACATACAGAT    | 1080   |     |
| Db | 1021 | AGGCTGAATTTCTGTAAATAAAGCAAAACAGCGTGGCTTAGCAAGAGGCAACATACAGAT    | 1080   |     |
| QY | 1081 | GGGCTGGAAGTAAAGAAACAATGTAATGATAGCGCGATCCCGACACAGAAAAAAGGTAG     | 1140   |     |
| Db | 1081 | GGGCTGGAAGTAAAGAAACAATGTAATGATAGCGCGATCCCGACACAGAAAAAAGGTAG     | 1140   |     |
| QY | 1141 | ATCTGAATGCTGATCCCTGTGTGAGAGAAAGATGGAATAGCAGAAATGCTCATGCT        | 1200   |     |
| Db | 1141 | ATCTGAATGCTGATCCCTGTGTGAGAGAAAGATGGAATAGCAGAAATGCTCATGCT        | 1200   |     |
| QY | 1201 | CAGAGAACTCTAAGATCTAGGAAGATGTTCTTGGATTAACCTTAATAAGCAGCTTACA      | 1260   |     |
| Db | 1201 | CAGAGAACTCTAAGATCTAGGAAGATGTTCTTGGATTAACCTTAATAAGCAGCTTACA      | 1260   |     |
| QY | 1261 | AGGTTAATGAGTGGTTTTCCAGAAAGTGATGAACGTGTAGGTTCTGATGACTCAGATAGT    | 1320   |     |
| Db | 1261 | AGGTTAATGAGTGGTTTTCCAGAAAGTGATGAACGTGTAGGTTCTGATGACTCAGATAGT    | 1320   |     |
| QY | 1321 | GGGAGTCTGATCAAAATGCCAAAGTAGCTGATATTGAGCGTTCTAATATGAGTAGATG      | 1380   |     |
| Db | 1321 | GGGAGTCTGATCAAAATGCCAAAGTAGCTGATATTGAGCGTTCTAATATGAGTAGATG      | 1380   |     |
| QY | 1381 | AATATTCTGGTCTTTCAGAGAAATATGACTTACGGCAGTAGCCCTCATGAGGCTTTAA      | 1440   |     |
| Db | 1381 | AATATTCTGGTCTTTCAGAGAAATATGACTTACGGCAGTAGCCCTCATGAGGCTTTAA      | 1440   |     |
| QY | 1441 | TATGTAAAAGTGAAGAGTTCACCTCCAAATCAGTAGAGATTAATTATGAGACAAAAATAT    | 1500   |     |
| Db | 1441 | TATGTAAAAGTGAAGAGTTCACCTCCAAATCAGTAGAGATTAATTATGAGACAAAAATAT    | 1500   |     |
| QY | 1501 | TTGGGAAAACTATCGGAAAGGCAAGCCTCCCAACTTAAGCCTATGTAACCTGAATAATC     | 1560   |     |
| Db | 1501 | TTGGGAAAACTATCGGAAAGGCAAGCCTCCCAACTTAAGCCTATGTAACCTGAATAATC     | 1560   |     |
| QY | 1561 | TAAATTTAGAGAGATTTGTTACTGAGGCAAGATTAATCAAGAGCGTCCCTCACAATA       | 1620   |     |
| Db | 1561 | TAAATTTAGAGAGATTTGTTACTGAGGCAAGATTAATCAAGAGCGTCCCTCACAATA       | 1620   |     |
| QY | 1621 | AATTAAGCGTAAAGAGACCTACATCAGGCGCTTCACTCTGAGAGATTTTATCAAGAAAG     | 1680   |     |
| Db | 1621 | AATTAAGCGTAAAGAGACCTACATCAGGCGCTTCACTCTGAGAGATTTTATCAAGAAAG     | 1680   |     |
| QY | 1681 | CAGATTTGGCAGTTCAAAAGACTCTGAAAATGATTAATCAAGGGAACCTAACCAACGAGGC   | 1740   |     |
| Db | 1681 | CAGATTTGGCAGTTCAAAAGACTCTGAAAATGATTAATCAAGGGAACCTAACCAACGAGGC   | 1740   |     |

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|----|------|---|------|
| Db | 1681 | CAGATTGCGACGTTAAAAAGACTCTGTAAGATGAATTAACAGGAATCAACACGAGCC       | 1740 |
| Qy | 1741 | AGAAATGCTCAAGTGTGATGATATTAATCAATAGTGTCAAGAAATAAAAAAGGTGAT       | 1800 |
| Db | 1741 | AGAAATGCTCAAGTGTGATGATATTAATCAATAGTGTCAAGAAATAAAAAAGGTGAT       | 1800 |
| Qy | 1801 | CTATTTCAGATGAGAAAAATCTCTAACCAATAGAAATCACTGGAAAAAGAAATCTGTTTCA   | 1860 |
| Db | 1801 | CTATTTCAGATGAGAAAAATCTCTAACCAATAGAAATCACTGGAAAAAGAAATCTGTTTCA   | 1860 |
| Qy | 1861 | AAAGCAAAAGCTGAACTTAATAGACGACGACTATAGCAATATGGAATCGAATTAATATCC    | 1920 |
| Db | 1861 | AAAGCAAAAGCTGAACTTAATAGACGACGACTATAGCAATATGGAATCGAATTAATATCC    | 1920 |
| Qy | 1921 | ACAAATTCAAAAAGCACCTTAATAAGATAGCGTGGAGAGGAAGTCTTCTACACGACATATTC  | 1980 |
| Db | 1921 | ACAAATTCAAAAAGCACCTTAATAAGATAGCGTGGAGAGGAAGTCTTCTACACGACATATTC  | 1980 |
| Qy | 1981 | ATGCGCTTGAACCTAGTACTCAGTGAATACTTAAGCCCACTTAATTTGTACTGAATTGCAGAA | 2040 |
| Db | 1981 | ATGCGCTTGAACCTAGTACTCAGTGAATACTTAAGCCCACTTAATTTGTACTGAATTGCAGAA | 2040 |
| Qy | 2041 | TTGATAGTGTCTCTAGCGATGAAGATTAAGAAAAAAGATGACACCAAAATGCGACATCA     | 2100 |
| Db | 2041 | TTGATAGTGTCTCTAGCGATGAAGATTAAGAAAAAAGATGACACCAAAATGCGACATCA     | 2100 |
| Qy | 2101 | GGCACAGACAGAAACCTTAACAATCAATGAGAGTTAAAGAACTGCAACTGAGCCCAAGAGA   | 2160 |
| Db | 2101 | GGCACAGACAGAAACCTTAACAATCAATGAGAGTTAAAGAACTGCAACTGAGCCCAAGAGA   | 2160 |
| Qy | 2161 | GTAACAAAGCCCAATGATGACAGACAAGTAAAGACATGACATGATATCTTCCAGAGCTGA    | 2220 |
| Db | 2161 | GTAACAAAGCCCAATGATGACAGACAAGTAAAGACATGACATGATATCTTCCAGAGCTGA    | 2220 |
| Qy | 2221 | AGTTAACAAATGACACTGTGTTCTTTTACTAGTGTTCAAATAACAGAGGAATCTTAAGAT    | 2280 |
| Db | 2221 | AGTTAACAAATGACACTGTGTTCTTTTACTAGTGTTCAAATAACAGAGGAATCTTAAGAT    | 2280 |
| Qy | 2281 | TTGTCAATCTCAGACCTTCCAGAGAGAAAGAAAGAGAAATCTAGAAACAGTTAAAGTGT     | 2340 |
| Db | 2281 | TTGTCAATCTCAGACCTTCCAGAGAGAAAGAAAGAGAAATCTAGAAACAGTTAAAGTGT     | 2340 |
| Qy | 2341 | CTAATTAATGCTGAAGACCCCAAGATCTCATGTTAATGAGAAAGGGTTTGCACATG        | 2400 |
| Db | 2341 | CTAATTAATGCTGAAGACCCCAAGATCTCATGTTAATGAGAAAGGGTTTGCACATG        | 2400 |
| Qy | 2401 | AAAGATCTGTAGAGAGTACAGATATTTCACTGTGTAACCTGTGATCTGATTAATGGCACTGAG | 2460 |
| Db | 2401 | AAAGATCTGTAGAGAGTACAGATATTTCACTGTGTAACCTGTGATCTGATTAATGGCACTGAG | 2460 |
| Qy | 2461 | AAAGATCTCGTTACTGTGAAGTGAACCTTAGGGAGAGCAAAAAACAGAACCAAAATTAAT    | 2520 |
| Db | 2461 | AAAGATCTCGTTACTGTGAAGTGAACCTTAGGGAGAGCAAAAAACAGAACCAAAATTAAT    | 2520 |
| Qy | 2521 | GTTGTAGTCAAGTGTGACAGCATTTTGAACCCCAAGGACCTAATTCATGTTGTTCCAAAG    | 2580 |
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| Qy | 2641 | GGGAACAAGCATGGAATGGAAGAGTGAACCTTGAATGCTCAGATTTGAGAAATACAT       | 2700 |
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| Qy | 2701 | TCAAGGTTTCAAAGGCGCAGTCAATTTGCTGTTTCAAATCCAGGAATCAGAAAGAG        | 2760 |
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| Qy | 2761 | AATGTGCAACATTTCTGCGCACTCTGGGTCCTTAAAGAAACAAAGTCAAAAGTCACTT      | 2820 |
| Db | 2761 | AATGTGCAACATTTCTGCGCACTCTGGGTCCTTAAAGAAACAAAGTCAAAAGTCACTT      | 2820 |



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RESULT 9
HSU14680 5711 bp mRNA linear prt 10-JUN-2002
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DEFINITION complete cds.
ACCESSION U14680
VERSION U14680.1 GI:555931
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
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REFERENCE
  1 (bases 1 to 5711)
  Miki,Y., Swensen,J., Shattuck-Eidens,D., Futreal,P.A., Harshman,K.,
  Tavtigian,S., Liu,Q., Cochran,C., Bennett,L.M., Ding,W., Bell,R.,
  Rosenhal,J., Husey,C., Tran,T., McClure,M., Frye,C., Hattier,T.,
  Phelps,R., Haugen-Strano,A., Katcher,H., Yakumo,K., Gholian,Z.,
  Shaffer,D., Stone,S., Beyer,S., Wray,C., Bogden,R., Dayanant,P.,
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  Helvering,L., Morrison,P., Rostock,P., Lai,M., Barrett,J.C.,

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 Kamb,A. and Skolnick,M.H.  
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 gene BRCA1  
 Science 266 (5182), 66-71 (1994)  
 MEDLINE 95025896  
 PUBMED 7545954  
 2 (bases 1 to 5711)  
 AUTHORS Skolnick,M.H.  
 TITLE Direct Submission  
 JOURNAL Submitted (14-SEP-1994) Mark H. Skolnick, Myriad Genetics Inc. and  
 the University of Utah, 421 Wakara Way, Suite 201, Salt Lake City,  
 UT 84108, USA

#### FEATURES

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QY 5341 TCAATGAAGAAACACCAAGGTCCAAAGCGAGCAAGAGAAATCCAGAGACAGAAAGATCT 5400
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|
Db 5341 TCAATGAAGAAACACCAAGGTCCAAAGCGAGCAAGAGAAATCCAGAGACAGAAAGATCT 5400
QY 5401 TCAGGGGGCTAGAAATCTGTTGCTATGAGGCTTCAACCAACATGCTTCAACATCTG 5460
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Db 5401 TCAGGGGGCTAGAAATCTGTTGCTATGAGGCTTCAACCAACATGCTTCAACATCTG 5460
QY 5461 AATGATGATACAGTGTGTGTGCTTCTGAGTGAAGAGAGTTCATCATCTTCAACCTT 5520
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|
Db 5461 AATGATGATACAGTGTGTGTGCTTCTGAGTGAAGAGAGTTCATCATCTTCAACCTT 5520
QY 5521 GCACAGTGTCCACCAATTTGTGTGTGACAGCCAGATGCTGACAGAGCAATGTGCT 5580
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Db 5521 GCACAGTGTCCACCAATTTGTGTGTGACAGCCAGATGCTGACAGAGCAATGTGCT 5580
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Db 5521 GCACAGGTGTCCACCCCAATTGGTGTGTGACCCGACGATCTCTGACAGAGGACCAATGCT 5580  
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Db 5581 TCCATGCAATTGGGAGATGTGTGAGGCACTGTGTGTGACCCGAGAGTGGGTGTGACA 5640  
Qy 5641 GTGTAGCACTCTACCAAGTCCGAGAGTGTGACACCTACTGATACCCCGAGATCCCCCA 5700  
Db 5641 GTGTAGCACTCTACCAAGTCCGAGAGTGTGACACCTACTGATACCCCGAGATCCCCCA 5700  
Qy 5701 GCCACTACTGA 5711  
Db 5701 GCCACTACTGA 5711  
RESULT 10  
AR070223 5712 bp DNA linear PAT 18-FEB-2000  
LOCUS AR070223  
DEFINITION Sequence 1 from patent US 5891857.  
ACCESSION AR070223  
VERSION AR070223.1 GI:7221111  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 5712)  
AUTHORS Holte,J.T., Jensen,R.A., King,M.-C., Page,D.L., Szabo,C.I.,  
Jelton,T.L., Robinson-Benion,C.L. and Thompson,M.E.  
TITLE Characterized BRCA1 and BRCA2 proteins and screening and  
therapeutic methods based on characterized BRCA1 and BRCA2 proteins  
JOURNAL Patent: US 5891857-A 1 06-APR-1999;  
FEATURES  
source Location/Qualifiers  
1..5712  
BASE COUNT 1956 a 1099 c 1274 g 1383 t  
ORIGIN  
Query Match 99.8%; Score 5639.8; DB 6; Length 5712;  
Best Local Similarity 99.9%; Pred.No. 0;  
Matches 5704; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 481 AAGTTTCTATGATCCAAAGTATGGGCTACAGAAACCGTCCCAAGACCTTCAAGAGTG 540  
Db 481 AAGTTTCTATGATCCAAAGTATGGGCTACAGAAACCGTCCCAAGACCTTCAAGAGTG 540  
Qy 541 AACCAGAAATCTCTCTTGGAGAGAAACCACTCAGTGTCCAATCTCTTAACCTTGAA 600  
Db 541 AACCAGAAATCTCTCTTGGAGAGAAACCACTCAGTGTCCAATCTCTTAACCTTGAA 600  
Qy 601 CTGTGAGAACTCTGAGACAAAGCAGGATTAACCTTCAAGAGAGCTCTGTCTACATTG 660  
Db 601 CTGTGAGAACTCTGAGACAAAGCAGGATTAACCTTCAAGAGAGCTCTGTCTACATTG 660  
Qy 661 AATTGGGATCTGATTTCTTCAAGATACCGTTAATTAAGGCAACTATTGGAGTGGAG 720  
Db 661 AATTGGGATCTGATTTCTTCAAGATACCGTTAATTAAGGCAACTATTGGAGTGGAG 720  
Qy 721 ATCAAGAATTGTACAAATCAACCCCTCAAGGACAGGAGTGAATCAGTTGGATTCTG 780  
Db 721 ATCAAGAATTGTACAAATCAACCCCTCAAGGACAGGAGTGAATCAGTTGGATTCTG 780  
Qy 781 CAAAAAGGCTGCTTGTGAATTTTCTGAGACGATGTACAAATCTGACATCATCAAC 840  
Db 781 CAAAAAGGCTGCTTGTGAATTTTCTGAGACGATGTACAAATCTGACATCATCAAC 840  
Qy 841 CCAGTAATTAATGATTGAAACCACTGAGAGCGTGCAGCTGAGAGGATCCAGAAAGT 900  
Db 841 CCAGTAATTAATGATTGAAACCACTGAGAGCGTGCAGCTGAGAGGATCCAGAAAGT 900  
Qy 901 ATCAGGATGATCTGTTTCAAACTTGATGAGAGGATGAGGACCAATATCTATGCCA 960  
Db 901 ATCAGGATGATCTGTTTCAAACTTGATGAGAGGATGAGGACCAATATCTATGCCA 960  
Qy 961 GCTCATTAACAGATGAGACACGAGTTTATTAATCACTAAGACAGAAATGATGAAAA 1020  
Db 961 GCTCATTAACAGATGAGACACGAGTTTATTAATCACTAAGACAGAAATGATGAAAA 1020  
Qy 1021 AGGCTGAATTCGTATTAATTAAGCAAAACGCTGCTTAGCAAGGACCAATACAGAT 1080  
Db 1021 AGGCTGAATTCGTATTAATTAAGCAAAACGCTGCTTAGCAAGGACCAATACAGAT 1080  
Qy 1081 GGGCTGGAAGTAAAGAAACATGTAATGATAGCGGAGCTCCACAGACAGAAAAAGTAG 1140  
Db 1081 GGGCTGGAAGTAAAGAAACATGTAATGATAGCGGAGCTCCACAGACAGAAAAAGTAG 1140  
Qy 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAGATGGAATTAACAGAAATCTGCATGCT 1200  
Db 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAGATGGAATTAACAGAAATCTGCATGCT 1200  
Qy 1201 CAGAGATCTAGAGATCTGAAGTGTCTCTGATTAACATTAATAGCAGCTTACAG 1260  
Db 1201 CAGAGATCTAGAGATCTGAAGTGTCTCTGATTAACATTAATAGCAGCTTACAG 1260  
Qy 1261 AAGTTAATGAGTGTCTTCCAGAAAGTGAATGTTAGTGTGATGACTCACATGATG 1320  
Db 1261 AAGTTAATGAGTGTCTTCCAGAAAGTGAATGTTAGTGTGATGACTCACATGATG 1320  
Qy 1321 GGAAGTCTGAATCAATTCCAAAGTGAATGTAATTTGAGAGCTTCAATAGAGTAATG 1380  
Db 1321 GGAAGTCTGAATCAATTCCAAAGTGAATGTAATTTGAGAGCTTCAATAGAGTAATG 1380  
Qy 1381 AATATTCTGATCTTCCAGAGAAATPAGACTTACTGCGCAGATGCTCATGAGGCTTAA 1440  
Db 1381 AATATTCTGATCTTCCAGAGAAATPAGACTTACTGCGCAGATGCTCATGAGGCTTAA 1440  
Qy 1441 TATGTAAAGTGAAGAGTCACTCCAAATCAGTAGAGATTAATTTGAAGACAAATAT 1500  
Db 1441 TATGTAAAGTGAAGAGTCACTCCAAATCAGTAGAGATTAATTTGAAGACAAATAT 1500  
Qy 1501 TTGGGAAAACTATTCGGAAGAGGACGCTCCCAACTTAAGCATGTATGAATATC 1560  
Db 1501 TTGGGAAAACTATTCGGAAGAGGACGCTCCCAACTTAAGCATGTATGAATATC 1560

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|----|------|---|------|
| QY | 1561 | TAATATAGGAGCACTTGTCTCTGAGCCACAGATTAATACAAAGAGCTCCCTCCAAATA    | 1620 |
| Db | 1561 | TAATTATAGACATTTTGTACTGAGCCACAGATATATCAAGAGCTCCCTCCAAATA       | 1620 |
| QY | 1621 | AATTAAACGTAATAAGAGACCTACATCAGGCTTCATCTGAGATTTTATCAAGAAG       | 1680 |
| Db | 1621 | AATTAAACGTAATAAGAGACCTACATCAGGCTTCATCTGAGATTTTATCAAGAAG       | 1680 |
| QY | 1681 | CAGATTTGGCACTTCAAAAAGACTCCTGAAATGATTAATCAGGAACTAACCAACGAGC    | 1740 |
| Db | 1681 | CAGATTTGGCACTTCAAAAAGACTCCTGAAATGATTAATCAGGAACTAACCAACGAGC    | 1740 |
| QY | 1741 | AGAATGTCGCAAGTGTATGTAATTTACTAATAGTGGTCATGAGAAATTAACAAAGTGA    | 1800 |
| Db | 1741 | AGAATGTCGCAAGTGTATGTAATTTACTAATAGTGGTCATGAGAAATTAACAAAGTGA    | 1800 |
| QY | 1801 | CTATTCAAAATGAGAAAAATCTCTAACCCATAGATCACTCGAAAAAATCTGCTTCA      | 1860 |
| Db | 1801 | CTATTCAAAATGAGAAAAATCTCTAACCCATAGATCACTCGAAAAAATCTGCTTCA      | 1860 |
| QY | 1861 | AAACGAAGCTGAACTTAATAGCAGCAGTATAGCAATATGGAATCTGAAATTAATATCC    | 1920 |
| Db | 1861 | AAACGAAGCTGAACTTAATAGCAGCAGTATAGCAATATGGAATCTGAAATTAATATCC    | 1920 |
| QY | 1921 | ACAATTTCAAAAGCACTTAAAAAGAATAGGCTGAGAGAGAACTCTTCCACGCAATATTC   | 1980 |
| Db | 1921 | ACAATTTCAAAAGCACTTAAAAAGAATAGGCTGAGAGAGAACTCTTCCACGCAATATTC   | 1980 |
| QY | 1981 | ATGCGCTTGAACCTAGTATGCTAGTAGTAATCTAAGGCCACTAATTTGTACTGAATTCGAA | 2040 |
| Db | 1981 | ATGCGCTTGAACCTAGTATGCTAGTAGTAATCTAAGGCCACTAATTTGTACTGAATTCGAA | 2040 |
| QY | 2041 | TTGATAGTGTCTTACGAGTGAAGATTAAGAAAAAAGATACAAACCAATATGCGACTCA    | 2100 |
| Db | 2041 | TTGATAGTGTCTTACGAGTGAAGATTAAGAAAAAAGATACAAACCAATATGCGACTCA    | 2100 |
| QY | 2101 | GGCAGAGAGAAACCTACACTCATGGAAGTTAAAGAACTTGCACTGAGCCCAAGAA       | 2160 |
| Db | 2101 | GGCAGAGAGAAACCTACACTCATGGAAGTTAAAGAACTTGCACTGAGCCCAAGAA       | 2160 |
| QY | 2161 | GTAACAAACCCAAATGAACAGACAAGTAATAAGACATGACAGTATCTTCCAGAGCTGA    | 2220 |
| Db | 2161 | GTAACAAACCCAAATGAACAGACAAGTAATAAGACATGACAGAGATCTTCCAGAGCTGA   | 2220 |
| QY | 2221 | AGTTAACAAATGACACTGCTGTCTTTACTAAGTGTTCAAATACACAGTGAATTAAAGAT   | 2280 |
| Db | 2221 | AGTTAACAAATGACACTGCTGTCTTTACTAAGTGTTCAAATACACAGTGAATTAAAGAT   | 2280 |
| QY | 2281 | TTGTCAATCTTACGCTTCCAAAGAGAAAAAGAAAGAACTTGAAACAGTTAAAGTGT      | 2340 |
| Db | 2281 | TTGTCAATCTTACGCTTCCAAAGAGAAAAAGAAAGAACTTGAAACAGTTAAAGTGT      | 2340 |
| QY | 2341 | CTAATTAATGCTGAAGAGCCCAAAAGATCTCATGTTAAGTGGAGAAAGGTTTGGAACTG   | 2400 |
| Db | 2341 | CTAATTAATGCTGAAGAGCCCAAAAGATCTCATGTTAAGTGGAGAAAGGTTTGGAACTG   | 2400 |
| QY | 2401 | AAAGATCTGTAGAGAGTAGCAGTATTTCACTGCTGACCTGTATGATTAATGCACTCAGG   | 2460 |
| Db | 2401 | AAAGATCTGTAGAGAGTAGCAGTATTTCACTGCTGACCTGTATGATTAATGCACTCAGG   | 2460 |
| QY | 2461 | AAAGTATCTGTTACTGGAAGTTAGCACTTAGGGAAGGCAAAAAACAGAACCAATTAAT    | 2520 |
| Db | 2461 | AAAGTATCTGTTACTGGAAGTTAGCACTTAGGGAAGGCAAAAAACAGAACCAATTAAT    | 2520 |
| QY | 2521 | GTTGAGAGCAGTGGCAGCACTTTGAAACCCCAAGGGACTAATTCATGCTTTGCCAAG     | 2580 |
| Db | 2521 | GTTGAGAGCAGTGGCAGCACTTTGAAACCCCAAGGGACTAATTCATGCTTTGCCAAG     | 2580 |
| QY | 2581 | ATAATAGAAATGACACAGAAAGCTTTAATGATTCATTGGGACATGAAGTTAACACAGCTC  | 2640 |
| Db | 2581 | ATAATAGAAATGACACAGAAAGCTTTAATGATTCATTGGGACATGAAGTTAACACAGCTC  | 2640 |
| QY | 2641 | GGGAAACACAGCATAGAAAATGGAAGAAAGTGAATTGATGCTCAGTATTTGCAGAATACAT | 2700 |

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|----|------|--|------|
| Db | 2641 | GGGAAACACAGATAGAAATGGAAGAAATGAACTTGATGCTCAGTATTTCAGAAATACAT    | 2700 |
| Qy | 2701 | TCAAAGTTTCAAAGGCCAGTCATTTGCTGTGTTTTCAAAATCGAAGAAATCGAAGAG      | 2760 |
| Db | 2701 | TCAAAGTTTCAAAGGCCAGTCATTTGCTGTGTTTTCAAAATCGAAGAAATCGAAGAG      | 2760 |
| Qy | 2761 | AATGTGCAACATTCTCTGCCCACTCTGGGTCTTTAAGAAACAAAGTCCTT             | 2820 |
| Db | 2761 | AATGTGCAACATTCTCTGCCCACTCTGGGTCTTTAAGAAACAAAGTCCTT             | 2820 |
| Qy | 2821 | TTGAATGTGAACAAAGAGAAATATCAGGAAAGAAATGAGTCTAATTCAGGCTGTAC       | 2880 |
| Db | 2821 | TTGAATGTGAACAAAGAGAAATATCAGGAAAGAAATGAGTCTAATTCAGGCTGTAC       | 2880 |
| Qy | 2881 | AGACAGTTAATATCACTGACAGCTTTCTGTGTGTGTCAGAAAGATAGCAGTTGATA       | 2940 |
| Db | 2881 | AGACAGTTAATATCACTGACAGCTTTCTGTGTGTGTCAGAAAGATAGCAGTTGATA       | 2940 |
| Qy | 2941 | ATGCCAAATGTAGTATCAAAGAGGCTTAGGTTTGTCTATCATCTCAGTTCAAGACA       | 3000 |
| Db | 2941 | ATGCCAAATGTAGTATCAAAGAGGCTTAGGTTTGTCTATCATCTCAGTTCAAGACA       | 3000 |
| Qy | 3001 | ACGAAACCTGGACTCAATTACTCCAAATAAACATGCACTTTTCAAAACCCATATGCTATAC  | 3060 |
| Db | 3001 | ACGAAACCTGGACTCAATTACTCCAAATAAACATGCACTTTTCAAAACCCATATGCTATAC  | 3060 |
| Qy | 3061 | CACACACTTTTCCCATCAAGTCATTTGTTTAAATCTAATGTAAAGAAATCTGCTAGAG     | 3120 |
| Db | 3061 | CACACACTTTTCCCATCAAGTCATTTGTTTAAATCTAATGTAAAGAAATCTGCTAGAG     | 3120 |
| Qy | 3121 | AAAACTTTAGAAACATTCAAATGTACCTGAGAAAGAAATGGAAATGAGAACTTCCAA      | 3180 |
| Db | 3121 | AAAACTTTAGAAACATTCAAATGTACCTGAGAAAGAAATGGAAATGAGAACTTCCAA      | 3180 |
| Qy | 3181 | GTAACAGTAGACAAATTAAGCCGTAAATACATTAAGAGAAATGTTTTTAAAGAGCCAGCT   | 3240 |
| Db | 3181 | GTAACAGTAGACAAATTAAGCCGTAAATACATTAAGAGAAATGTTTTTAAAGAGCCAGCT   | 3240 |
| Qy | 3241 | CAAGCAATATTAATGAAGTAGGTTCCAGTACTAATGAAGTGGGCTCCAGTATTATGAAA    | 3300 |
| Db | 3241 | CAAGCAATATTAATGAAGTAGGTTCCAGTACTAATGAAGTGGGCTCCAGTATTATGAAA    | 3300 |
| Qy | 3301 | TAGGTTCCAGTGATGAAAAACATTCAGCAGAACTAGGTAGAAACAGAGGCCCAAAATTTGA  | 3360 |
| Db | 3301 | TAGGTTCCAGTGATGAAAAACATTCAGCAGAACTAGGTAGAAACAGAGGCCCAAAATTTGA  | 3360 |
| Qy | 3361 | ATGCTATGCTTAGATTAGGGGTTTTGCAACCTGAGGTCATTAACAAAGTCTTCTGGAA     | 3420 |
| Db | 3361 | ATGCTATGCTTAGATTAGGGGTTTTGCAACCTGAGGTCATTAACAAAGTCTTCTGGAA     | 3420 |
| Qy | 3421 | GTAATTTGTAACATCCGGAATTAAGAAACAGAAATGTGAAGAGTGTGAGACTGTTA       | 3480 |
| Db | 3421 | GTAATTTGTAACATCCGGAATTAAGAAACAGAAATGTGAAGAGTGTGAGACTGTTA       | 3480 |
| Qy | 3481 | ATAACAGATTTCTCTCCATATCTGATTTTCAGATTAACCTTAAGAACAGCTATGGAAGTATC | 3540 |
| Db | 3481 | ATAACAGATTTCTCTCCATATCTGATTTTCAGATTAACCTTAAGAACAGCTATGGAAGTATC | 3540 |
| Qy | 3541 | ATGCATCTCAGGTTTGTCTGAGACACCTGATGACTGTTAGATGATGTTGAATTAAG       | 3600 |
| Db | 3541 | ATGCATCTCAGGTTTGTCTGAGACACCTGATGACTGTTAGATGATGTTGAATTAAG       | 3600 |
| Qy | 3601 | AAGATCTAGTTTGTGGAATAACATTAAGAAAGTGTGCGTGTTTTAGCAAAAGCG         | 3660 |
| Db | 3601 | AAGATCTAGTTTGTGGAATAACATTAAGAAAGTGTGCGTGTTTTAGCAAAAGCG         | 3660 |
| Qy | 3661 | TCGAGAGAGAGACCTTAGCAGAGAGTCTAGCCCTTTCACCCATACACATTTGGCTCAGG    | 3720 |
| Db | 3661 | TCGAGAGAGAGACCTTAGCAGAGAGTCTAGCCCTTTCACCCATACACATTTGGCTCAGG    | 3720 |
| Qy | 3721 | GTTACCGAAGAGGGGCCAAGAAATTAGAGTCTTCAAGAAAGAACTTATCTAAGTGAAGATG  | 3780 |
| Db | 3721 | GTTACCGAAGAGGGGCCAAGAAATTAGAGTCTTCAAGAAAGAACTTATCTAAGTGAAGATG  | 3780 |



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| D | 3721 | GTATCCGAAGAGGGCCCAAGAAATTAGAGTCTCAGAAAGAGACTTATCTAGTGAAGT      | 3780 |
| O | 3781 | AAGAGCTTCCTGCTTCCAAACACTTGTTATTTGGTAAAGTAAACATATACCTTCTCAGT    | 3840 |
| D | 3781 | AAGAGCTTCCTGCTTCCAAACACTTGTTATTTGGTAAAGTAAACATATACCTTCTCAGT    | 3840 |
| O | 3841 | CTACTAGGCAATAGCACCGCTTGCTACCGAGTGTCTGTCTAAGAACACAGAGAAATTTAT   | 3900 |
| O | 3901 | TATCATTAAGAATATGCTTAAATGACCTGACAGTAACCAAGTAAATATGGCAAAAGCATCTC | 3960 |
| D | 3901 | TATCATTAAGAATATGCTTAAATGACCTGACAGTAACCAAGTAAATATGGCAAAAGCATCTC | 3960 |
| O | 3961 | AGGAACATCACCTTAGTAGGAAACMAAATGTTCTGTAGAGTGTGTTTCTTCAAGTGA      | 4020 |
| D | 3961 | AGGAACATCACCTTAGTAGGAAACMAAATGTTCTGTAGAGTGTGTTTCTTCAAGTGA      | 4020 |
| O | 4021 | GTGAATTGGAAAGACTTGACTGCAATACAAACCCAGAGTCTTTCTTGAATTGGTCTT      | 4080 |
| D | 4021 | GTGAATTGGAAAGACTTGACTGCAATACAAACCCAGAGTCTTTCTTGAATTGGTCTT      | 4080 |
| O | 4081 | CCAAACAATGAGGATAGTGTGAAGCCAGGGAGTTGTCGTGATCAAGAAATTTGG         | 4140 |
| D | 4081 | CCAAACAATGAGGATAGTGTGAAGCCAGGGAGTTGTCGTGATCAAGAAATTTGG         | 4140 |
| O | 4141 | TTTCAGATGATGTAAGAAAGAGAACGGGCTTGGAAAGAAATTAATCAAGAAAGCA        | 4200 |
| D | 4141 | TTTCAGATGATGTAAGAAAGAGAACGGGCTTGGAAAGAAATTAATCAAGAAAGCA        | 4200 |
| O | 4201 | TGGAATCAAACCTTAGGTGAGCAGCATCTGGGTGTGAAGTGAACAAGCGTCTGTGA       | 4260 |
| D | 4201 | TGGAATCAAACCTTAGGTGAGCAGCATCTGGGTGTGAAGTGAACAAGCGTCTGTGA       | 4260 |
| O | 4261 | ACTGCTAAGGGGTATCTCTCAGAGTGAATTTTAAACACTCAGAGAGGATATCCAGC       | 4320 |
| D | 4261 | ACTGCTAAGGGGTATCTCTCAGAGTGAATTTTAAACACTCAGAGAGGATATCATGC       | 4320 |
| O | 4321 | AACATTAACCTGATTAAGCTCCAGCAGAAATGGCTGAACCTGATGAAGCTGTAGAACAGC   | 4380 |
| D | 4321 | AACATTAACCTGATTAAGCTCCAGCAGAAATGGCTGAACCTGATGAAGCTGTAGAACAGC   | 4380 |
| O | 4381 | ATGGAGCCAGGCTTCTTAACAGCTACCTTCCATCAATGAAGACTCTTCTGCCCTTGAG     | 4440 |
| D | 4381 | ATGGAGCCAGGCTTCTTAACAGCTACCTTCCATCAATGAAGACTCTTCTGCCCTTGAG     | 4440 |
| O | 4441 | ACCTGCCGAATCCCAAGAACATATAGAAAAGCAGTATTAATCTTCAAGAAAAGTA        | 4500 |
| D | 4441 | ACCTGCCGAATCCCAAGAACATATAGAAAAGCAGTATTAATCTTCAAGAAAAGTA        | 4500 |
| O | 4501 | GTTGAATACCTTATAAGCAGAAATCAGAAAGGCTTCTGTGACAAAGTTGAGGTGTG       | 4560 |
| D | 4501 | GTTGAATACCTTATAAGCAGAAATCAGAAAGGCTTCTGTGACAAAGTTGAGGTGTG       | 4560 |
| O | 4561 | CAGATAGTTCTACACGTAATAAAGAACCAAGAGTGAAGGTCATCCCTCTTAAT          | 4620 |
| D | 4561 | CAGATAGTTCTACACGTAATAAAGAACCAAGAGTGAAGGTCATCCCTCTTAAT          | 4620 |
| O | 4621 | GCCCATCTATAGATATAGGTGTAATGCAAGTGTCTTGGAAGTCTTCAAGAAATAAA       | 4680 |
| D | 4621 | GCCCATCTATAGATATAGGTGTAATGCAAGTGTCTTGGAAGTCTTCAAGAAATAAA       | 4680 |
| O | 4681 | ACTACCCATCTCAAGAGAGCTCATTTAAGTTGTGATGTGGAGAGCAACAGCTGAA        | 4740 |
| D | 4681 | ACTACCCATCTCAAGAGAGCTCATTTAAGTTGTGATGTGGAGAGCAACAGCTGAA        | 4740 |
| O | 4741 | AGTCTGGGCAACAGATTTGAAGGAACATCTTACTTCCAAAGCAAGATCTAAGGGAA       | 4800 |
| D | 4741 | AGTCTGGGCAACAGATTTGAAGGAACATCTTACTTCCAAAGCAAGATCTAAGGGAA       | 4800 |
| O | 4801 | CCCCTACTTGGAATCTGGAATCAGAGCTTCTCTGATGACCTTAATCTGATCTTCTG       | 4860 |
| D | 4801 | CCCCTACTTGGAATCTGGAATCAGAGCTTCTCTGATGACCTTCTGATCTGATCTTCTG     | 4860 |

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|---|--|------|--------------|--|------------------------------|-------|
| OY  |  | 4861 | AAGACAGA     | GCCCCCAGAGTCACTGTTGTGGCAA                                | CATPCCATCTTTCAACCCTCTGCATTGA | 49220 |
| Db  |  | 4861 | AAGACAGAGCCC | CAGAGTCACCTGTTGGCAACATPCCATCTTTCAACCCTCTGCATTGA          |                              | 49220 |
| OY  |  | 4921 | AAGTCCCCCAT  | TGAAAGTTGCAGATCTGCGCCAGGGGCCAGCTGCTCTATACTACTG           |                              | 49800 |
| Db  |  | 4921 | AAGTCCCCCAT  | TGAAAGTTGCAGANTCTGCCAGAGTCCAGCTGCTCTATACTACTG            |                              | 49800 |
| OY  |  | 4981 | ATACTGCTGGG  | TATATGCAATGGAAAGAGTGAGCAGGGAGAAAGCCAGAATTGACAG           |                              | 50400 |
| Db  |  | 4981 | ATACTGCTGGG  | TATATGCAATGGAAAGAGTGAGCAGGGAGAAAGCCAGAATTGACAG           |                              | 50400 |
| OY  |  | 5041 | CTTCAACA     | GAAAGGGTCACAAAAGAAAGTCCATGCTGCTGCTGCCCCAGAG              |                              | 51000 |
| Db  |  | 5041 | CTTCAACA     | GAAAGGGTCACAAAAGAAAGTCCATGCTGCTGCTGCCCCAGAG              |                              | 51000 |
| OY  |  | 5101 | AATTATATCTG  | TGTAACAAGTTTGGCCAGAAACACACATCACTTAATCTAATTA              |                              | 51600 |
| Db  |  | 5101 | AATTATATCTG  | TGTAACAAGTTTGGCCAGAAACACACATCACTTAATCTAATTA              |                              | 51600 |
| OY  |  | 5161 | CTGAAGAGAC   | TACTCATGTTATGAAAAAGATGCTGAATGTTGTGTGAACGGACAC            |                              | 52200 |
| Db  |  | 5161 | CTGAAGAGAC   | TACTCATGTTATGAAAAAGATGCTGAATGTTGTGTGAACGGACAC            |                              | 52200 |
| OY  |  | 5221 | TGAATATATTT  | CTAGGAATTCGGGAGAGAAATGGTAGTAGTATTTCTGGGTGACCC            |                              | 52800 |
| Db  |  | 5221 | TGAATATATTT  | CTAGGAATTCGGGAGAGAAATGGTAGTAGTATTTCTGGGTGACCC            |                              | 52800 |
| OY  |  | 5281 | AGCTATTATTA  | AGAAAGAAAAATGCTGATGAGCATGATTTTGAAGTCAGAGAGATGTGG         |                              | 53400 |
| Db  |  | 5281 | AGCTATTATTA  | AGAAAGAAAAATGCTGATGAGCATGATTTTGAAGTCAGAGAGATGTGG         |                              | 53400 |
| OY  |  | 5341 | TCAATGGA     | AGAAACCAACCAAGGTCCTCAAGCGACAGAGAAATCCAGAGACGAAAGATCT     |                              | 54000 |
| Db  |  | 5341 | TCAATGGA     | AGAAACCAACCAAGGTCCTCAAGCGACAGAGAAATCCAGAGACGAAAGATCT     |                              | 54000 |
| OY  |  | 5401 | TCAGGGGGCT   | TGAAATCTGTTGCTATGAGGCGCTTCCACCAATGCGCCACAGATCAACTGG      |                              | 54600 |
| Db  |  | 5401 | TCAGGGGGCT   | TGAAATCTGTTGCTATGAGGCGCTTCCACCAATGCGCCACAGATCAACTGG      |                              | 54600 |
| OY  |  | 5461 | AATGATGGA    | TACAGCTGTGTGCTTCTGTGTGAAGAGCTTTTCATCATTCACCCTTG          |                              | 55200 |
| Db  |  | 5461 | AATGATGGA    | TACAGCTGTGTGCTTCTGTGTGAAGAGCTTTTCATCATTCACCCTTG          |                              | 55200 |
| OY  |  | 5521 | GCACAGGTG    | TCCACCCAATTTGTGTTGTGACCCAGATGCTTGACAGAGAACATGGCT         |                              | 55800 |
| Db  |  | 5521 | GCACAGGTG    | TCCACCCAATTTGTGTTGTGACCCAGATGCTTGACAGAGAACATGGCT         |                              | 55800 |
| OY  |  | 5581 | TCCATGCA     | TAATTTGGGAGATGTGTGAGGCACTGTGTGTGTAACCCGAGAGTGGGTGTTGGACA |                              | 56400 |
| Db  |  | 5581 | TCCATGCA     | TAATTTGGGAGATGTGTGAGGCACTGTGTGTGTAACCCGAGAGTGGGTGTTGGACA |                              | 56400 |
| OY  |  | 5641 | GTTAGCA      | CTCTACCAAGTCCAGAGAGCTGACACCTTACTGATACCCCAATGCCCAACA      |                              | 57000 |
| Db  |  | 5641 | GTTAGCA      | CTCTACCAAGTCCAGAGAGCTGACACCTTACTGATACCCCAATGCCCAACA      |                              | 57000 |
| OY  |  | 5701 | GCCACTACTGA  | 5711   |                              |       |
| Db  |  | 5701 | GCCACTACTGA  | 5711   |                              |       |
| <hr/>   |  |      |              |  |                              |       |
| RESULT 11   |  |      |              |  |                              |       |
| AR118507  |  |      |              |  |                              |       |
| LOCUS AR118507 5712 bp DNA linear PAT 16-MAY-2001 |  |      |              |  |                              |       |
| DEFINITION Sequence 1 from patent US 6149903.     |  |      |              |  |                              |       |
| ACCESSION AR118507                                |  |      |              |  |                              |       |
| VERSION AR118507.1 GI:14100417                    |  |      |              |  |                              |       |
| KEYWORDS  |  |      |              |  |                              |       |
| SOURCE unknown.                                   |  |      |              |  |                              |       |
| ORGANISM unknown.                                 |  |      |              |  |                              |       |
| REFERENCE 1 (bases 1 to 5712)                     |  |      |              |  |                              |       |

| RESULT 11 | LOCUS    | DEFINITION                         | ACCESSION | VERSION    | GI:14100417 | 5712 bp | DNA | linear | PAT 16-MAY-2001 |
|-----------|----------|------------------------------------|-----------|------------|-------------|---------|-----|--------|-----------------|
| AR118507  | AR118507 | Sequence 1 from patent US 6149903. | AR118507  | AR118507.1 | GI:14100417 |         |     |        |                 |

| KEYWORDS | SOURCE   | ORGANISM | REFERENCE           |
|----------|----------|----------|---------------------|
| unknown. | unknown. | unknown. | 1 (bases 1 to 5712) |



AUTHORS Holt, J.T., Jensen, R.A., King, M.-C., Page, D.L., Szabo, C.I.,  
Jettison, J.L., Robinson-Benion, C.L. and Thompson, M.E.  
TITLE Characterized BRCA1 and BRCA2 proteins and screening and  
JOURNAL therapeutic methods based on characterized BRCA1 and BRCA2 proteins  
FEATURES Patent: US 6149903-A 1 21-NOV-2000;  
Location/Qualifiers  
source 1.5712  
/Organism="unknown"

BASE COUNT 1956 a 1099 c 1274 g 1383 t  
ORIGIN

Query Match 99.8%; Score 5699.8; DB 6; Length 5712;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 5704; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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QY 181 TCTTAAGTGTCCATCTGTGAGAGTATGATCAAGAACTGTCTCCAAAGTGTGAGC 240
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DB 181 TCTTAAGTGTCCATCTGTGAGAGTATGATCAAGAACTGTCTCCAAAGTGTGAGC 240
QY 241 ACATATTTTGCAAATTTTGCATGCTGAACTTCTCAACAGAAAGAGGCTTTCACAGT 300
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DB 361 AACTGTGTAAGAGCTATGAAATGATTTGTGCTTTGAGCTGTGACAGAGTTGGAGT 420
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QY 541 AACCCGAAATCCCTCTCTGAGAGAAACAGTCTGAGTCCCAACTCTTAACCTTTGAA 600
DB 541 AACCCGAAATCCCTCTCTGAGAGAAACAGTCTGAGTCCCAACTCTTAACCTTTGAA 600
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QY 841 CCAATTAATGATTTGAACCACTGAGAGGCTGAGAGGATTCAGAAAGT 900
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QY 1801 CTATTCAAGATGAGAAAAATCTTAACCAATAGAAATCTGAAAAAAGAAATCTGTTTCA 1860
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QY 1861 AAACGAAAGCTGAACCTTAAGCAGAGTATTAAGCAATATGAACTCGAATTAATATATCC 1920
DB 1861 AAACGAAAGCTGAACCTTAAGCAGAGTATTAAGCAATATGAACTCGAATTAATATATCC 1920
QY 1921 ACAATTCAAAGCACTTAAGAAATAGCTGAGAGGAGAGTCTTCTACAGGCAATATTC 1980
DB 1921 ACAATTCAAAGCACTTAAGAAATAGCTGAGAGGAGAGTCTTCTACAGGCAATATTC 1980
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QY 1981 ATGGGCTTGAATCTAGTACGTAGAAATCTAAGCCCACTTAATTGTACTGAAATTCGAA 2040  
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QY 2041 TTGATAGTGTCTTGTGACGTAGAGATTAAGAAAAAAGTACAAACCAATGCCAGTCA 2100  
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QY 2521 GTGTGAGTCAGTGTGACAGATTTGAAAAACCCCAAGAGCAATATTCATGGTGTTCGAAAG 2580  
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Db AATGTGCAACATTTCTGCCCCACTGCGGTCTTTAAGAAACAAAGTCCAAAAGTCACTT 2820  
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QY 3421 GTAAATGTAGCATCTCGAATTAATAAAGCAGAAATGAGAAAGTACAGACTGTTA 3480  
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QY 3481 ATACAGATTTCTCCATATCTGATTTCAATTAATTAGAAACAGCTTATGAGAAATGATC 3540  
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QY 4141 TTTCAGATGATGAAGAAAGAGAAACGGGCTTGAAGAAATTAATCAAGAAAGCAAGCA 4200

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|----|------|---|------|
| Db | 4141 | TTTCAGATGATGAAAGAGGAACGGGCTTGAAAGAAAATATCAAGAGCAAGCA          | 4200 |
| OY | 4201 | TGGATTCAAACTTAGGTGAAGCAGCATCTGGGTGTGAAGTGAACAAGCGTCTCTGAAG    | 4260 |
| Db | 4201 | TGGATTCAAACTTAGGTGAAGCAGCATCTGGGTGTGAAGTGAACAAGCGTCTCTGAAG    | 4260 |
| OY | 4261 | ACTGCTCAGGGGTATTCCTCTCAGAGTGCATTTTAAACCACTCAGAGAGGGATACATGC   | 4320 |
| Db | 4261 | ACTGCTCAGGGGTATTCCTCTCAGAGTGCATTTTAAACCACTCAGAGAGGGATACATGC   | 4320 |
| OY | 4321 | AACATAACCTGATTAAGCTCCGACGAGAAATGGCTGAACCTGAAGCTGTGTAGAACGC    | 4380 |
| Db | 4321 | AACATAACCTGATTAAGCTCCGACGAGAAATGGCTGAACCTGAAGCTGTGTAGAACGC    | 4380 |
| OY | 4331 | AACATTAACCTGATTAAGCTCCGACGAGAAATGGCTGAACCTGAAGCTGTGTAGAACGC   | 4380 |
| Db | 4331 | AACATTAACCTGATTAAGCTCCGACGAGAAATGGCTGAACCTGAAGCTGTGTAGAACGC   | 4380 |
| OY | 4391 | ATGGAGGCGAGCTTTCTAACAGCTAACCTTCCATCATTAAGTACCTCTGCGCTTGAGG    | 4440 |
| Db | 4391 | ATGGAGGCGAGCTTTCTAACAGCTAACCTTCCATCATTAAGTACCTCTGCGCTTGAGG    | 4440 |
| OY | 4441 | ACCTGCGAAATTCAGAAACAAAGCAGATCAAGAAAAAGCATTTAACTTCAAGAAAACTA   | 4500 |
| Db | 4441 | ACCTGCGAAATTCAGAAACAAAGCAGATCAAGAAAAAGCATTTAACTTCAAGAAAACTA   | 4500 |
| OY | 4501 | GTGAATACCTCTATAAGCCAGAAATCCAGAAAGGCTTTCTGCTGACAAAGTTTAGAGTGTG | 4560 |
| Db | 4501 | GTGAATACCTCTATAAGCCAGAAATCCAGAAAGGCTTTCTGCTGACAAAGTTTAGAGTGTG | 4560 |
| OY | 4561 | CAGATAGTTCCTAACCGATAAAAATTAAGAACAGAGTGAAGGTCATCCCCCTCTAAAT    | 4620 |
| Db | 4561 | CAGATAGTTCCTAACCGATAAAAATTAAGAACAGAGTGAAGGTCATCCCCCTCTAAAT    | 4620 |
| OY | 4621 | GCCCATCTATTAGATGATGCTGGTGCATGACACAGTTGCTCTGGAGTCTTCAAGATTGAA  | 4680 |
| Db | 4621 | GCCCATCTATTAGATGATGCTGGTGCATGACACAGTTGCTCTGGAGTCTTCAAGATTGAA  | 4680 |
| OY | 4661 | ACTACCCATCTCAAGAGAGGCGCATTAAGTGTGTTGATGTGAGGAGCAACAGCTGGAG    | 4740 |
| Db | 4661 | ACTACCCATCTCAAGAGAGGCGCATTAAGTGTGTTGATGTGAGGAGCAACAGCTGGAG    | 4740 |
| OY | 4741 | AGCTGGGCGCACAGCATTTGACGAAACATCTTACTTCCCAAGCGAAGATCTAAGGGAA    | 4800 |
| Db | 4741 | AGCTGGGCGCACAGCATTTGACGAAACATCTTACTTCCCAAGCGAAGATCTAAGGGAA    | 4800 |
| OY | 4801 | CCCCCTTACCTTGAATCTGGAATCAGCCCTCTCTGTAAGACCGTGAATCTATCCTTCTG   | 4860 |
| Db | 4801 | CCCCCTTACCTTGAATCTGGAATCAGCCCTCTCTGTAAGACCGTGAATCTATCCTTCTG   | 4860 |
| OY | 4861 | AAGACAGAGCCCCAGAGTCAGCTGCTGTGGCAACATACATCTTCAACCTCTGCAATTGA   | 4920 |
| Db | 4861 | AAGACAGAGCCCCAGAGTCAGCTGCTGTGGCAACATACATCTTCAACCTCTGCAATTGA   | 4920 |
| OY | 4921 | AAGTTCGCCCAATTGAAATTTGCAGAAATTTGCCAGAGGTCAGAGCTGCTCATACACTG   | 4980 |
| Db | 4921 | AAGTTCGCCCAATTGAAATTTGCAGAAATTTGCCAGAGGTCAGAGCTGCTCATACACTG   | 4980 |
| OY | 4991 | ATACTGCTGGGTATTAATCAATGGAAGAAATGTGAAGCAGGAGAGAGCCAGAAATTTGACG | 5040 |
| Db | 4991 | ATACTGCTGGGTATTAATCAATGGAAGAAATGTGAAGCAGGAGAGAGCCAGAAATTTGACG | 5040 |
| OY | 5041 | CTTCAACGAAAGGCTCAACAAAGAAATGTCATATGAGTGTGTGCGCTGACCCCAAGAG    | 5100 |
| Db | 5041 | CTTCAACGAAAGGCTCAACAAAGAAATGTCATATGAGTGTGTGCGCTGACCCCAAGAG    | 5100 |
| OY | 5101 | AATTTATCTCGTGTACAAGTTTGCAGAAAAACACACATCACTTAACTTAATCTAAATTA   | 5160 |
| Db | 5101 | AATTTATCTCGTGTACAAGTTTGCAGAAAAACACACATCACTTAACTTAATCTAAATTA   | 5160 |
| OY | 5161 | CTGAAGAGACTACTCATGTTGTGTAAGAAAAAGATGCTGAGTTTGTGTGAACGACAC     | 5220 |
| Db | 5161 | CTGAAGAGACTACTCATGTTGTGTAAGAAAAAGATGCTGAGTTTGTGTGAACGACAC     | 5220 |
| OY | 5221 | TGAATATTTCTAGGAATTCGGGAGGAAATGGGTAGTTAGTATTTCTGGGTGACCC       | 5280 |
| Db | 5221 | TGAATATTTCTAGGAATTCGGGAGGAAATGGGTAGTTAGTATTTCTGGGTGACCC       | 5280 |

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|----------------------------|---|--|--------|
| Db                         | 5221  | GGAAATATTTCTGAGAAATGCGGGAGAGAAATGGAGTAGTACGTATTTCTGGGTGACC   | 5280   |
| Qy                         | 5281  | AGTCATTAAAGAAAGAAAAATGCTGATGATGACATGATTTTGAATCAGAGAGATGTGG   | 5340   |
| Db                         | 5281  | AGTCATTAAAGAAAGAAAAATGCTGATGATGACATGATTTTGAATCAGAGAGATGTGG   | 5340   |
| Qy                         | 5341  | TCATTCGAAAGAAACCCACCAAGTCCAAAGCAGAAAGAAATCCACAGAACGAAAGATCT  | 5400   |
| Db                         | 5341  | TCATTCGAAAGAAACCCACCAAGTCCAAAGCAGAAAGAAATCCACAGAACGAAAGATCT  | 5400   |
| Qy                         | 5401  | TCAGGGGGCTGGAATCTGTGTGATGAGGCCCTTACCAACATGSCCCACAGATCAATCG   | 5460   |
| Db                         | 5401  | TCAGGGGGCTGGAATCTGTGTGATGAGGCCCTTACCAACATGSCCCACAGATCAATCG   | 5460   |
| Qy                         | 5461  | AATGATATGATCAGACTGTGTGTCTTCTGTGTGAAGAGCTTTCATTCATCCCTTG      | 5520   |
| Db                         | 5461  | AATGATATGATCAGACTGTGTGTCTTCTGTGTGAAGAGCTTTCATTCATCCCTTG      | 5520   |
| Qy                         | 5521  | GCAAGATGTCCACCCAAATTTGTGTTTGTGACCCAGATGCTGTGACAGAGAACATGGCT  | 5580   |
| Db                         | 5521  | GCAAGATGTCCACCCAAATTTGTGTTTGTGACCCAGATGCTGTGACAGAGAACATGGCT  | 5580   |
| Qy                         | 5581  | TCCATGCAATGGGCAAGTGTGTAGGACCACTGTGTGTGACCCGAGATGGGTGTGGACA   | 5640   |
| Db                         | 5581  | TCCATGCAATGGGCAAGTGTGTAGGACCACTGTGTGTGACCCGAGATGGGTGTGGACA   | 5640   |
| Qy                         | 5641  | GTGTAGCACTCTTACAGTCCAGAGAGCTGACACCTACCTGATACCCAGATCCCCACA    | 5700   |
| Db                         | 5641  | GTGTAGCACTCTTACAGTCCAGAGAGCTGACACCTACCTGATACCCAGATCCCCACA    | 5700   |
| Qy                         | 5701  | GCACCTACTGA 5711   |        |
| Db                         | 5701  | GCACCTACTGA 5711   |        |
| RESULT 12                  |   |  |        |
| ARI25601                   | ARI25601  | 5712 bp  | DNA    |
| LOCUS                      | Definition  | Sequence 1 from patent US 6177410.                           | linear |
| LOCUS                      | Accession   | ARI25601   |        |
| VERSION                    | ARI25601.1  | GI:14111663  |        |
| KEYWORDS                   | Unknown.  |  |        |
| SOURCE                     | Unknown.  |  |        |
| ORGANISM                   | Unclassified.                                     |  |        |
| REFERENCE                  | 1 (bases 1 to 5712)                               |  |        |
| AUTHORS                    | Holt,J.T., Jensen,R.A., King,M.-C., Steiner,M.S., |  |        |
| TITLE                      | Robinson-Bennon,C.U. and Thompson,M.E.            |  |        |
| JOURNAL                    | Therapeutic methods for prostate cancer           |  |        |
| FEATURES                   | Patent: US 6177410-A 1 23-JAN-2001;               |  |        |
| source                     | Location/Qualifiers                               |  |        |
|                            | 1..5712   |  |        |
|                            | /organism="unknown"                               |  |        |
| BASE COUNT                 | 1956 a 1099 c 4274 g 1383 t                       |  |        |
| ORIGIN                     |   |  |        |
| Query Match                | 99.8%; Score 5699.8; DB 6; Length 5712;           |  |        |
| Best Local Similarity      | 99.9%; Pred. No. 0;                               |  |        |
| Matches 5704; Conservative | 0; Mismatches 7; Indels 0; Gaps 0;                |  |        |
| Qy                         | 1   | AGCTGCTGAGACTCTCTGAGACCCCGACACGAGCTGTGGGGTTTCTCAGATTAATGGGCC | 60     |
| Db                         | 1   | AGCTGCTGAGACTTCTGAGACCCCGACACGAGCTGTGGGGTTTCTCAGATTAATGGGCC  | 60     |
| Qy                         | 61  | CTGCGCTCAGAGAGCCTTCAACCTCTGCTCTGGGTAAATTTATTGGAAACAGAAAGAA   | 120    |
| Db                         | 61  | CTGCGCTCAGAGAGCCTTCAACCTCTGCTCTGGGTAAATTTATTGGAAACAGAAAGAA   | 120    |
| Qy                         | 121   | TGATTTATCTGCTCTCGGCTTGAAGAAATGATCAATTAATGCTATGACAGAAA        | 180    |
| Db                         | 121   | TGATTTATCTGCTCTCGGCTTGAAGAAATGATCAATTAATGCTATGACAGAAA        | 180    |
| Qy                         | 181   | TCCTTAGAGTGTCCACTGTCTGTGAGATTGATCAGAGAACTGTCTCCACAAAGTGTACC  | 240    |

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Db 181 TCTTGAAGTCCCATCTGTCTGGAGTGTATCAAGAACTCTCTCCAAAGTGTGACC 240
Qy 241 ACATATTTTGGCAATTTTGCATGCTGAAAATTCTCAACGAGAAAGGGCTTCACAGT 300
Db 241 ACATATTTTGGCAATTTTGCATGCTGAAAATTCTCAACGAGAAAGGGCTTCACAGT 300
Qy 301 GTCTTTTATGTAAATATATTAACCAAAAGAGCTTACAAAGATCGAATTTAGTC 360
Db 301 GTCTTTTATGTAAATATATTAACCAAAAGAGCTTACAAAGATCGAATTTAGTC 360
Qy 361 AACTTGTGAAGAGTATTTGAAAATCATTTTGTCTTTTCAAGCTTACAGGTTTGAAT 420
Db 361 AACTTGTGAAGAGTATTTGAAAATCATTTTGTCTTTTCAAGCTTACAGGTTTGAAT 420
Qy 421 ATGCAAAACAGCTATATTTTGGCAAAAAGAAAATTAATCTCTCTGAACATCTTAAAGATG 480
Db 421 ATGCAAAACAGCTATATTTTGGCAAAAAGAAAATTAATCTCTCTGAACATCTTAAAGATG 480
Qy 481 AAGTTTCTATCATCCAAAGTATGGGCTACAGAAACGGTCCAAAAGACTTCTTACAGAGTG 540
Db 481 AAGTTTCTATCATCCAAAGTATGGGCTACAGAAACGGTCCAAAAGACTTCTTACAGAGTG 540
Qy 541 AACCAGAAATCTCTTCTTGGAGAAACAGTCTCAGTGTCCAACTCTTAACTTGGAA 600
Db 541 AACCAGAAATCTCTTCTTGGAGAAACAGTCTCAGTGTCCAACTCTTAACTTGGAA 600
Qy 601 CTGTGAGAACTCTGAGCAAAAGCAGCGGATCAAACTTCAAAAAGCTGTCTTCAATTG 660
Db 601 CTGTGAGAACTCTGAGCAAAAGCAGCGGATCAAACTTCAAAAAGCTGTCTTCAATTG 660
Qy 661 AATTGGGATCTGATTTCTTGAAGTACGGTAAATAGGCACTTATGCACTGTGGGAG 720
Db 661 AATTGGGATCTGATTTCTTGAAGTACGGTAAATAGGCACTTATGCACTGTGGGAG 720
Qy 721 ATCAAGATTTGTTCAAATCAACCCCTCAAGAAACAGGATGAAATCAAGTTGATTCG 780
Db 721 ATCAAGATTTGTTCAAATCAACCCCTCAAGAAACAGGATGAAATCAAGTTGATTCG 780
Qy 781 CAAAAAAGGCTGCTTGTGAATTTTCTGAGACGATGTAACTGAATCTCATCAAC 840
Db 781 CAAAAAAGGCTGCTTGTGAATTTTCTGAGACGATGTAACTGAATCTCATCAAC 840
Qy 841 CCAGTAATTAATGATTTGAAACCACTGAGAAAGCTGAGAGGCACTCCAGAAAAT 900
Db 841 CCAGTAATTAATGATTTGAAACCACTGAGAAAGCTGAGAGGCACTCCAGAAAAT 900
Qy 901 ATCAGGAGTATTTCTGTTTCAAACTTGCATGTGAGACCATGTGGCAAAATACTCATGCA 960
Db 901 ATCAGGAGTATTTCTGTTTCAAACTTGCATGTGAGACCATGTGGCAAAATACTCATGCA 960
Qy 961 GCTATTATCAGATGAGAAACAGCACTTATTAATCTCACTAAAGACGAATGTGAAA 1020
Db 961 GCTATTATCAGATGAGAAACAGCACTTATTAATCTCACTAAAGACGAATGTGAAA 1020
Qy 1021 AGGCTGAATTTCTGTAATAAAGCAAAAGCTGCTTACAGAGGCACTTAACAGAT 1080
Db 1021 AGGCTGAATTTCTGTAATAAAGCAAAAGCTGCTTACAGAGGCACTTAACAGAT 1080
Qy 1081 GGGCTGGAAGTAAAGAAAATGTATGATAGGCGGACTCCAGCACAGAAAAGGTG 1140
Db 1081 GGGCTGGAAGTAAAGAAAATGTATGATAGGCGGACTCCAGCACAGAAAAGGTG 1140
Qy 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAAGAAATGGAATAGCAAACTGCCATGCT 1200
Db 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAAGAAATGGAATAGCAAACTGCCATGCT 1200
Qy 1201 CAGAGAAATCTGAGAAATCTGAGAAATGTTCTTGGATTAACATTAATATACACATTCACA 1260
Db 1201 CAGAGAAATCTGAGAAATCTGAGAAATGTTCTTGGATTAACATTAATATACACATTCACA 1260
Qy 1261 AAGTTAATGATGTTTTCAGAAAGTGAATCTGTAGGTTCTGATGATCATGATG 1320
Db 1261 AAGTTAATGATGTTTTCAGAAAGTGAATCTGTAGGTTCTGATGATCATGATG 1320
Db 1261 AAGTTAATGATGTTTTCAGAAAGTGAATCTGTAGGTTCTGATGATCATGATG 1320
Qy 1321 GGGAGTCTGATTCAAATATGCCAAATAGCTGATGATTTGAGACGTTTAAAGATGATG 1380
Db 1321 GGGAGTCTGATTCAAATATGCCAAATAGCTGATGATTTGAGACGTTTAAAGATGATG 1380
Qy 1381 AATAATTCGTTCTTACAGAGAAATATAGCTTACCTGAGAGATCTCATGAGCTTTAA 1440
Db 1381 AATAATTCGTTCTTACAGAGAAATATAGCTTACCTGAGAGATCTCATGAGCTTTAA 1440
Qy 1441 TATGTAAGTGAAGAGTCTTCAATCAATGATGAGATATATTTGAAGACAAATAT 1500
Db 1441 TATGTAAGTGAAGAGTCTTCAATCAATGATGAGATATATTTGAAGACAAATAT 1500
Qy 1501 TTGGGAAAACCTATCGGAAGAGGCAAGCTCCCACTTAAGCCATGATGAAATC 1560
Db 1501 TTGGGAAAACCTATCGGAAGAGGCAAGCTCCCACTTAAGCCATGATGAAATC 1560
Qy 1561 TAAATATAGAGCAATTTGTTACTGAGCCACAGATATATACAAGAGCTCCCTCAATA 1620
Db 1561 TAAATATAGAGCAATTTGTTACTGAGCCACAGATATATACAAGAGCTCCCTCAATA 1620
Qy 1621 AATTAAAGCTTAAAGAGACCTTACATCAGGCTTCAATCTGAGAGATTTTATCAAGAG 1680
Db 1621 AATTAAAGCTTAAAGAGACCTTACATCAGGCTTCAATCTGAGAGATTTTATCAAGAG 1680
Qy 1681 CAGATTTGGAGTTTCAAAAAGCTCTGAAATGATTAATCAAGGAACTTAAACGAGG 1740
Db 1681 CAGATTTGGAGTTTCAAAAAGCTCTGAAATGATTAATCAAGGAACTTAAACGAGG 1740
Qy 1741 AGAATGTCTAGATGATATTTACTTAATAGTGTCTGAGAAATTAACAAAGGTGAT 1800
Db 1741 AGAATGTCTAGATGATATTTACTTAATAGTGTCTGAGAAATTAACAAAGGTGAT 1800
Qy 1801 CTATTCAGATGAGAAAATCTTAAACCAATAGATTAATCTGAGAAAAGATTCGCTTCA 1860
Db 1801 CTATTCAGATGAGAAAATCTTAAACCAATAGATTAATCTGAGAAAAGATTCGCTTCA 1860
Qy 1861 AAAGGAAAGCTGAACCTTAAAGAGAGTATTAAGCAATAGGAACTGAAATTAATATCC 1920
Db 1861 AAAGGAAAGCTGAACCTTAAAGAGAGTATTAAGCAATAGGAACTGAAATTAATATCC 1920
Qy 1921 ACAAATTCAAAAGCACTTAAAGAAATAGGCTGAGAGAGGCTTCTTACAGGCAATTC 1980
Db 1921 ACAAATTCAAAAGCACTTAAAGAAATAGGCTGAGAGAGGCTTCTTACAGGCAATTC 1980
Qy 1981 ATGGCTTGAACCTGATGATCTGATGAAATCTTAAAGCTTAAATTTGATGAAATTCG 2040
Db 1981 ATGGCTTGAACCTGATGATCTGATGAAATCTTAAAGCTTAAATTTGATGAAATTCG 2040
Qy 2041 TTGATAGTGTCTTACAGAGTGAAGATTAAGAAAAGAAAAGTAAACCAATATGCACTCA 2100
Db 2041 TTGATAGTGTCTTACAGAGTGAAGATTAAGAAAAGAAAAGTAAACCAATATGCACTCA 2100
Qy 2101 GGCAAGCAGAAACCTTCAACTCATGAGGTAAGAACTGCAATCTGAGCCAAAGAA 2160
Db 2101 GGCAAGCAGAAACCTTCAACTCATGAGGTAAGAACTGCAATCTGAGCCAAAGAA 2160
Qy 2161 GTAACAGCCCAATGAGACAGCAAGTAAAGACATGACAGTATCTTTCCAGAGCTGA 2220
Db 2161 GTAACAGCCCAATGAGACAGCAAGTAAAGACATGACAGTATCTTTCCAGAGCTGA 2220
Qy 2221 AGTTAACAATGACACTGCTTCTTCTAAGTTCCTAATTAACAGTGAATTAAGAT 2280
Db 2221 AGTTAACAATGACACTGCTTCTTCTAAGTTCCTAATTAACAGTGAATTAAGAT 2280
Qy 2281 TTGTCAATCTTACGCTTCAAGAGAGAAAAGAGAACTAGAAACAGTTAAAGTGT 2340
Db 2281 TTGTCAATCTTACGCTTCAAGAGAGAAAAGAGAACTAGAAACAGTTAAAGTGT 2340
Qy 2341 CTAATATATGCTGAAGACCCCAAGATCTCATGTTAATGAGAAAGGGTTTTCGAACTG 2400
Db 2341 CTAATATATGCTGAAGACCCCAAGATCTCATGTTAATGAGAAAGGGTTTTCGAACTG 2400
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QY 2401 AAAGATCTGAGAGATAGACGATTTCTAGTACCTGGTACTGATTAATGCGACTCAGG 2460  
DB 2401 AAAGATCTGAGAGATAGACGATTTCTAGTACCTGGTACTGATTAATGCGACTCAGG 2460  
QY 2461 AAGGATCTGCTTACTGGAAGTTAGCACTCTAGGGAAGGCAAAACAGAACCAATTAAT 2520  
DB 2461 AAGGATCTGCTTACTGGAAGTTAGCACTCTAGGGAAGGCAAAACAGAACCAATTAAT 2520  
QY 2521 GGTGAGTCAAGTGTGAGCACTTGAAGCCCAAGGACCTAATCTGTTGTTCCAAAG 2580  
DB 2521 GGTGAGTCAAGTGTGAGCACTTGAAGCCCAAGGACCTAATCTGTTGTTCCAAAG 2580  
QY 2581 ATATAGAAATGACACAGAAAGCTTAAATGATTCATTGGGACATGAAATCCACAGTC 2640  
DB 2581 ATATAGAAATGACACAGAAAGCTTAAATGATTCATTGGGACATGAAATCCACAGTC 2640  
QY 2641 GGGAAACAAGCATAGAAATGGAAGAAAGTGAATGCTGATGCTGATATTTGACAGATACAT 2700  
DB 2641 GGGAAACAAGCATAGAAATGGAAGAAAGTGAATGCTGATGCTGATATTTGACAGATACAT 2700  
QY 2701 TCAAGGTTTCAAGCCGACGTCATTTGCTCTGTTTCAATCCAGGAAATGCGAAGAGG 2760  
DB 2701 TCAAGGTTTCAAGCCGACGTCATTTGCTCTGTTTCAATCCAGGAAATGCGAAGAGG 2760  
QY 2761 AATGTGCAACATTCCTGCCCCACTGCGGTCTTAAAGAAACAAAGTCCAAAGTCACTT 2820  
DB 2761 AATGTGCAACATTCCTGCCCCACTGCGGTCTTAAAGAAACAAAGTCCAAAGTCACTT 2820  
QY 2821 TTGAATGTGAACAAAGAAAGAAATCAAGAAAGATGATCTAATATCAAGCTGTAC 2880  
DB 2821 TTGAATGTGAACAAAGAAAGAAATCAAGAAAGATGATCTAATATCAAGCTGTAC 2880  
QY 2881 AGACATTAATATCACTGAGGCTTCTGTGTTGTGTGTCAGAAAGATAGCCAGTTGAT 2940  
DB 2881 AGACATTAATATCACTGAGGCTTCTGTGTTGTGTGTCAGAAAGATAGCCAGTTGAT 2940  
QY 2941 ATGCCAAATGTAGTATCAAGAGAGGCTAGGTTTGTCTATCATCTCAGTTGAGGCA 3000  
DB 2941 ATGCCAAATGTAGTATCAAGAGAGGCTAGGTTTGTCTATCATCTCAGTTGAGGCA 3000  
QY 3001 ACAGAACTGGAATCTTACCTCCAAATTAACATGACCTTTTACAAACCCATATCGTATAC 3060  
DB 3001 ACAGAACTGGAATCTTACCTCCAAATTAACATGACCTTTTACAAACCCATATCGTATAC 3060  
QY 3061 CACCACTTTTCCCACTCAAGTCACTTTGTTAAACTTAATGTAAGAAATCTGCTAGAGG 3120  
DB 3061 CACCACTTTTCCCACTCAAGTCACTTTGTTAAACTTAATGTAAGAAATCTGCTAGAGG 3120  
QY 3121 AAAAATTTGAGGAACATTCGATGTCAGTGAAGAAATGGGAAATGGAACATTCGAA 3180  
DB 3121 AAAAATTTGAGGAACATTCGATGTCAGTGAAGAAATGGGAAATGGAACATTCGAA 3180  
QY 3181 GATCAGTGAACAATTAAGCCGTAATTAATGAGAAATGTTTAAAGAGCCAGCT 3240  
DB 3181 GATCAGTGAACAATTAAGCCGTAATTAATGAGAAATGTTTAAAGAGCCAGCT 3240  
QY 3241 CAAGCAATATTAATGAAGTTCAGTACTAATGAAGTGGCTCCAGTATTAATGAA 3300  
DB 3241 CAAGCAATATTAATGAAGTTCAGTACTAATGAAGTGGCTCCAGTATTAATGAA 3300  
QY 3301 TAGGTTCCAGTGAAGAAATCAAGCAAGAACTAGTAGAAACAGAGGCCAAATTTGA 3360  
DB 3301 TAGGTTCCAGTGAAGAAATCAAGCAAGAACTAGTAGAAACAGAGGCCAAATTTGA 3360  
QY 3361 ATGCTATGCTTAGATTAAGGGGTTTGCACCTGAGAGTCTATTAACAAAGTCTTCTGGA 3420  
DB 3361 ATGCTATGCTTAGATTAAGGGGTTTGCACCTGAGAGTCTATTAACAAAGTCTTCTGGA 3420  
QY 3421 GTAATGTAGCATCTGTAATTAAGAAAGCAAGAAATGTAAGAAAGTGTGAGAGTGTGA 3480  
DB 3421 GTAATGTAGCATCTGTAATTAAGAAAGCAAGAAATGTAAGAAAGTGTGAGAGTGTGA 3480

QY 3481 ATACAGATTTCTTCCATATCTGATTTAGATTAATGAGAAAGCTTATGGAAGTATGTC 3540  
DB 3481 ATACAGATTTCTTCCATATCTGATTTAGATTAATGAGAAAGCTTATGGAAGTATGTC 3540  
QY 3541 ATGCACTCAGGTTTGTCTGAGACCTGATGACCTGTTAGATGATGTTGAATTAAGG 3600  
DB 3541 ATGCACTCAGGTTTGTCTGAGACCTGATGACCTGTTAGATGATGTTGAATTAAGG 3600  
QY 3601 AAGATACATGTTTGTGTAAGAAATGACATTAAGAAAGTCTGCTGTTTATGCAAAAGG 3660  
DB 3601 AAGATACATGTTTGTGTAAGAAATGACATTAAGAAAGTCTGCTGTTTATGCAAAAGG 3660  
QY 3661 TCCAGAGAGAGAGCTTACAGAGTCTAGCCCTTTCACCCATACATTTGGCTCAGG 3720  
DB 3661 TCCAGAGAGAGAGCTTACAGAGTCTAGCCCTTTCACCCATACATTTGGCTCAGG 3720  
QY 3721 GTTACCGAAGAGGGCCAAAGAAATTAAGTCTCAGAGAGAACTTATCTAGTACGATG 3780  
DB 3721 GTTACCGAAGAGGGCCAAAGAAATTAAGTCTCAGAGAGAACTTATCTAGTACGATG 3780  
QY 3781 AAGAGCTTCCGCTTCCAACTGTTATTTGTAAGTAAACAATACCTTCTCAGT 3840  
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DB 3841 CTACTAGGATAGCACCGTGTCTACCGAGTCTGTCTAAGAACACAGAGAGAAATTTAT 3900  
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DB 3961 AGGAATCATACCTTGTAGAGAAACAAATGTTGCTGATGCTGTTTCTTCAAGTGA 4020  
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DB 4021 GTGAATTTGAAGATCTGACGAAATACCAACCCAGATCTTCTGATTTGTTCTT 4080  
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DB 4081 CCAAAACAAATGAGCATCAGTCTGAAAGCCAGGAGTTGCTGAGTCAAGAAATTTGG 4140  
QY 4141 TTTGATGATGATGAAGAAAGAGAAAGGCTTGAAGAAATTAATGAAGAGCAAGAA 4200  
DB 4141 TTTGATGATGATGAAGAAAGAGAAAGGCTTGAAGAAATTAATGAAGAGCAAGAA 4200  
QY 4201 TGGATTTCAAATTAAGTGAAGAGCATCTGGGTGTGAGAGTGAACAAAGCTCTGAGG 4260  
DB 4201 TGGATTTCAAATTAAGTGAAGAGCATCTGGGTGTGAGAGTGAACAAAGCTCTGAGG 4260  
QY 4261 ACTGCTCAGGGCTATCTCTCAGAGTGAATTTAAACAATGAGAGAGATACCATGC 4320  
DB 4261 ACTGCTCAGGGCTATCTCTCAGAGTGAATTTAAACAATGAGAGAGATACCATGC 4320  
QY 4321 AACATTAACCTGAATTAAGCTCCAGAGAGAAATGAGTGAACCTGTTTGAACAGC 4380  
DB 4321 AACATTAACCTGAATTAAGCTCCAGAGAGAAATGAGTGAACCTGTTTGAACAGC 4380  
QY 4381 ATGGAGCAGAGCTTCTAAACAGTACCTTCCATATAGTGAATCTTCTGCTTGAAG 4440  
DB 4381 ATGGAGCAGAGCTTCTAAACAGTACCTTCCATATAGTGAATCTTCTGCTTGAAG 4440  
QY 4441 ACCTCGAAATCCAGAACAAAGCAATCAAGAAAGAGTATTAATTTCAAGAAAGTA 4500  
DB 4441 ACCTCGAAATCCAGAACAAAGCAATCAAGAAAGAGTATTAATTTCAAGAAAGTA 4500  
QY 4501 GTGAATACCTTAAGCCAGAAATCCAGAAAGGCTTCTGCTGACAGAGTTGAGGTTGTCG 4560  
DB 4501 GTGAATACCTTAAGCCAGAAATCCAGAAAGGCTTCTGCTGACAGAGTTGAGGTTGTCG 4560  
QY 4561 CAGATAGTTCTACAGTAAAAATTAAGAACAGAGAGTGAAGAGTCAATCCCTTAAAT 4620

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Db      4561  CAGATAGTTCTACAGTAAATAAAGAACGAGAGTGAAGAAAGTCATCCCTTCTAAAT 4620
Qy      4621  GCGCATCTTTAGATGATAGTGTGTCATGACAGATTGCTCTGGAGTCTTCAGATAGAA 4680
Db      4621  GCGCATCTTTAGATGATAGTGTGTCATGACAGATTGCTCTGGAGTCTTCAGATAGAA 4680
Qy      4681  ACTACCCCTCTCAAGAGAGGCTCATTAAGTGTGTAAGTGTGAGAGCAACAGCTGGAAG 4740
Db      4681  ACTACCCCTCTCAAGAGAGGCTCATTAAGTGTGTAAGTGTGAGAGCAACAGCTGGAAG 4740
Qy      4741  AGTCTGGGCAACAGATTGACGAAACATCTTACTTGGCAAGGCAAGATCTTAGAGGAA 4800
Db      4741  AGTCTGGGCAACAGATTGACGAAACATCTTACTTGGCAAGGCAAGATCTTAGAGGAA 4800
Qy      4801  CCCCTTACCTGGAATCTGGAATCAGCTCTTCTCTGATGACCTGATCTGATCTCTG 4860
Db      4801  CCCCTTACCTGGAATCTGGAATCAGCTCTTCTCTGATGACCTGATCTGATCTCTG 4860
Qy      4861  AAGACAGAGCCCAAGAGTCAAGTGTGTCAGACATACATCTTCAACCTCTGATGGA 4920
Db      4861  AAGACAGAGCCCAAGAGTCAAGTGTGTCAGACATACATCTTCAACCTCTGATGGA 4920
Qy      4921  AAGTTCCTCAATTTGAAGTTGCAAGATCTGCCAGAGTCCAGCTGCTCTCATACTG 4980
Db      4921  AAGTTCCTCAATTTGAAGTTGCAAGATCTGCCAGAGTCCAGCTGCTCTCATACTG 4980
Qy      4981  ATACTGCTGGGTATTAATGCAATGGAAGAAAGTGTGACGAGGAGAAAGCCAGATTGACG 5040
Db      4981  ATACTGCTGGGTATTAATGCAATGGAAGAAAGTGTGACGAGGAGAAAGCCAGATTGACG 5040
Qy      5041  CTTCAACAGAAAGGTCACAAACAAAGATGTCATGATGTCGCTGAGTCCCAAGAG 5100
Db      5041  CTTCAACAGAAAGGTCACAAACAAAGATGTCATGATGTCGCTGAGTCCCAAGAG 5100
Qy      5101  AATTATGCTGCTGATCAAGATTGTCAGAAACACACATCACTTAACTAATCTAATTA 5160
Db      5101  AATTATGCTGCTGATCAAGATTGTCAGAAACACACATCACTTAACTAATCTAATTA 5160
Qy      5161  CTGAAGAGCTATCTATGTTATGAAACAGATGTCGAGTTGTGTGAAAGGAGCAC 5220
Db      5161  CTGAAGAGCTATCTATGTTATGAAACAGATGTCGAGTTGTGTGAAAGGAGCAC 5220
Qy      5221  TGAATATATTTCTAGAAATGCGGAGGAAATGGTGTAGTCTATTTCTGGGTGACCC 5280
Db      5221  TGAATATATTTCTAGAAATGCGGAGGAAATGGTGTAGTCTATTTCTGGGTGACCC 5280
Qy      5281  AGTCTATTTAAAGAAAGAAATGCTGAATGAGCATGATTTGAAGTCAGAGAGATGTGG 5340
Db      5281  AGTCTATTTAAAGAAAGAAATGCTGAATGAGCATGATTTGAAGTCAGAGAGATGTGG 5340
Qy      5341  TCAATGGAAGAAACCAACCAAGTCCAAACCGAGCAAGAGATCCCAAGACAAAGATCT 5400
Db      5341  TCAATGGAAGAAACCAACCAAGTCCAAACCGAGCAAGAGATCCCAAGACAAAGATCT 5400
Qy      5401  TCAGGGGGCTAGAAATCTGTGCTATGAGGCTTCAACCAATGCCCCAGATCAACTGG 5460
Db      5401  TCAGGGGGCTAGAAATCTGTGCTATGAGGCTTCAACCAATGCCCCAGATCAACTGG 5460
Qy      5461  AATGATGTGACAGCTGTGTGTGCTCTGTGTGTAAGAGGCTTTCATCATTCACCTTG 5520
Db      5461  AATGATGTGACAGCTGTGTGTGCTCTGTGTGTAAGAGGCTTTCATCATTCACCTTG 5520
Qy      5521  GCACAGGTGTCACACCAATTTGTGTTGTCAGCAGATGCTGTGACAGAGGCAAGTGGT 5580
Db      5521  GCACAGGTGTCACACCAATTTGTGTTGTCAGCAGATGCTGTGACAGAGGCAAGTGGT 5580
Qy      5581  TCCATGCAATTTGGGAGAGATGTGTGAGGACCTGTGGTGAACCCGAGAGTGGGTGGACA 5640
Db      5581  TCCATGCAATTTGGGAGAGATGTGTGAGGACCTGTGGTGAACCCGAGAGTGGGTGGACA 5640
Qy      5641  GTGTAGCACTTACAGAGTCCAGAGCTGACACCTTACTGATACCCAGATCCCCACA 5700

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Db      5641  GTGTAGCACTTACAGAGTCCAGAGAGTGCAGACCTAATGATACCCAGATCCCCACA 5700
Qy      5701  GCGACTACTGA 5711
Db      5701  GCGACTACTGA 5711

RESULT 13
AR184044
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DEFINITION Sequence 47 from patent US 6342483.
ACCESSION AR184044
VERSION AR184044.1 GI:20228013
KEYWORDS
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 5712)
AUTHORS     Holt,J.T., Jensen,R.A., Page,D.L., Obermiller,P.S.,
            Robinson-Bentley,C.L. and Thompson,M.E.
TITLE       Method for detection and treatment of breast cancer
JOURNAL     Patent: US 6342483-A 47 29-JUN-2002;
            Location/Qualifiers
FEATURES
source      1..5712
            /organism="unknown"
BASE COUNT  1956 a 1099 c 1274 g 1383 t
ORIGIN
Query Match 99.8%; Score 5699.8; DB 6; Length 5712;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 5704; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy      1  AGCTGCTGAGACCTTCTGAGACCCCGACAGGCTGTGGGTTCTCAGATTAATGAGGCC 60
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Qy      61  CTTGGCTCAGAGAGGCTTCACTCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
Db      61  CTTGGCTCAGAGAGGCTTCACTCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
Qy      121  TGGATTTATCTGCTCTTCTGCGTTGAGAGAGTACAAATGTCATTAATGCTATGAGAAA 180
Db      121  TGGATTTATCTGCTCTTCTGCGTTGAGAGAGTACAAATGTCATTAATGCTATGAGAAA 180
Qy      181  TCTTGAAGTGTCCATCTGCTGAGAGTATCAAGAACTGTCTCCAGAAAGTGTGACC 240
Db      181  TCTTGAAGTGTCCATCTGCTGAGAGTATCAAGAACTGTCTCCAGAAAGTGTGACC 240
Qy      241  ACATATTTTGAAGAAATTTGCAATGCTGAATCTTCAACAGAGAAAGGCTTTCACAGT 300
Db      241  ACATATTTTGAAGAAATTTGCAATGCTGAATCTTCAACAGAGAAAGGCTTTCACAGT 300
Qy      301  GTCTTTATGTAAGATGATTAACCAAAAGAGCTTCAAGAAAGTACAGATTTAGTC 360
Db      301  GTCTTTATGTAAGATGATTAACCAAAAGAGCTTCAAGAAAGTACAGATTTAGTC 360
Qy      361  AACTGTGGAAGAGCTATTTGAAGTCAATTTGCTTTTCAAGTCAACAGAGTTGAGT 420
Db      361  AACTGTGGAAGAGCTATTTGAAGTCAATTTGCTTTTCAAGTCAACAGAGTTGAGT 420
Qy      421  ATGCAACAGCTATTAATTTTGAAGAAAGAAATTAATCTCTCTGAACATCTAAAGATG 480
Db      421  ATGCAACAGCTATTAATTTTGAAGAAAGAAATTAATCTCTCTGAACATCTAAAGATG 480
Qy      481  AAGTTTCTATCATCAAGATATGAGGCTACAGAAACGCTGCAAAAGACTTCAAGAGTG 540
Db      481  AAGTTTCTATCATCAAGATATGAGGCTACAGAAACGCTGCAAAAGACTTCAAGAGTG 540
Qy      541  AACCAGAAATCTCTCTGTCAGAGAAACAGTCTCAGTGTCAACTCTTAACTTGAAG 600
Db      541  AACCAGAAATCTCTCTGTCAGAGAAACAGTCTCAGTGTCAACTCTTAACTTGAAG 600
Qy      601  CTGTGAGAACTCTGAGGACAAAGGAGGATACAACTCAAAAGAGCTGTCTAATTTG 660

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Db 601 CTGTGGAACCTCGAGAGCAAAAGCAGCGGATACAACTCAAAAGAGTCTGTCTACATGG 660  
Qy 661 AATTGGATCTGATCTTCTCGAAGATACGGTTAATAAGCACTTATTCGAGTGGGAG 720  
Db 661 AATTGGATCTGATCTTCTCGAAGATACGGTTAATAAGCACTTATTCGAGTGGGAG 720  
Qy 721 ATCAAGATTTGTAACAATCACCCCTCAAGGAACGAGGATGAATCAGTTGATTCG 780  
Db 721 ATCAAGATTTGTAACAATCACCCCTCAAGGAACGAGGATGAATCAGTTGATTCG 780  
Qy 781 CAAAAAGGCTGCTTGTAATTTTCTGAGACGAGATGTAACAATCTGAAATCATCAAC 840  
Db 781 CAAAAAGGCTGCTTGTAATTTTCTGAGACGAGATGTAACAATCTGAAATCATCAAC 840  
Qy 841 CCGATTAATAATGATTTTGAACACCACTGAGAGGCTGAGTGAGGATCCGAAAGT 900  
Db 841 CCGATTAATAATGATTTTGAACACCACTGAGAGGCTGAGTGAGGATCCGAAAGT 900  
Qy 901 ATCAGGATAGTCTGTTTCAAACTTGATGAGGCAATGAGCAAAATCTCATGCCA 960  
Db 901 ATCAGGATAGTCTGTTTCAAACTTGATGAGGCAATGAGCAAAATCTCATGCCA 960  
Qy 961 GCTCATTAAGCAGTGAAGACAGCAGTTTATTCTCACTAAAGACAGATGATGAGAA 1020  
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Qy 1021 AGGCTAAATTCGTATTAATAAGCAAGCCTGGCTTAGACAGAGCCCAATACAGAT 1080  
Db 1021 AGGCTAAATTCGTATTAATAAGCAAGCCTGGCTTAGACAGAGCCCAATACAGAT 1080  
Qy 1081 GGGCTGAAGTGAAGAAACATGTAATGATAGCGGATCCGAGCAGAGAAAAAGTAG 1140  
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Db 4441 ACTGCGAAATCCAGAAACAAACATCAAGAAAGCACTATTAATTCAAGAAAGTA 4500  
QY 4501 GTGAATACCCCTTAAGCCAGAAATCCAGAAAGGCTTTCTGCTGAACAAGTTGAGTCTG 4560  
Db 4501 GTGAATACCCCTTAAGCCAGAAATCCAGAAAGGCTTTCTGCTGAACAAGTTGAGTCTG 4560  
QY 4561 CAGATAGTTCTACAGTAATAAATAAAGAACAGAGTGAAGAGTCAATCCCTTCAAT 4620  
Db 4561 CAGATAGTTCTACAGTAATAAATAAAGAACAGAGTGAAGAGTCAATCCCTTCAAT 4620  
QY 4621 GCCCATCATTAATGATGATGAGTGTACATGCAAGTTGCTTGGAGTCTTCAAGATGA 4680  
Db 4621 GCCCATCATTAATGATGATGAGTGTACATGCAAGTTGCTTGGAGTCTTCAAGATGA 4680  
QY 4681 ACTACCATCTCAAGAGAGCTCATTAAGGTTGTTGATGAGAGGCAACAGCTGGA 4740  
Db 4681 ACTACCATCTCAAGAGAGCTCATTAAGGTTGTTGATGAGAGGCAACAGCTGGA 4740  
QY 4741 AGCTGGGCGACAGATTTGAGGAAACATCTTACTTGGCAAGGCAAGATCTAGAGGA 4800  
Db 4741 AGCTGGGCGACAGATTTGAGGAAACATCTTACTTGGCAAGGCAAGATCTAGAGGA 4800  
QY 4801 CCCCTTACTGGAATCTGGAATCAGCCTTTCTTGATGACCTGATCTGATCTTCTG 4860  
Db 4801 CCCCTTACTGGAATCTGGAATCAGCCTTTCTTGATGACCTGATCTGATCTTCTG 4860  
QY 4861 AAGACAGAGCCCCCAGAGTACGCTGTTGGCAATACATCTTCAACTCTGCACTGA 4920  
Db 4861 AAGACAGAGCCCCCAGAGTACGCTGTTGGCAATACATCTTCAACTCTGCACTGA 4920  
QY 4921 AAGTTCCCAATTTGAAGTTGAGAACTGCCCAGAGTCCAGTCTGCTCACTACTG 4980  
Db 4921 AAGTTCCCAATTTGAAGTTGAGAACTGCCCAGAGTCCAGTCTGCTCACTACTG 4980  
QY 4981 ATACTGCTGGTATTAATGCAATGGAAGAAAGTGTAGCAGGAGAAAGCCAGAAATGAC 5040  
Db 4981 ATACTGCTGGTATTAATGCAATGGAAGAAAGTGTAGCAGGAGAAAGCCAGAAATGAC 5040  
QY 5041 CTTCAACAGAAAGGCTCAACAAAGATGTCATGCTGCTGCTGAGCCGACCCAGAG 5100  
Db 5041 CTTCAACAGAAAGGCTCAACAAAGATGTCATGCTGCTGCTGAGCCGACCCAGAG 5100  
QY 5101 AATTTATGCTCGTGTACAAATTTGCGAGAAACACCAATCACTTAACTAATTA 5160  
Db 5101 AATTTATGCTCGTGTACAAATTTGCGAGAAACACCAATCACTTAACTAATTA 5160  
QY 5161 CTGAAGAGACTACTATGTTGTTATGAACAGATGCTGAGTTGTGTGAACGACAC 5220  
Db 5161 CTGAAGAGACTACTATGTTGTTATGAACAGATGCTGAGTTGTGTGAACGACAC 5220  
QY 5221 TGAATATTTTCTAGAAATTTGGGAGGAAATGGGTGTTGTAATTTCTGGGTGACCC 5280  
Db 5221 TGAATATTTTCTAGAAATTTGGGAGGAAATGGGTGTTGTAATTTCTGGGTGACCC 5280  
QY 5281 AGCTATTTAAAGAAAGAAATGCTGAATGAGCATGATTTTGAAGTCAAGAGATGTGG 5340  
Db 5281 AGCTATTTAAAGAAAGAAATGCTGAATGAGCATGATTTTGAAGTCAAGAGATGTGG 5340  
QY 5341 TCAATGGAAGAAACCAAGGTTCCAAAGCCAGCAAGAAATCCAGAGCAGAAAGATCT 5400  
Db 5341 TCAATGGAAGAAACCAAGGTTCCAAAGCCAGCAAGAAATCCAGAGCAGAAAGATCT 5400

|    |      |  |      |
|----|------|--|------|
| Qy | 5401 | TCAGGGGGCTAGAAATCTGTTCTCATATGGGCCCTTACCACAACTGGCCACAGATCAACTGG | 5460 |
| Db | 5401 | TCAGGGGGCTAGAAATCTGTTCTCATATGGGCCCTTACCACAACTGGCCACAGATCAACTGG | 5460 |
| Qy | 5461 | AATGATGATGACAGCTGTGTGTGCTTCTGTGTGACAGAGCTTTCATCATTCACCTTG      | 5520 |
| Db | 5461 | AATGATGATGACAGCTGTGTGTGCTTCTGTGTGACAGAGCTTTCATCATTCACCTTG      | 5520 |
| Qy | 5521 | GCACAGGTGTCCACCCTAATTGTGTGTGTGTGCAGCCAGATGCTCGACAGAGGACATGTGCT | 5580 |
| Db | 5521 | GCACAGGTGTCCACCCTAATTGTGTGTGTGTGCAGCCAGATGCTCGACAGAGGACATGTGCT | 5580 |
| Qy | 5581 | TCCATGCAATTGGGCGAGATGTGTGAGGCCACCTGTGTGTACCCGAGAGTGGGTGTGGACA  | 5640 |
| Db | 5581 | TCCATGCAATTGGGCGAGATGTGTGAGGCCACCTGTGTGTACCCGAGAGTGGGTGTGGACA  | 5640 |
| Qy | 5641 | GTGTGCACTCTACACAGTGCACGAGAGCTGCACACTACTGTGATACCCAGATCCCCACACA  | 5700 |
| Db | 5641 | GTGTGCACTCTACACAGTGCACGAGAGCTGCACACTACTGTGATACCCAGATCCCCACACA  | 5700 |
| Qy | 5701 | GCCACTACTGA 5711   |      |
| Db | 5701 | GCCACTACTGA 5711   |      |

|            |                                    |            |        |
|------------|------------------------------------|------------|--------|
| RESULT 15  |                                    |            |        |
| AR008159   |                                    |            |        |
| LOCUS      | AR008159                           | 5914 bp    | DNA    |
| DEFINITION | Sequence 1 from patent US 5753441. |            | linear |
| ACCESSION  | AR008159                           |            |        |
| VERSION    | AR008159.1                         | GI:3967268 |        |

| ORGANISM  | Unknown.   |
|-----------|--|
| REFERENCE | Unclassified.  |
| AUTHORS   | 1 (bases 1 to 5914)  |
| TITLE     | Skolnick, K.H., Goldgar, D.E., Miki, Y., Swenson, J., Kamb, A., Harshman, M.D., Shattuck-Eidens, D.M., Tavtiglian, S.V., Wiseman, R.W. and Futreal, P. Andrew. |
| JOURNAL   | 170-linked breast and ovarian cancer susceptibility gene   |
| FEATURES  | Patent: US 5753441-A 1.19-MAY-1998;  |
| source    | Location/Qualifiers  |
|           | 1..5914  |

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/organism="unknown"
BASE COUNT      2006 a      1156 c      1316 g      1436 t
ORIGIN

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|                       |                |              |          |             |
|-----------------------|----------------|--------------|----------|-------------|
| Query Match           | 99.8%          | Score 5699.8 | DB 6     | Length 5914 |
| Best Local Similarity | 99.9%          | Pred. No. 0  |          |             |
| Matches 5704          | Conservative 0 | Mismatches 7 | Indels 0 | Gaps 0      |

|    |     |  |     |
|----|-----|--|-----|
| OY | 1   | AGCTGCGTAGAGCTTCCTGGAAACCCGACACAGGCGTGGGGGTTCTCAGATPAACCTGGGCC | 60  |
| Db | 1   | AGCTGCGTAGAGCTTCCTGGAAACCCGACACAGGCGTGGGGGTTCTCAGATPAACCTGGGCC | 60  |
| OY | 61  | CCTGCGCTCAGAGAGCCTTCACCCCTCTGCTCTGGGTAAAGTTCAATTGGAACAGAAAGAAA | 120 |
| Db | 61  | CCTGCGCTCAGAGAGCCTTCACCCCTCTGCTCTGGGTAAAGTTCAATTGGAACAGAAAGAAA | 120 |
| OY | 121 | TGGATTATCTGCTCTTTGGCGTTGAAAGAGTCAAAATGTCAATTAAGTATGCAGAAA      | 180 |
| Db | 121 | TGGATTATCTGCTCTTTGGCGTTGAAAGAGTCAAAATGTCAATTAAGTATGCAGAAA      | 180 |
| OY | 181 | TCTTAGAGTGTCCTCATCTGTCTGGAGTTGATCAAGAAACCTGTCCACAAAGTGTGACC    | 240 |
| Db | 181 | TCTTAGAGTGTCCTCATCTGTCTGGAGTTGATCAAGAAACCTGTCCACAAAGTGTGACC    | 240 |
| OY | 241 | ACATATTTTTCGAAATTTTTCATGCTGAAACCTTCTCAACGAGAAGAAAGGCGCTTCACAGT | 300 |
| Db | 241 | ACATATTTTTCGAAATTTTTCATGCTGAAACCTTCTCAACGAGAAGAAAGGCGCTTCACAGT | 300 |
| OY | 301 | GTCCTTATGTGAAGATGATATACCAAAAGAGCGCTACAGAAAGTACGAGATTAGTC       | 360 |
| Db | 301 | GTCCTTATGTGAAGATGATATACCAAAAGAGCGCTACAGAAAGTACGAGATTAGTC       | 360 |

|    |      |   |      |
|----|------|---|------|
| Dp | 301  | GTCCCTTAATGTAAGAAATGATATTAACCAAAAAGACCTTACAAGAAAGTACAGGATTTGATC   | 360  |
| Oy | 361  | AACCTGTGAAGACCTATGGAATCAATTTGTGCTTTTCAGCTTGACACAGCTTTGAGT         | 420  |
| Dp | 361  | AACCTGTGAAGACCTATGGAATCAATTTGTGCTTTTCAGCTTGACACAGCTTTGAGT         | 420  |
| Oy | 421  | ATGCAAAACAGCTATAATTTTGCAAAAAGAAAAATTAACCTCTCTGAACATCTTAAGAATG     | 480  |
| Dp | 421  | ATGCAAAACAGCTATAATTTTGCAAAAAGAAAAATTAACCTCTCTGAACATCTTAAGAATG     | 480  |
| Oy | 481  | AAGTTTCTATATCCAAAGTATGGGCTACAGAAACCGTGCCAAAAGACTTCTACAGAGTG       | 540  |
| Dp | 481  | AAGTTTCTATATCCAAAGTATGGGCTACAGAAACCGTGCCAAAAGACTTCTACAGAGTG       | 540  |
| Oy | 541  | AAACCGAAAAATCCCTTCCCTGAGAGAAACCAAGTCTCAGTGTCCAACCTCTTAACCTTGAA    | 600  |
| Dp | 541  | AAACCGAAAAATCCCTTCCCTGAGAGAAACCAAGTCTCAGTGTCCAACCTCTTAACCTTGAA    | 600  |
| Oy | 601  | CTGTGAGAACTCTGAGAGCAAAAGCAGCGGATACAACTCAAAAGACCTCTGTCTACATTG      | 660  |
| Dp | 601  | CTGTGAGAACTCTGAGAGCAAAAGCAGCGGATACAACTCAAAAGACCTCTGTCTACATTG      | 660  |
| Oy | 661  | AATTGGATCTGATTTCTTCTGAAATACCTGTAATTAAGGCAACTATTTGCAAGTGTGGAG      | 720  |
| Dp | 661  | AATTGGATCTGATTTCTTCTGAAATACCTGTAATTAAGGCAACTATTTGCAAGTGTGGAG      | 720  |
| Oy | 721  | ATCAAGAATTTGTTCAAAATCACCCCTCAAGGAAACAGGGAATGAATCAGTTTGGATTCTG     | 780  |
| Dp | 721  | ATCAAGAATTTGTTCAAAATCACCCCTCAAGGAAACAGGGAATGAATCAGTTTGGATTCTG     | 780  |
| Oy | 781  | CAAAAAAGGCTGCTTGTGGAATTTTCTGAGACGGAATGTAACAAATACGAAACATCATATAC    | 840  |
| Dp | 781  | CAAAAAAGGCTGCTTGTGGAATTTTCTGAGACGGAATGTAACAAATACGAAACATCATATAC    | 840  |
| Oy | 841  | CCAGTAAATTAATGATTTTGAACACCACTGAGAAACCGTGCAGCTGAGAGGCATTCAGAAAAAGT | 900  |
| Dp | 841  | CCAGTAAATTAATGATTTTGAACACCACTGAGAAACCGTGCAGCTGAGAGGCATTCAGAAAAAGT | 900  |
| Oy | 901  | ATCAGGGTAGTTCCTGTTTCAAACTTGTCATGTGAGCCATGTGGACAAATATCTATGCCA      | 960  |
| Dp | 901  | ATCAGGGTAGTTCCTGTTTCAAACTTGTCATGTGAGCCATGTGGACAAATATCTATGCCA      | 960  |
| Oy | 961  | GCTCATTTACAGCATGAGAAACAGCACTTTATTTACTCACTAAAGACAGATGATTAAGAAA     | 1020 |
| Dp | 961  | GCTCATTTACAGCATGAGAAACAGCACTTTATTTACTCACTAAAGACAGATGATTAAGAAA     | 1020 |
| Oy | 1021 | AGGCTGAATTTCTGTATTAAGCAAAACAGCCCTGCTTAGCAAGGAGCCAAATATACAGAT      | 1080 |
| Dp | 1021 | AGGCTGAATTTCTGTATTAAGCAAAACAGCCCTGCTTAGCAAGGAGCCAAATATACAGAT      | 1080 |
| Oy | 1081 | GGGCTGGAAGTAAAGAAACATGTAAATGATATAGCGCGAATCCACAGACAGAAAAAAGGTAG    | 1140 |
| Dp | 1081 | GGGCTGGAAGTAAAGAAACATGTAAATGATATAGCGCGAATCCACAGACAGAAAAAAGGTAG    | 1140 |
| Oy | 1141 | ATCTGAATGCGATCCCCCTGTGTGAGAGAAAAAGATGGAATTAAGCAGAAAAATGCGCATCT    | 1200 |
| Dp | 1141 | ATCTGAATGCGATCCCCCTGTGTGAGAGAAAAAGATGGAATTAAGCAGAAAAATGCGCATCT    | 1200 |
| Oy | 1201 | CAGAGAAATCTAGAGATCTGAAAGATGTTCTCTTGATTAACAATAATAGCAGCATTCAGA      | 1260 |
| Dp | 1201 | CAGAGAAATCTAGAGATCTGAAAGATGTTCTCTTGATTAACAATAATAGCAGCATTCAGA      | 1260 |
| Oy | 1261 | AAGTTAATGAGTGTATTTCCAGAAAGATGAACCTGTAGGTTCTGATGACTCAGCATGATG      | 1320 |
| Dp | 1261 | AAGTTAATGAGTGTATTTCCAGAAAGATGAACCTGTGTAGGTTCTGATGACTCAGCATGATG    | 1320 |
| Oy | 1321 | GGGAGTCTGAATCAAAATCCAAAGTACGTATGATGACGTTCTAAATAGAGTATGATG         | 1380 |
| Dp | 1321 | GGGAGTCTGAATCAAAATCCAAAGTACGTATGATGACGTTCTAAATAGAGTATGATG         | 1380 |
| Oy | 1381 | AATTTCTGCTTCTTCAGAGAAAAATACATTTACGCGCAATGATCCCATGAGGCTTTAA        | 1440 |
| Dp | 1381 | AATTTCTGCTTCTTCAGAGAAAAATACATTTACGCGCAATGATCCCATGAGGCTTTAA        | 1440 |



|    |      |  |      |
|----|------|--|------|
| QY | 1441 | TATGTAAAGGAAAAGACTTCATCCCAATCAGTAGAGAGATTAATTGGAACAATAAT         | 1500 |
| Db | 1441 | TATGTAAAGGAAAAGACTTCATCCCAATCAGTAGAGAGATTAATTGGAACAATAAT         | 1500 |
| QY | 1501 | TTGGGAAAACCTATCGAAGAAAGGCAAGCCTCCCACTTAAGCATTGACTGAATAATC        | 1560 |
| Db | 1501 | TTGGGAAAACCTATCGAAGAAAGGCAAGCCTCCCACTTAAGCATTGACTGAATAATC        | 1560 |
| QY | 1561 | TAAATTATGGAGCATTTTGTTACTGAGCCACAGATTAATCANAAGCTCCCTCAATAA        | 1620 |
| Db | 1561 | TAAATTATGGAGCATTTTGTTACTGAGCCACAGATTAATCANAAGCTCCCTCAATAA        | 1620 |
| QY | 1621 | AATTAAACGTAAGAAAGAGACCTTCATAGAGCCTTCACTCGAAGATTTTATCAAGAAAG      | 1680 |
| Db | 1621 | AATTAAACGTAAGAAAGAGACCTTCATAGAGCCTTCACTCGAAGATTTTATCAAGAAAG      | 1680 |
| QY | 1681 | CAGATTTTGGCAGTTCAAAAGAATCCCTGTAATGATTAATCAGGGAATTAACCAACGAGNC    | 1740 |
| Db | 1681 | CAGATTTTGGCAGTTCAAAAGAATCCCTGTAATGATTAATCAGGGAATTAACCAACGAGNC    | 1740 |
| QY | 1741 | AGAATGGTCAGTGAATGAATTAATTAAGTGGTCATGAGAAATTAACAAAGGTGATT         | 1800 |
| Db | 1741 | AGAATGGTCAGTGAATGAATTAATTAAGTGGTCATGAGAAATTAACAAAGGTGATT         | 1800 |
| QY | 1801 | CTATTTCGAATAGAGAAAAAATCTTAACCCAAATAGAAATCTCGAAAAAGAAATCTGTTCA    | 1860 |
| Db | 1801 | CTATTTCGAATAGAGAAAAAATCTTAACCCAAATAGAAATCTCGAAAAAGAAATCTGTTCA    | 1860 |
| QY | 1861 | AAACGAAAGCTGAACCTTAAGACAGCATTAAGCAATATGGAATCTGAATTAATATCC        | 1920 |
| Db | 1861 | AAACGAAAGCTGAACCTTAAGACAGCATTAAGCAATATGGAATCTGAATTAATATCC        | 1920 |
| QY | 1921 | ACAATTTCAAAGCACTTAAAAAGATAGGCTGAGAGAGAAAGTCTTCAACGAGCATATTC      | 1980 |
| Db | 1921 | ACAATTTCAAAGCACTTAAAAAGATAGGCTGAGAGAGAAAGTCTTCAACGAGCATATTC      | 1980 |
| QY | 1981 | ATGCGCTTGAACCTAGTAGTCAGTAGAAATCTAAGCCCACTTAATTTGTACTGAATTGGCAA   | 2040 |
| Db | 1981 | ATGCGCTTGAACCTAGTAGTCAGTAGAAATCTAAGCCCACTTAATTTGTACTGAATTGGCAA   | 2040 |
| QY | 2041 | TTGATATGATGTTTCTAGACGTAGTAAGAAAGATTAAGAAAAAAAGTACAACCAATGGCACTCA | 2100 |
| Db | 2041 | TTGATATGATGTTTCTAGACGTAGTAAGAAAGATTAAGAAAAAAAGTACAACCAATGGCACTCA | 2100 |
| QY | 2101 | GGCAGCAGCAAAACCTCAACACTCAATGGAAGGTAAAGAACTCGCAACTGAGCCCAAGAGA    | 2160 |
| Db | 2101 | GGCAGCAGCAAAACCTCAACACTCAATGGAAGGTAAAGAACTCGCAACTGAGCCCAAGAGA    | 2160 |
| QY | 2161 | GTAACCAAGCCCAATGAAACAGACAAAGTAAGAATGACATGACATGTAATCTTCCAGAGCTGA  | 2220 |
| Db | 2161 | GTAACCAAGCCCAATGAAACAGACAAAGTAAGAATGACATGACATGTAATCTTCCAGAGCTGA  | 2220 |
| QY | 2221 | AGTTAAACAAATGACACCTGTTCTTTTACTAGTGTCAAAATACCAAGTAACTTTAAAGAT     | 2280 |
| Db | 2221 | AGTTAAACAAATGACACCTGTTCTTTTACTAGTGTCAAAATACCAAGTAACTTTAAAGAT     | 2280 |
| QY | 2281 | TTGTCAATCTAGCCTTGCAGAGAGAAAGAAAGAAAGAACTAGAAACAGTTAAAGTGT        | 2340 |
| Db | 2281 | TTGTCAATCTAGCCTTGCAGAGAGAAAGAAAGAAAGAACTAGAAACAGTTAAAGTGT        | 2340 |
| QY | 2341 | CTAATTAATGCTGAAGAGACCCCAAAATCTCAAGTTAAGTGAAGGAAGGGTTTGGAACTG     | 2400 |
| Db | 2341 | CTAATTAATGCTGAAGAGACCCCAAAATCTCAAGTTAAGTGAAGGAAGGGTTTGGAACTG     | 2400 |
| QY | 2401 | AAAGATCTGTAGAGAGTAGCAGTATTTCACTGTACTCTGTACTGATTAATGCACTCAGG      | 2460 |
| Db | 2401 | AAAGATCTGTAGAGAGTAGCAGTATTTCACTGTACTCTGTACTGATTAATGCACTCAGG      | 2460 |
| QY | 2461 | AAAGATCTCTTACTGGAATTTAGCACTTAGGGAAGGCAAAAACGAACCAATTAAT          | 2520 |
| Db | 2461 | AAAGATCTCTTACTGGAATTTAGCACTTAGGGAAGGCAAAAACGAACCAATTAAT          | 2520 |

|    |      |  |      |
|----|------|--|------|
| QY | 2521 | ATGAGAGTCAGTGGGACGACATTTGAAAAACCCCAAGGGGCTTAATTCATGCTGTTCCAAAG   | 2580 |
| Db | 2521 | GTGGAGTCAGTGGACGACATTTGAAAAACCCCAAGGGGCTTAATTCATGCTGTTCCAAAG     | 2580 |
| QY | 2581 | ATAATAGAAATGACACAGAGAGCTTTAAAGTATCCATTGGGACATGAAGTTAAACACAGTC    | 2640 |
| Db | 2581 | ATAATAGAAATGACACAGAGAGCTTTAAAGTATCCATTGGGACATGAAGTTAAACACAGTC    | 2640 |
| QY | 2641 | GGGAAACAGCATAGAAATGGAGAAGAGTGAATGCTCAGTATTTGCAGAAATCAT           | 2700 |
| Db | 2641 | GGGAAACAGCATAGAAATGGAGAAGAGTGAATGCTCAGTATTTGCAGAAATCAT           | 2700 |
| QY | 2701 | TCAAGGTTTCAAAACCGCCAGTCATTTTGCTCTGTTTCCAAATCCAGGAAATGCAGAAAGG    | 2760 |
| Db | 2701 | TCAAGGTTTCAAAACCGCCAGTCATTTTGCTCTGTTTCCAAATCCAGGAAATGCAGAAAGG    | 2760 |
| QY | 2761 | AATGTGCAACATTCCTGCGCCACTCTGGGTCCTTAAAGAAACAAAGTCCAAAGATCACTT     | 2820 |
| Db | 2761 | AATGTGCAACATTCCTGCGCCACTCTGGGTCCTTAAAGAAACAAAGTCCAAAGATCACTT     | 2820 |
| QY | 2821 | TTGAATGTGAACAAAGGAGAGAAATCAAGGAAAGAAATGAGTCTAATATATCAAGCTGTAC    | 2880 |
| Db | 2821 | TTGAATGTGAACAAAGGAGAGAAATCAAGGAAAGAAATGAGTCTAATATATCAAGCTGTAC    | 2880 |
| QY | 2881 | AGACAGTTAATATCACTGTCAGGCTTTCTGTGCTGTGTCAGAAAGATATAGCCAGTTGATA    | 2940 |
| Db | 2881 | AGACAGTTAATATCACTGTCAGGCTTTCTGTGCTGTGTCAGAAAGATATAGCCAGTTGATA    | 2940 |
| QY | 2941 | ATGCCAAATGAGTATCAAAAGAGAGCTTAGGTTTGTCTCATCTCAGTTCAGAGGCA         | 3000 |
| Db | 2941 | ATGCCAAATGAGTATCAAAAGAGAGCTTAGGTTTGTCTCATCTCAGTTCAGAGGCA         | 3000 |
| QY | 3001 | ACGAAATCGAGCTCATTAATCTCAAAATAAACATGAGACTTTTAAACAAACCCATATGCTATAC | 3060 |
| Db | 3001 | ACGAAATCGAGCTCATTAATCTCAAAATAAACATGAGACTTTTAAACAAACCCATATGCTATAC | 3060 |
| QY | 3061 | CACCACTTTTCCCATCAAGTCATTTGTGTTAAACCTAATGTAGAAAAATCTGTAAGG        | 3120 |
| Db | 3061 | CACCACTTTTCCCATCAAGTCATTTGTGTTAAACCTAATGTAGAAAAATCTGTAAGG        | 3120 |
| QY | 3121 | AAAACTTTGAGGAACATTCATATGTCACCTGAAAGAGAAATGGGAAATGAGAACATTCGCA    | 3180 |
| Db | 3121 | AAAACTTTGAGGAACATTCATATGTCACCTGAAAGAGAAATGGGAAATGAGAACATTCGCA    | 3180 |
| QY | 3181 | GTACAGTGGACACATTAGCCGTAAATAACATTTAGAGAAATGTTTTTAAAGSAGCCAGCT     | 3240 |
| Db | 3181 | GTACAGTGGACACATTAGCCGTAAATAACATTTAGAGAAATGTTTTTAAAGSAGCCAGCT     | 3240 |
| QY | 3241 | CAAGCAATATTTAAAGAGTAGGTTCAGTACTAATGAAAGGGGCTCCAGTATTTAATGAA      | 3300 |
| Db | 3241 | CAAGCAATATTTAAAGAGTAGGTTCAGTACTAATGAAAGGGGCTCCAGTATTTAATGAA      | 3300 |
| QY | 3301 | TAGGTTCCAGTAGAAGAAACATTCACACAGAACTAGGTAGAAACAGAGGGCCAAATTTGA     | 3360 |
| Db | 3301 | TAGGTTCCAGTAGAAGAAACATTCACACAGAACTAGGTAGAAACAGAGGGCCAAATTTGA     | 3360 |
| QY | 3361 | ATGCTATGCTTAGATTAGGGGTTTTGCAACCTGAGGCTCTAATAACAAAGCTCTTCTGGAA    | 3420 |
| Db | 3361 | ATGCTATGCTTAGATTAGGGGTTTTGCAACCTGAGGCTCTAATAACAAAGCTCTTCTGGAA    | 3420 |
| QY | 3421 | GTAATTTGATGATCTCTGAAAATTAAGAACAGAGATATGAAAGAGTATGTTCCAGCTGTTA    | 3480 |
| Db | 3421 | GTAATTTGATGATCTCTGAAAATTAAGAACAGAGATATGAAAGAGTATGTTCCAGCTGTTA    | 3480 |
| QY | 3481 | ATACAGATTTCTCTCCATATCTGATTTCCATATTACTTAGAACAGCCATATGGGAAAGTAGTC  | 3540 |
| Db | 3481 | ATACAGATTTCTCTCCATATCTGATTTCCATATTACTTAGAACAGCCATATGGGAAAGTAGTC  | 3540 |
| QY | 3541 | ATGCATCTCAAGGTTGTGTTCTGAGACACCTGATGACCTGTTAAGATGAGTGTAATTAAGG    | 3600 |
| Db | 3541 | ATGCATCTCAAGGTTGTGTTCTGAGACACCTGATGACCTGTTAAGATGAGTGTAATTAAGG    | 3600 |
| QY | 3601 | AAGATCTAGTTTTGCTGAAAATGACATTAAGGAAGTCTGCTGTTTTTAACAAAAACGC       | 3660 |

Db 3601 AAGATACGATTTTCTGTAATGATGATTAAGAAAGTTCTCTGTTTACGAAAGG 3660  
 Qy 3661 TCCAGAGAGAGAGCTTAGCAGAGAGCTTACGCTTTTACCAATACATTTGGCTCAG 3720  
 Db 3661 TCCAGAAAGAGAGAGCTTAGCAGAGAGCTTACGCTTTTACCAATACATTTGGCTCAG 3720  
 Qy 3721 GTTACCGAGAGAGAGAGCTTAGCAGAGAGCTTACGAGAGAGCTTACGAGAGAG 3780  
 Db 3721 GTTACCGAGAGAGAGAGCTTAGCAGAGAGCTTACGAGAGAGCTTACGAGAGAG 3780  
 Qy 3781 AAGAGCTTCCCTGCTTCCAAACCTTGTATTTGTAAATTAATATACCTTCTCAGT 3840  
 Db 3781 AAGAGCTTCCCTGCTTCCAAACCTTGTATTTGTAAATTAATATACCTTCTCAGT 3840  
 Qy 3841 CTACTAGGAGAGAGAGCTTACGAGAGAGCTTACGAGAGAGCTTACGAGAGAG 3900  
 Db 3841 CTACTAGGAGAGAGAGCTTACGAGAGAGCTTACGAGAGAGCTTACGAGAGAG 3900  
 Qy 3901 TATCATTTGAAGAAATAGCTTAATATGATGATGATGATGATGATGATGATGATG 3960  
 Db 3901 TATCATTTGAAGAAATAGCTTAATATGATGATGATGATGATGATGATGATGATG 3960  
 Qy 3961 AGGAACATCACCTTAGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4020  
 Db 3961 AGGAACATCACCTTAGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4020  
 Qy 4021 GTGAATTTGAAG 4080  
 Db 4021 GTGAATTTGAAG 4080  
 Qy 4081 CCAAAACAAATGAG 4140  
 Db 4081 CCAAAACAAATGAG 4140  
 Qy 4141 TTTGAGATGATGAG 4200  
 Db 4141 TTTGAGATGATGAG 4200  
 Qy 4201 TGGATTTCAAATCTAGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4260  
 Db 4201 TGGATTTCAAATCTAGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4260  
 Qy 4261 ACTGCTGAG 4320  
 Db 4261 ACTGCTGAG 4320  
 Qy 4321 AACATTAACCTGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4380  
 Db 4321 AACATTAACCTGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4380  
 Qy 4381 ATGGAG 4440  
 Db 4381 ATGGAG 4440  
 Qy 4441 ACCGCGAG 4500  
 Db 4441 ACCGCGAG 4500  
 Qy 4501 GTGAATACCTGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4560  
 Db 4501 GTGAATACCTGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4560  
 Qy 4561 CAGATAG 4620  
 Db 4561 CAGATAG 4620  
 Qy 4621 GCCCATCTTGAAG 4680  
 Db 4621 GCCCATCTTGAAG 4680  
 Qy 4681 ACTACCATCTTGAAG 4740  
 Db 4681 ACTACCATCTTGAAG 4740

Db 4681 ACTACCATCTTGAAG 4740  
 Qy 4741 AGTCTGGGAG 4800  
 Db 4741 AGTCTGGGAG 4800  
 Qy 4801 CCCCTTACCTGAG 4860  
 Db 4801 CCCCTTACCTGAG 4860  
 Qy 4861 AAGACAG 4920  
 Db 4861 AAGACAG 4920  
 Qy 4921 AAGTCTGGGAG 4980  
 Db 4921 AAGTCTGGGAG 4980  
 Qy 4981 ATACTGCTGGGAG 5040  
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 12, 2003, 23:57:10 / Search time 283 Seconds

(without alignments)  
6188.802 Million cell updates/sec

Title: US-09-734-672-3

Perfect score: 5711

Sequence: 1 AGCTCGCTGAGACTTCTTG.....TCCCCACAGCCTACTGTA 5711

Scoring table: IDENTITY\_NUC

Gapop 10.0, Gapext 1.0

Searched: 441362 seqs, 15338361 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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| 2          | 5711   | 100.0       | 5711   | 3  | US-08-825-487A-3 Sequence 3, Appl1   |
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#### ALIGNMENTS

RESULT 1  
US-08-798-691-3  
Sequence 3, Application US/08798691  
Patent No. 5750400  
GENERAL INFORMATION:  
APPLICANT: Murphy, Patricia D.  
APPLICANT: Allen, Antoinette C.  
APPLICANT: Alvares, Christopher P.  
APPLICANT: Critz, Brenda S.  
APPLICANT: Olson, Sheri J.  
APPLICANT: Schelter, Denise B.  
APPLICANT: Zeng, Bin  
TITLE OF INVENTION: Coding Sequences of the Human  
NUMBER OF SEQUENCES: 72  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ONCOMED  
STREET: 200 Perry Parkway  
CITY: Gaithersburg  
STATE: MD  
COUNTRY: USA  
ZIP: 20877  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/798,691  
FILING DATE: 12-Feb-97  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Thomas Gallegos  
REGISTRATION NUMBER: 32,692  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 301-527-2051  
TELEFAX: 301-208-6997  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5711 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
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ORGANISM: Homo sapiens  
STRAIN: BRCA1  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: 17

MAP POSITION: 17g21  
US-08-798-691-3

Query Match 100.0%; Score 5711; DB 1; Length 5711;  
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RESULT 2  
US-08-825-487A-3  
Sequence 3, Application US/08825487A  
Patent No. 6048689  
GENERAL INFORMATION:  
Applicant: Murphy, Patricia D.  
Applicant: White, Marga B.  
Title of Invention: METHODS FOR IDENTIFYING VARIATIONS IN POLYNUCLEOTIDE SEQUENC.  
Number of Sequences: 110  
Correspondence Address:  
Addressee: Howrey & Simon  
Street: 1299 Pennsylvania Avenue., N.W.  
City: Washington,  
State: DC  
Country: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
Medium Type: Floppy disk  
Computer: IBM PC compatible  
Operating System: PC-DOS/MS-DOS  
Software: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
Application Number: US/08/825,487A  
Filing Date: 28-MAR-1997  
Classification: 435  
Prior Application Data:  
Application Number: PCT/US98/060002  
Filing Date: 26-Mar-1998  
Classification: 435  
Attorney/Agent Information:  
Name: Albert P. Halluin  
Registration Number: 25,227  
Reference/Docket Number: 05371.0012.999  
Telecommunication Information:  
Telephone: 650-463-8100  
Telefax: 650-463-8400  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
Length: 5711 base pairs  
Type: nucleic acid  
Strandedness: not relevant  
Topology: linear  
Molecule Type: CDNA  
Original Source:  
Organism: Homo sapiens  
Strain: BRC41

POSITION IN GENOME:  
CHROMOSOME/SEGMENT: 17  
MAP POSITION: 17q21  
US-08-825-487A-3

Query Match 100.0%; Score 5711; DB 3; Length 5711;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 5711; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 4981 ATACTGCTGGGTATTAATGCAATGGAAGAAAGTGTGAGCAGAGAGAGCCAGATTTGACAG 5040  
QY 5041 CTTCACAGAAAGGCTCAACAAAGAAATGTCATGTGTGTGCTGAGCTTGAACCCAGAG 5100  
Db 5041 CTTCACAGAAAGGCTCAACAAAGAAATGTCATGTGTGTGCTGAGCTTGAACCCAGAG 5100  
QY 5101 AATTATGCTGCTGATCAAGTTTGCAGAAAAACACACATCACTTAACTTAATTAATTA 5160  
Db 5101 AATTATGCTGCTGATCAAGTTTGCAGAAAAACACACATCACTTAACTTAATTAATTA 5160  
QY 5161 CTGAAGAGACTACTCATGTGTATGAAAAACAGATGCTGAGTTGTGTGAGAGAGAC 5220  
Db 5161 CTGAAGAGACTACTCATGTGTATGAAAAACAGATGCTGAGTTGTGTGAGAGAGAC 5220  
QY 5221 TGAATATTTTCTAGGAATTCGGGAGAGAAATGGGTAGTTACTATTTCTGGGTACCC 5280  
Db 5221 TGAATATTTTCTAGGAATTCGGGAGAGAAATGGGTAGTTACTATTTCTGGGTACCC 5280  
QY 5281 AGTCTATTAAAGAAAGAAATGCTGAATGAGATATTTTGAAGTCAGAGAGAGATGTGG 5340  
Db 5281 AGTCTATTAAAGAAAGAAATGCTGAATGAGATATTTTGAAGTCAGAGAGAGATGTGG 5340

QY 5341 TCAATGGAAGAAACCAACAGAGTCCAAAGCAGAAAGAAATCCAGAGCAGAAAGATCT 5400  
Db 5341 TCAATGGAAGAAACCAACAGAGTCCAAAGCAGAAAGAAATCCAGAGCAGAAAGATCT 5400  
QY 5401 TCAGGGGGCTAGAAATCTGTGTATAGGGCCCTTTCACCAACATGCCCCAGATCACTGG 5460  
Db 5401 TCAGGGGGCTAGAAATCTGTGTATAGGGCCCTTTCACCAACATGCCCCAGATCACTGG 5460  
QY 5461 AATGATGATGACAGCTGTGTGTGTCTGTGTGTAAGAGAGCTTTCATCAATCACTTGC 5520  
Db 5461 AATGATGATGACAGCTGTGTGTGTCTGTGTGTAAGAGAGCTTTCATCAATCACTTGC 5520  
QY 5521 GCACAGGTGTCACCCCAATTTGTGTGTGTCAGAGCAGATGCTGAGCAGAGCAATGGCT 5580  
Db 5521 GCACAGGTGTCACCCCAATTTGTGTGTGTCAGAGCAGATGCTGAGCAGAGCAATGGCT 5580  
QY 5581 TCCATGCAATTTGGGCGAGATGTGTAGGACACTGTGTGACCCGAGAGTGGGTGTGACA 5640  
Db 5581 TCCATGCAATTTGGGCGAGATGTGTAGGACACTGTGTGACCCGAGAGTGGGTGTGACA 5640  
QY 5641 GTGTAGCACTTACACAGTCCGAGAGAGTGGACACCTGATATACCCAGATCCCCACA 5700  
Db 5641 GTGTAGCACTTACACAGTCCGAGAGAGTGGACACCTGATATACCCAGATCCCCACA 5700  
QY 5701 GCCACTACTGA 5711  
Db 5701 GCCACTACTGA 5711

RESULT 3  
US-09-074-476-5  
Sequence 5, Application US/09074476  
Patent No. 6130322  
GENERAL INFORMATION:  
APPLICANT: Murphy, Patricia D.  
APPLICANT: Allen, Antoinette C.  
APPLICANT: Alvares, Christopher P.  
APPLICANT: Critz, Brenda S.  
APPLICANT: Olson, Sheri J.  
APPLICANT: Thurber, Denise  
APPLICANT: Zeng, Bin  
TITLE OF INVENTION: Coding Sequences of the Human  
TITLE OF INVENTION: BRC1 Gene  
NUMBER OF SEQUENCES: 72  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Howrey & Simon  
STREET: 1299 Pennsylvania Avenue N. W.  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/074,476  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/074,453  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Albert P. Halluin  
REGISTRATION NUMBER: 25,227  
REFERENCE/DOCKET NUMBER: 5371.34.US01  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-463-8109  
TELEFAX: 650-463-8400  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5711 base pairs

TYPE: nucleic acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
STRAIN: BRCA1 (om13)  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: 17  
MAP POSITION: 17q21  
US-09-074-476-5

Query Match 100.0%; Score 5711; DB 3; Length 5711;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 5711; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGCTGAGACTTCTCTGAGACCCGACACAGGCTGTGGGTTTCTCAGATAAATGCGGCC 60  
DB 1 AGCTGCTGAGACTTCTCTGAGACCCGACACAGGCTGTGGGTTTCTCAGATAAATGCGGCC 60  
QY 61 CCTGGCTCAGAGAGCCTTCAACCTCTGCTCTGGGTAAGTTCATTGGAAACAGAAAGAA 120  
DB 61 CCTGGCTCAGAGAGCCTTCAACCTCTGCTCTGGGTAAGTTCATTGGAAACAGAAAGAA 120  
QY 121 TGGATTATCTGCTCTTCCGCTTGAAGAGTACAAATGTCAATTAATGCTATGCAAGAAA 180  
DB 121 TGGATTATCTGCTCTTCCGCTTGAAGAGTACAAATGTCAATTAATGCTATGCAAGAAA 180  
QY 121 TGGATTATCTGCTCTTCCGCTTGAAGAGTACAAATGTCAATTAATGCTATGCAAGAAA 180  
DB 121 TGGATTATCTGCTCTTCCGCTTGAAGAGTACAAATGTCAATTAATGCTATGCAAGAAA 180  
QY 181 TCTTAGAGTGTCCATCTGTCTGTGAGTTGATCAAGAACTGTCTTCCACAAAGTGTGACC 240  
DB 181 TCTTAGAGTGTCCATCTGTCTGTGAGTTGATCAAGAACTGTCTTCCACAAAGTGTGACC 240  
QY 241 ACATATTTTGGCAATTTTGCATGCTGAAACCTTCTCAACAGAAAGAAAGGCCCTTCACAT 300  
DB 241 ACATATTTTGGCAATTTTGCATGCTGAAACCTTCTCAACAGAAAGAAAGGCCCTTCACAT 300  
QY 301 GTCTTTATGTAGATGATATATACCAAAAGAGCCTTACAGAAAGTACGAGATTATGTC 360  
DB 301 GTCTTTATGTAGATGATATATACCAAAAGAGCCTTACAGAAAGTACGAGATTATGTC 360  
QY 361 AACTTTGTGAAGAGCTATTTGAAATCATTTTGTGCTTTTCAGCTTGAACAAGTTTGGAGT 420  
DB 361 AACTTTGTGAAGAGCTATTTGAAATCATTTTGTGCTTTTCAGCTTGAACAAGTTTGGAGT 420  
QY 421 ATGCAAGAGCTATTAATTTTGAAGAAAGAAATTAATCTCTCTGAAACATCTPAAAGATG 480  
DB 421 ATGCAAGAGCTATTAATTTTGAAGAAAGAAATTAATCTCTCTGAAACATCTPAAAGATG 480  
QY 481 AAGTTTCTATCATCCAAAGTATGGGCTACAGAAACCGTGCAGAAAGACTTCTACAGAGTG 540  
DB 481 AAGTTTCTATCATCCAAAGTATGGGCTACAGAAACCGTGCAGAAAGACTTCTACAGAGTG 540  
QY 541 AACCAGAAATCTCTTCTTGGCAGAAACCAAGTCTCAGTCTCAAACTCTTAACTTTGGAA 600  
DB 541 AACCAGAAATCTCTTCTTGGCAGAAACCAAGTCTCAGTCTCAAACTCTTAACTTTGGAA 600  
QY 601 CTGTGAGAACTGTGAGAACAAAGCAGCGGATCAACCTCAAAAGAGTGTGCTTCAATG 660  
DB 601 CTGTGAGAACTGTGAGAACAAAGCAGCGGATCAACCTCAAAAGAGTGTGCTTCAATG 660  
QY 661 AATTGGAGTCTGATCTTCTGAAGATACCGTTAATTAAGCAACTTAATTCAGTGTGGAG 720  
DB 661 AATTGGAGTCTGATCTTCTGAAGATACCGTTAATTAAGCAACTTAATTCAGTGTGGAG 720  
QY 721 ATCAAGAAATTTGTAACAATCACCCCTCAAGGAAACCGGATGAAATCAATTTGGATCTG 780  
DB 721 ATCAAGAAATTTGTAACAATCACCCCTCAAGGAAACCGGATGAAATCAATTTGGATCTG 780  
QY 781 CAAAAAAGGCTGCTGTGAAATTTTCTGAGACGATGTAAACAATATCTGAACATCATCAAC 840  
DB 781 CAAAAAAGGCTGCTGTGAAATTTTCTGAGACGATGTAAACAATATCTGAACATCATCAAC 840  
QY 841 CCAGTAATATGATTTGAAACCACTGAGAAAGCTGACGTGAGAGCATCCAGAAAGT 900

DB 841 CCAGTAATATGATTTGAAACCACTGAGAAAGCTGAGAGGATCCAGAAAGT 900  
QY 901 ATCAGGGATGTTCTGTTTCAAACTTGCATGTGGAGCCATGTGGCAAAATCTCATGCCA 960  
DB 901 ATCAGGGATGTTCTGTTTCAAACTTGCATGTGGAGCCATGTGGCAAAATCTCATGCCA 960  
QY 961 GCTCATTAAGATGAGAAACAGAGTTTATTAATCACTAAGACAGATGAATAGTAA 1020  
DB 961 GCTCATTAAGATGAGAAACAGAGTTTATTAATCACTAAGACAGATGAATAGTAA 1020  
QY 1021 AGGCTGAATTTCTGTATTAATAAGCAACGCTGCTTACAGAGAGCCCAATTAACGAT 1080  
DB 1021 AGGCTGAATTTCTGTATTAATAAGCAACGCTGCTTACAGAGAGCCCAATTAACGAT 1080  
QY 1081 GGGCTGGAAGTGAAGAAACATGTATGATTAAGGCGCATCCAGACACAGAAAGGATG 1140  
DB 1081 GGGCTGGAAGTGAAGAAACATGTATGATTAAGGCGCATCCAGACACAGAAAGGATG 1140  
QY 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAGATGGAATTAAGCAGAAACTGCGATGCT 1200  
DB 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAGATGGAATTAAGCAGAAACTGCGATGCT 1200  
QY 1201 CAGAGAAATCTAGAGATACCTGAAGATGTTCTTGGATTAACAATAAGCAGATTGAGA 1260  
DB 1201 CAGAGAAATCTAGAGATACCTGAAGATGTTCTTGGATTAACAATAAGCAGATTGAGA 1260  
QY 1261 AAGTTAATGAGTGTGTTTCCAGAAAGTGAATGATGATGTTGATGATGATGATGATG 1320  
DB 1261 AAGTTAATGAGTGTGTTTCCAGAAAGTGAATGATGATGATGATGATGATGATGATG 1320  
QY 1321 GGGAGTCTGATCAAAATGCCAAAGTGTGATGATGATGATGATGATGATGATGATG 1380  
DB 1321 GGGAGTCTGATCAAAATGCCAAAGTGTGATGATGATGATGATGATGATGATGATG 1380  
QY 1381 AATATTTGCTGTTCTTCAAGAAATATGACTTACGCGCAGATGATCTCATGAGCTTTAA 1440  
DB 1381 AATATTTGCTGTTCTTCAAGAAATATGACTTACGCGCAGATGATCTCATGAGCTTTAA 1440  
QY 1441 TATGTAAGAGTGAAGAAAGTCTTCAATCCAAATGATGAGAGATTAATTAAGAGCAAAATAT 1500  
DB 1441 TATGTAAGAGTGAAGAAAGTCTTCAATCCAAATGATGAGAGATTAATTAAGAGCAAAATAT 1500  
QY 1501 TTGGGAAAACCTATGGAAGAGCAAGCCTCCCAACTTAAGCATGTAAGTAAATC 1560  
DB 1501 TTGGGAAAACCTATGGAAGAGCAAGCCTCCCAACTTAAGCATGTAAGTAAATC 1560  
QY 1561 TAATTATAGAGCAATTTGTTACTGAGCCAGATPAATCAAGAGCGTCCCTCAAAATA 1620  
DB 1561 TAATTATAGAGCAATTTGTTACTGAGCCAGATPAATCAAGAGCGTCCCTCAAAATA 1620  
QY 1621 AATTAAACGTTAAAGAGACCTTACATGAGGCTTCAATCCAGATTTTATCAAGAAAG 1680  
DB 1621 AATTAAACGTTAAAGAGACCTTACATGAGGCTTCAATCCAGATTTTATCAAGAAAG 1680  
QY 1681 CAGATTTGGCAGTTCAAAAGACTCCTGAAATGATTAATCAAGGGAATTAACCAAGAGC 1740  
DB 1681 CAGATTTGGCAGTTCAAAAGACTCCTGAAATGATTAATCAAGGGAATTAACCAAGAGC 1740  
QY 1741 AGAATGTCATGATGATTAATTAATTAATGATGATGATGATGATGATGATGATGATG 1800  
DB 1741 AGAATGTCATGATGATTAATTAATTAATGATGATGATGATGATGATGATGATGATG 1800  
QY 1801 CTATTCAAGATGAGAAAAATCTCTAACCAGATTAATGATGATGATGATGATGATGATG 1860  
DB 1801 CTATTCAAGATGAGAAAAATCTCTAACCAGATTAATGATGATGATGATGATGATGATG 1860  
QY 1861 AAACGAAGCTGAAGCTTAAGCAGAGTATTAAGCAATATGGAATTAATTAATTC 1920  
DB 1861 AAACGAAGCTGAAGCTTAAGCAGAGTATTAAGCAATATGGAATTAATTAATTC 1920  
QY 1921 ACAATTCAAAAGCACCTTAAGAAATGAGCTGAGAGAGAGTCTTCTTACAGGCAATATTC 1980



D 1921 ACAATTCAGAACCTTAAAAAGATAGCTGAGGAGAAAGCTTTTACCAAGGCATATTC 1980  
Q 1981 ATGGCTTGAATAGTAGTACATGAGAAATCTAAGCCACCTAATGTGATGAAATGGCAA 2040  
D 1981 ATGGCTTGAATAGTAGTACATGAGAAATCTAAGCCACCTAATGTGATGAAATGGCAA 2040  
Q 2041 TTGATAGTTGTTCTAGCAGTGAAGAGATAAAGAAAAAGTACACCAATGCCAGTCA 2100  
D 2041 TTGATAGTTGTTCTAGCAGTGAAGAGATAAAGAAAAAGTACACCAATGCCAGTCA 2100  
Q 2101 GGCACAGCAGAAACCTTCAACTCATGAGAGTAAAGAACTCGCACTGAGCCAGAGAA 2160  
D 2101 GGCACAGCAGAAACCTTCAACTCATGAGAGTAAAGAACTCGCACTGAGCCAGAGAA 2160  
Q 2161 GTACACAGCCAAATGAAACAGACAGTAAAGACATGACAGCTACTCTTCCAGAGTGA 2220  
D 2161 GTACACAGCCAAATGAAACAGACAGTAAAGACATGACAGCTACTCTTCCAGAGTGA 2220  
Q 2221 AGTTAACAAATGACACCTGCTTCTTTTAACTAAGTTCAAATACAGTGAATTTAAAGAT 2280  
D 2221 AGTTAACAAATGACACCTGCTTCTTTTAACTAAGTTCAAATACAGTGAATTTAAAGAT 2280  
Q 2281 TTGTCAATCTTACCTTCCAGAGAGAGAAAAAGAGAACTTGAACACGTTAAAGTGT 2340  
D 2281 TTGTCAATCTTACCTTCCAGAGAGAGAAAAAGAGAACTTGAACACGTTAAAGTGT 2340  
Q 2341 CTATATATGCTGAAGAGACCCCAAGATCTCATGTTAATGAGAGAAAGGGTTTGCAGACTG 2400  
D 2341 CTATATATGCTGAAGAGACCCCAAGATCTCATGTTAATGAGAGAAAGGGTTTGCAGACTG 2400  
Q 2401 AAAAGATCTGAGAGAGTGAAGATTTTCAATGCTACCTGCTAGTATGATGAGCACTCAG 2460  
D 2401 AAAAGATCTGAGAGAGTGAAGATTTTCAATGCTACCTGCTAGTATGATGAGCACTCAG 2460  
Q 2461 AAAGTATCTGCTTACTGAGAGAGTGAACCTTAGGAGAGCCAAAGCCAAATTAAT 2520  
D 2461 AAAGTATCTGCTTACTGAGAGAGTGAACCTTAGGAGAGCCAAAGCCAAATTAAT 2520  
Q 2521 GTGTGAGTCACTGTCAGCATTTGAAAACCCCAAGGACCTAATTCATGTTTCCAAAG 2580  
D 2521 GTGTGAGTCACTGTCAGCATTTGAAAACCCCAAGGACCTAATTCATGTTTCCAAAG 2580  
Q 2581 ATATAGAAATGACACAGAGAGCTTTAAGTATCATTTGAGCATGAAATTAACACAGTC 2640  
D 2581 ATATAGAAATGACACAGAGAGCTTTAAGTATCATTTGAGCATGAAATTAACACAGTC 2640  
Q 2641 GGGAAACAGCATGAAATGAAAGAAAGTGAACCTTGATGCTCAGTATTTGCAAGATACAT 2700  
D 2641 GGGAAACAGCATGAAATGAAAGAAAGTGAACCTTGATGCTCAGTATTTGCAAGATACAT 2700  
Q 2701 TCAAGGTTTCAAGCGCAGTCACTTGTCTGTTCCTAATTCAGAGAAATGCAAGAGAG 2760  
D 2701 TCAAGGTTTCAAGCGCAGTCACTTGTCTGTTCCTAATTCAGAGAAATGCAAGAGAG 2760  
Q 2761 AATGTGCAACATTTCTGCCCACCTGAGTCTTTAAAGAAACAAAGTCCAAAGTCACTT 2820  
D 2761 AATGTGCAACATTTCTGCCCACCTGAGTCTTTAAAGAAACAAAGTCCAAAGTCACTT 2820  
Q 2821 TTGAATGTGAACAAAGAAAGAAATCAAGAGAAAGATGATGCTAATATCAAGCTGTAC 2880  
D 2821 TTGAATGTGAACAAAGAAAGAAATCAAGAGAAAGATGATGCTAATATCAAGCTGTAC 2880  
Q 2881 AGACAGTTAATATCACTGACGAGCTTCTGTGTGTGTGTCAGAAAGATGAGCCAGTTGAT 2940  
D 2881 AGACAGTTAATATCACTGACGAGCTTCTGTGTGTGTGTCAGAAAGATGAGCCAGTTGAT 2940  
Q 2941 ATGCCAAATGTATATCAAGAGAGCTCTAGGTTTGTCTATCATCTCAGTTCAAGAGCA 3000  
D 2941 ATGCCAAATGTATATCAAGAGAGCTCTAGGTTTGTCTATCATCTCAGTTCAAGAGCA 3000  
Q 3001 ACAGAACTGACATCTATCTCCAAATTAACATGAGACTTTTACAAAACCCATATCTGATAC 3060  
D 3001 ACAGAACTGACATCTATCTCCAAATTAACATGAGACTTTTACAAAACCCATATCTGATAC 3060

Q 3061 CACCACTTTTCCCATCAAGTCACTTGTAAAACTAATATGTAAGAAAAATCTGAGAG 3120  
D 3061 CACCACTTTTCCCATCAAGTCACTTGTAAAACTAATATGTAAGAAAAATCTGAGAG 3120  
Q 3121 AAAACTTGAAGAACATTCATGATGTCACCTGAAAAGAGAAATGGGAAATGAGACATTCOA 3180  
D 3121 AAAACTTGAAGAACATTCATGATGTCACCTGAAAAGAGAAATGGGAAATGAGACATTCOA 3180  
Q 3181 GTACAGTGAACCAATTAACCCGTAATTAACATTAAGAAAATGTTTTTAAAGAGCCAGCT 3240  
D 3181 GTACAGTGAACCAATTAACCCGTAATTAACATTAAGAAAATGTTTTTAAAGAGCCAGCT 3240  
Q 3241 CAAGCAATATTAATGAAGTAGTTCAGTACTAATGAAGGGCTCCAGTATTAATGAA 3300  
D 3241 CAAGCAATATTAATGAAGTAGTTCAGTACTAATGAAGGGCTCCAGTATTAATGAA 3300  
Q 3301 TAGGTTCCAGTAGTGAACCAATTCAGAGAACCTAGTGAACACAGAGGCCCCAAATTTGA 3360  
D 3301 TAGGTTCCAGTAGTGAACCAATTCAGAGAACCTAGTGAACACAGAGGCCCCAAATTTGA 3360  
Q 3361 ATGCTATGCTTATGATTAAGGGGTTTGCACCTGAGTCTATTAACAAAGTCTTCCGGA 3420  
D 3361 ATGCTATGCTTATGATTAAGGGGTTTGCACCTGAGTCTATTAACAAAGTCTTCCGGA 3420  
Q 3421 GTATATGTAAGCATCTGAAATTAAGAAACAGAAATATGAAGAGTAGTTCACTGTTA 3480  
D 3421 GTATATGTAAGCATCTGAAATTAAGAAACAGAAATATGAAGAGTAGTTCACTGTTA 3480  
Q 3481 ATACAGATTTCTCTCCATATCTGATTTACGATTAATTAAGAACAGCTATGGAAGTAGTC 3540  
D 3481 ATACAGATTTCTCTCCATATCTGATTTACGATTAATTAAGAACAGCTATGGAAGTAGTC 3540  
Q 3541 ATGCACTCAGGTTTGTCTGAGAACCTGATGACCTGTTAAGTAGTGTGAATTAAGG 3600  
D 3541 ATGCACTCAGGTTTGTCTGAGAACCTGATGACCTGTTAAGTAGTGTGAATTAAGG 3600  
Q 3601 AAGATCTAGTTTGTGTAAGAAATGACATTAAGAAAGTCTGCTGTTTAAAGCAAAAGC 3660  
D 3601 AAGATCTAGTTTGTGTAAGAAATGACATTAAGAAAGTCTGCTGTTTAAAGCAAAAGC 3660  
Q 3661 TCCAGAAAGAGAGCTTTAGCAGAGAGTCTAGCCCTTTCAACCATACATTTGGCTCAG 3720  
D 3661 TCCAGAAAGAGAGCTTTAGCAGAGAGTCTAGCCCTTTCAACCATACATTTGGCTCAG 3720  
Q 3721 GTTACCGAAGAGGGGCAAGAAATTTAGAGTCTCTCAGAAAGAACTTATCTAGTGAAGATG 3780  
D 3721 GTTACCGAAGAGGGGCAAGAAATTTAGAGTCTCTCAGAAAGAACTTATCTAGTGAAGATG 3780  
Q 3781 AAGAGCTTCCCTGCTCCAAACCTGTTATTTGGTAAAGTAAACATTAACCTTCAAGT 3840  
D 3781 AAGAGCTTCCCTGCTCCAAACCTGTTATTTGGTAAAGTAAACATTAACCTTCAAGT 3840  
Q 3841 CTACTAGGATAGACCCGTTGTCTACCGAGTGTCTGTAAAGAACACAGAGAGAAATTTAT 3900  
D 3841 CTACTAGGATAGACCCGTTGTCTACCGAGTGTCTGTAAAGAACACAGAGAGAAATTTAT 3900  
Q 3901 TATCATTTGAAGAAATAGCTTAAATGATGACAGTAAATATTTGGCAAGAGCATCTC 3960  
D 3901 TATCATTTGAAGAAATAGCTTAAATGATGACAGTAAATATTTGGCAAGAGCATCTC 3960  
Q 3961 AGGACATCACCTTGTGAGAGAAACAAATGTTGCTGAGTCTGTTTCTTCAAGTGA 4020  
D 3961 AGGACATCACCTTGTGAGAGAAACAAATGTTGCTGAGTCTGTTTCTTCAAGTGA 4020  
Q 4021 GTGAATGGAAGACTGACCTGCAAAATACAAACACCCAGAGATCTTCTTGAATGTTCTT 4080  
D 4021 GTGAATGGAAGACTGACCTGCAAAATACAAACACCCAGAGATCTTCTTGAATGTTCTT 4080  
Q 4081 CCAGAACTAGGAGATCAGTCTGAAGCCAGAGAGTGTGTGAGTGAAGAGAAATTTGG 4140  
D 4081 CCAGAACTAGGAGATCAGTCTGAAGCCAGAGAGTGTGTGAGTGAAGAGAAATTTGG 4140



MOLECULE TYPE: DNA (genomic)  
 ; HYPOTHEITICAL: NO  
 ; ANTI-SENSE: NO  
 US-08-658-322-1

Query Match 100.0%; Score 5709.4; DB 2; Length 5711;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 5710; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

|    |     |  |     |
|----|-----|--|-----|
| Qy | 1   | AGCTCGTGAAGCTTCTGACCCCGACACAGCGTGGGTTTCTAGTAATCTGGGCC      | 60  |
| Db | 1   | AGCTCGTGAAGCTTCTGACCCCGACACAGCGTGGGTTTCTAGTAATCTGGGCC      | 60  |
| Qy | 61  | CTGCGCTCAGAGGCGCTTCACTCTGCTCTGGGTAAGTTCATTGGAACAGAAAGAA    | 120 |
| Db | 61  | CTGCGCTCAGAGGCGCTTCACTCTGCTCTGGGTAAGTTCATTGGAACAGAAAGAA    | 120 |
| Qy | 121 | TGGATTATCTGCTCTTGGCGTTGAGAGATCAAAATGTCATTATGCTATSCAGAAA    | 180 |
| Db | 121 | TGGATTATCTGCTCTTGGCGTTGAGAGATCAAAATGTCATTATGCTATSCAGAAA    | 180 |
| Qy | 181 | TCTTAGAGTCCCATCTGTCTGGAGTTGATCAAGAACCTGTCTCCAGAAAGTGGACC   | 240 |
| Db | 181 | TCTTAGAGTCCCATCTGTCTGGAGTTGATCAAGAACCTGTCTCCAGAAAGTGGACC   | 240 |
| Qy | 241 | ACATATTTTCAAAATTTTGCATGCTGAACTTCTCAACAGAAAGAGGCTTTCACAGT   | 300 |
| Db | 241 | ACATATTTTCAAAATTTTGCATGCTGAACTTCTCAACAGAAAGAGGCTTTCACAGT   | 300 |
| Qy | 301 | GTCCTTTATGTAAAGATGATATACCAAAAGAGCCTTCAAGAAAGTACGAGATTTAGTC | 360 |
| Db | 301 | GTCCTTTATGTAAAGATGATATACCAAAAGAGCCTTCAAGAAAGTACGAGATTTAGTC | 360 |
| Qy | 361 | AACCTGTGAAGAGCTATTAATAATCATTTTGTCTTTCAGCTTGAACAGGTTTGGAGT  | 420 |
| Db | 361 | AACCTGTGAAGAGCTATTAATAATCATTTTGTCTTTCAGCTTGAACAGGTTTGGAGT  | 420 |
| Qy | 421 | ATGCAAAACAGCTAATTTTGGCAAAAAGGAAATAACTCTCTGAAACATCTAAAGATG  | 480 |
| Db | 421 | ATGCAAAACAGCTAATTTTGGCAAAAAGGAAATAACTCTCTGAAACATCTAAAGATG  | 480 |
| Qy | 481 | AACTTCTATCATCAAAAGATGGGCTACAGAAACCGTCCAAAGACTTCTACAGAGTG   | 540 |
| Db | 481 | AACTTCTATCATCAAAAGATGGGCTACAGAAACCGTCCAAAGACTTCTACAGAGTG   | 540 |
| Qy | 541 | AACTTCTATCATCAAAAGATGGGCTACAGAAACCGTCCAAAGACTTCTACAGAGTG   | 600 |
| Db | 541 | AACTTCTATCATCAAAAGATGGGCTACAGAAACCGTCCAAAGACTTCTACAGAGTG   | 600 |
| Qy | 601 | CTGTGAGAACTCTGAGGACAAAGAGGAGTCAAACTCAAAAGAGCGTCTGTACATTG   | 660 |
| Db | 601 | CTGTGAGAACTCTGAGGACAAAGAGGAGTCAAACTCAAAAGAGCGTCTGTACATTG   | 660 |
| Qy | 661 | AATTGGAGTCTGATCTTCTGAGAGATACCGTTAATAAGCACTTATGCAAGTGGAG    | 720 |
| Db | 661 | AATTGGAGTCTGATCTTCTGAGAGATACCGTTAATAAGCACTTATGCAAGTGGAG    | 720 |
| Qy | 721 | ATCAAGATTTGTTACAAATACCCCTCAAGAACCAAGGATGAATTCAGTTGGATTCTG  | 780 |
| Db | 721 | ATCAAGATTTGTTACAAATACCCCTCAAGAACCAAGGATGAATTCAGTTGGATTCTG  | 780 |
| Qy | 781 | CAAAAAGGCTGCTGTGAAATTTTCTGAGAGGATGTAACAATACTGAACATCATCAAC  | 840 |
| Db | 781 | CAAAAAGGCTGCTGTGAAATTTTCTGAGAGGATGTAACAATACTGAACATCATCAAC  | 840 |
| Qy | 841 | CCAGTATATATGATTGGAACACCACTGAGAGGCTGAGAGGCAATCCAGAAAGT      | 900 |
| Db | 841 | CCAGTATATATGATTGGAACACCACTGAGAGGCTGAGAGGCAATCCAGAAAGT      | 900 |
| Qy | 901 | ATAGGGATGTTCTGTTTCAACTTGACATGAGGCAATGCGCAAAATCTCATGCA      | 960 |
| Db | 901 | ATAGGGATGTTCTGTTTCAACTTGACATGAGGCAATGCGCAAAATCTCATGCA      | 960 |

|    |      |   |      |
|----|------|---|------|
| Qy | 961  | GCTCATTAAGCATGAGAAACAGCAGTTTATTACTCACTAATAAGCAGAAATGATAGAAA | 1020 |
| Db | 961  | GCTCATTAAGCATGAGAAACAGCAGTTTATTACTCACTAATAAGCAGAAATGATAGAAA | 1020 |
| Qy | 1021 | AGGCTGAATTTCTGTAATTAAGCAAAACAGCTGGCTTACAGAGAGCCCAATACAGAT   | 1080 |
| Db | 1021 | AGGCTGAATTTCTGTAATTAAGCAAAACAGCTGGCTTACAGAGAGCCCAATACAGAT   | 1080 |
| Qy | 1081 | GGGCTGGAAGTAAAGAAACATGTAATAGTGGCGGCTCCCGACACAGAAAAAAGGTAG   | 1140 |
| Db | 1081 | GGGCTGGAAGTAAAGAAACATGTAATAGTGGCGGCTCCCGACACAGAAAAAAGGTAG   | 1140 |
| Qy | 1141 | ATCTGAATCTGATCCCTGTGTGAGAGAAAAAGATGAATAGCAGAAATGCGCATGCT    | 1200 |
| Db | 1141 | ATCTGAATCTGATCCCTGTGTGAGAGAAAAAGATGAATAGCAGAAATGCGCATGCT    | 1200 |
| Qy | 1201 | CAGAGATCTTGAAGATCTGAAGATGTTCTTGATTAACACTAATATGACAGATTCAAG   | 1260 |
| Db | 1201 | CAGAGATCTTGAAGATCTGAAGATGTTCTTGATTAACACTAATATGACAGATTCAAG   | 1260 |
| Qy | 1261 | AACTTAATGAGTGTTCACAGAGTGAATCTGTTAGGTTCTGATGACTCACATGATG     | 1320 |
| Db | 1261 | AACTTAATGAGTGTTCACAGAGTGAATCTGTTAGGTTCTGATGACTCACATGATG     | 1320 |
| Qy | 1321 | GGGAGTCTGAATCAAAATGCGCAAGTATGATGATTTGACGCTTCAATATGAGTATG    | 1380 |
| Db | 1321 | GGGAGTCTGAATCAAAATGCGCAAGTATGATGATTTGACGCTTCAATATGAGTATG    | 1380 |
| Qy | 1381 | AATATTCTGTTCTTCAAGAAAAATGACTTAACGCGAGTATCTCATGAGGCTTTAA     | 1440 |
| Db | 1381 | AATATTCTGTTCTTCAAGAAAAATGACTTAACGCGAGTATCTCATGAGGCTTTAA     | 1440 |
| Qy | 1441 | TATGTAAAGTAAAGAGCTTCACTCAATTCAGTGAAGGTAATTTGAAGCAAAATAT     | 1500 |
| Db | 1441 | TATGTAAAGTAAAGAGCTTCACTCAATTCAGTGAAGGTAATTTGAAGCAAAATAT     | 1500 |
| Qy | 1501 | TTGGGAAAACTATCGAAGAAAGCAGAGCCTCCCAACTTAAGCCATGTAACGAAATATC  | 1560 |
| Db | 1501 | TTGGGAAAACTATCGAAGAAAGCAGAGCCTCCCAACTTAAGCCATGTAACGAAATATC  | 1560 |
| Qy | 1561 | TAAATTAGAGCAATTTGTTACTGAGCCACAGATTAATACAGAGCGTCCCTCACAAATA  | 1620 |
| Db | 1561 | TAAATTAGAGCAATTTGTTACTGAGCCACAGATTAATACAGAGCGTCCCTCACAAATA  | 1620 |
| Qy | 1621 | AATTAAGGTTAAAGAGAGACCTATACATGAGGCTTCACTCCAGATTTTATCAAGAAAG  | 1680 |
| Db | 1621 | AATTAAGGTTAAAGAGAGACCTATACATGAGGCTTCACTCCAGATTTTATCAAGAAAG  | 1680 |
| Qy | 1681 | CAGATTTGCACTTCAAAAAGACTCTGAAATGATTAATCAGGGAACCTAACCGAGAC    | 1740 |
| Db | 1681 | CAGATTTGCACTTCAAAAAGACTCTGAAATGATTAATCAGGGAACCTAACCGAGAC    | 1740 |
| Qy | 1741 | AGAAATGCTCAAGTGAATTAATTAATAGTGTGATGAGATTAATAAAGAGTGATT      | 1800 |
| Db | 1741 | AGAAATGCTCAAGTGAATTAATTAATAGTGTGATGAGATTAATAAAGAGTGATT      | 1800 |
| Qy | 1801 | CTAATCAGAAAGAAAAATCCTTAACCAATGGAATCACTCGAAAAAAGATCTGCTTCA   | 1860 |
| Db | 1801 | CTAATCAGAAAGAAAAATCCTTAACCAATGGAATCACTCGAAAAAAGATCTGCTTCA   | 1860 |
| Qy | 1861 | AAACGAAAGCTGAACTTAATAGCAGAGTATAGCAATATGGAATCTCGAAATTAATATCC | 1920 |
| Db | 1861 | AAACGAAAGCTGAACTTAATAGCAGAGTATAGCAATATGGAATCTCGAAATTAATATCC | 1920 |
| Qy | 1921 | ACAATTTCAAAAGCACTTAATAAGGATAGGCTGAGAGAGAGCTTCTACAGAGCATATTC | 1980 |
| Db | 1921 | ACAATTTCAAAAGCACTTAATAAGGATAGGCTGAGAGAGAGCTTCTACAGAGCATATTC | 1980 |
| Qy | 1981 | ATGCGCTTGAATTAATAGTCAATGAATCTTAAGCCCACTTAATTTGTAATTTGCAAA   | 2040 |
| Db | 1981 | ATGCGCTTGAATTAATAGTCAATGAATCTTAAGCCCACTTAATTTGTAATTTGCAAA   | 2040 |
| Qy | 2041 | TTGATAGTTGTTCTAGCAGTGAAGATTAAGAAAAAAGTAAACCAAAATGCGCAGTCA   | 2100 |

Db 2041 TTGATAGTTGTTCTGACGATGAAGATTAAGAAAAAGTACCAACCAATCCAGTCA 2100  
Qy 2101 GGCACAGAGAAACCTTACACTCATGGAAGGTAAAGACCTGCACTGAGCCCAAGAGA 2160  
Db 2101 GGCAAGAGAAACCTACACTCATGGAAGGTAAAGACCTGCACTGAGCCCAAGAGA 2160  
Qy 2161 GTAAACAAGCCAAATGAACAGACAGTAAAGACATGACAGCGATCTTTCCAGAGCTGA 2220  
Db 2161 GTAAACAAGCCAAATGAACAGACAGTAAAGACATGACAGCGATCTTTCCAGAGCTGA 2220  
Qy 2221 AGTTACAAATGACCTGCTTTCTTTACTAAGTGTCAATACCAATGCACTTAAGAAT 2280  
Db 2221 AGTTACAAATGACCTGCTTTCTTTACTAAGTGTCAATACCAATGCACTTAAGAAT 2280  
Qy 2281 TTGTCAATCTGACCTTCCAAAGAGAAAGAAAGAAAGAACTAGAAACAGTTAAAGTGT 2340  
Db 2281 TTGTCAATCTGACCTTCCAAAGAGAAAGAAAGAAAGAACTAGAAACAGTTAAAGTGT 2340  
Qy 2341 CTAATAATGCTGAAGACCCCAAGATCTGATGTTAAGTGAAGAGGTTTGGCAACTG 2400  
Db 2341 CTAATAATGCTGAAGACCCCAAGATCTGATGTTAAGTGAAGAGGTTTGGCAACTG 2400  
Qy 2401 AAAGATCTGTAGAGATGACAGTATTCATTGGTACCTGTACTGATTAAGCACTCAG 2460  
Db 2401 AAAGATCTGTAGAGATGACAGTATTCATTGGTACCTGTACTGATTAAGCACTCAG 2460  
Qy 2461 AAAGATCTGTTACTGGAAGTTAGCACTCTAGAGAGGCAAAACAGAAACCAATTAAT 2520  
Db 2461 AAAGATCTGTTACTGGAAGTTAGCACTCTAGAGAGGCAAAACAGAAACCAATTAAT 2520  
Qy 2521 GTGTAGTCAAGTGTGACAGATTTGAAACCCCAAGGACCTAATCAAGTGTGTTCCAAAG 2580  
Db 2521 GTGTAGTCAAGTGTGACAGATTTGAAACCCCAAGGACCTAATCAAGTGTGTTCCAAAG 2580  
Qy 2581 ATATAGAAATGACACAGAGGCTTTAAGTATTCATTGGGACATGAGTTAACCAAGTTC 2640  
Db 2581 ATATAGAAATGACACAGAGGCTTTAAGTATTCATTGGGACATGAGTTAACCAAGTTC 2640  
Qy 2641 GGGAAACAGACATGAAATGGAAGAAAGTAACTGATGCTCGATTTTGGCAAGTATCAT 2700  
Db 2641 GGGAAACAGACATGAAATGGAAGAAAGTAACTGATGCTCGATTTTGGCAAGTATCAT 2700  
Qy 2701 TCAAGTTTCAAGGCGCAGTCAATTTGCTGTTTCAATCCAGAAATGCGAGAGAG 2760  
Db 2701 TCAAGTTTCAAGGCGCAGTCAATTTGCTGTTTCAATCCAGAAATGCGAGAGAG 2760  
Qy 2761 AATGTCAACATTTCTCTGCCCACTCTGGGTCTTTAAGAAACAAAGTCCAAAAGTCACTT 2820  
Db 2761 AATGTCAACATTTCTCTGCCCACTCTGGGTCTTTAAGAAACAAAGTCCAAAAGTCACTT 2820  
Qy 2821 TTGAATGTGAACAAAAGAAAGAAATCAAGAAAGATGATTAATATCAGCCTGTAC 2880  
Db 2821 TTGAATGTGAACAAAAGAAAGAAATCAAGAAAGATGATTAATATCAGCCTGTAC 2880  
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Db 2881 AGACAGTTAATATCACTGAGGCTTCTGTTGTTGTCAGAAAGATTAAGCCAGTTGATA 2940  
Qy 2941 ATGCCAAATGTAGTATCAAGAGAGGCTCTAGGTTTGTCTATCATCTCAGTTTCAGAGCA 3000  
Db 2941 ATGCCAAATGTAGTATCAAGAGAGGCTCTAGGTTTGTCTATCATCTCAGTTTCAGAGCA 3000  
Qy 3001 ACGAATCTGAGCTCATTTCTCCAAATTAACATGACCTTTTACAAAACCAATATCGTATAC 3060  
Db 3001 ACGAATCTGAGCTCATTTCTCCAAATTAACATGACCTTTTACAAAACCAATATCGTATAC 3060  
Qy 3061 CACCACTTTTCCATCAAGTCAATTTGTTAAACCTAAATGTAAAGAAATCTGCTAGAG 3120  
Db 3061 CACCACTTTTCCATCAAGTCAATTTGTTAAACCTAAATGTAAAGAAATCTGCTAGAG 3120  
Qy 3121 AAAACTTTGAGGAACATTCATATGTCACCTGAAGAAATGCGAAATGAGAACATTCCAA 3180  
Db 3121 AAAACTTTGAGGAACATTCATATGTCACCTGAAGAAATGCGAAATGAGAACATTCCAA 3180

Db 3121 AAACTTTGAGGAACATTCATATGTCACCTGAAGAAATGCGAAATGAGAACATTCCAA 3180  
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Db 3181 GTACAGTGAACACATTTAGCCGTAAATACATTTAGAGAAATGTTTTTAAGAACCCAGCT 3240  
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Db 3241 CAAGCAATATTATGAAGTAGGTTCCAGTACATTAATGAAGTGGGCTCCAGTATTAATGAA 3300  
Qy 3301 TAGGTTCCAGTATGAAGAAACATTCAGCAGAACTAGTAGAAGAGGCGCAAAATTTGA 3360  
Db 3301 TAGGTTCCAGTATGAAGAAACATTCAGCAGAACTAGTAGAAGAGGCGCAAAATTTGA 3360  
Qy 3361 ATGCTATGCTAGATTTAGGGTTTTGCAACCTGAGGCTATTAACAAAGTCTCTGGA 3420  
Db 3361 ATGCTATGCTAGATTTAGGGTTTTGCAACCTGAGGCTATTAACAAAGTCTCTGGA 3420  
Qy 3421 GTAAATGTAGCATCTGAAATTAAGAAAGCAAGAAATGAAGAGTAGTTCCAGCTGTA 3480  
Db 3421 GTAAATGTAGCATCTGAAATTAAGAAAGCAAGAAATGAAGAGTAGTTCCAGCTGTA 3480  
Qy 3481 ATACAGATTTCTCTCATATCTGATTTCAATTAAGAAACAGCTTAAGGAAATGATC 3540  
Db 3481 ATACAGATTTCTCTCATATCTGATTTCAATTAAGAAACAGCTTAAGGAAATGATC 3540  
Qy 3541 ATGCACTTCAGGTTTGTCTGAGACACCTGATGACCTGTTGATGATGATGTAATTAAG 3600  
Db 3541 ATGCACTTCAGGTTTGTCTGAGACACCTGATGACCTGTTGATGATGATGTAATTAAG 3600  
Qy 3601 AAGATACTAGTTTCTGAAATGACATTAAGAAAGTCTGCTGTTTTTACAAAACG 3660  
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Qy 3661 TCCAGAAAGAGAGCTTAGCAGAGCTCTAGCCCTTTTCAACCATACACATTTGCTCAG 3720  
Db 3661 TCCAGAAAGAGAGCTTAGCAGAGCTCTAGCCCTTTTCAACCATACACATTTGCTCAG 3720  
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Db 3721 GTTACCGAAGAGGCGCAAGAAATTAAGAGTCTCAGAAAGAACTTAATCTAGTAGAGT 3780  
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Db 3781 AAGACCTTCCCTGCTTCCAAACATTTGTTTGGTAAAGTAAACATATACCTTCAGT 3840  
Qy 3841 CTACTAGGATAGCACCGTGTCTACCGAGTGTCTGTAAAGAACAGAGAGAAATTTAT 3900  
Db 3841 CTACTAGGATAGCACCGTGTCTACCGAGTGTCTGTAAAGAACAGAGAGAAATTTAT 3900  
Qy 3901 TATCATTAAGAAATGCTTAATAGCTGACATTAACAGGTAATTTGGCAAGGATCTC 3960  
Db 3901 TATCATTAAGAAATGCTTAATAGCTGACATTAACAGGTAATTTGGCAAGGATCTC 3960  
Qy 3961 AGGAACATCACCTTAGTAGAGAAACAAATGTTCTGCTAGCTTTGTTCTTACAGTGA 4020  
Db 3961 AGGAACATCACCTTAGTAGAGAAACAAATGTTCTGCTAGCTTTGTTCTTACAGTGA 4020  
Qy 4021 GTGAATTTGGAAGACTTGACCTGAAATACAAACACCCAGAGATCTTTCTGTAAGTGGCTT 4080  
Db 4021 GTGAATTTGGAAGACTTGACCTGAAATACAAACACCCAGAGATCTTTCTGTAAGTGGCTT 4080  
Qy 4081 CCAACCAATGAGGATGAGTGTGAAGCCAGGGAGTGTGCTGAGTACAGAAATTTGG 4140  
Db 4081 CCAACCAATGAGGATGAGTGTGAAGCCAGGGAGTGTGCTGAGTACAGAAATTTGG 4140  
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Db 4141 TTTCAAGATGAAGAAAGAGAGAGCGGCTTGAAGAAATATCAAGAAAGCA 4200  
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QY 4261 ACTGCTCAGGGGCTATCCTCTCAGAGTGCATTTTAACTCACTCAGCAGAGGATACCACTGC 4320  
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DB 4381 ATGGAGGCCAGCCTTCTTAACAGTACCTCTCCATCATTAATGACTCTTCTGCCCCCTTGAGG 4440  
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DB 4441 ACCTGGGAATTCAGAACCAAGACATCAGAAAAAGAGATTTAACTTTCAGAAAAAGTA 4500  
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DB 4501 GTGAATTAACCTTATTAAGCAGAAATCCAGAAAGCCTTCTGCTGCAAGTTTGAAGTGTCTG 4560  
QY 4561 CAGATAGTCTTACAGTAAATAAAGAACAGAGAGTGAAGAGTCACTCCCTTCTAAAT 4620  
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DB 4741 AGTCTGGGCCACACGATTTTGAACGAAACATCTTACTTGGCAAGCAAGATCTTGAGGAA 4800  
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DB 4801 CCCCTTACCTGGAATCTGGAATCAGCCTCTTCTGTGATGACCTGTGATCTGATCTTCTG 4860  
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DB 4861 AAGACAGAGGCCAGAGTCACTGCTGTGGAACAATACCATCTTCAACCTCTGCAATGA 4920  
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DB 4921 AAGTTCCTCCCAATGGAAGTTCGCAATCTGCGCAGAGTCCAGCTGCTGCTCATACTG 4980  
QY 4981 ATACTGCTGGGTATTAATGCAATGGAAGAAATGTGAGCAGAGGAGCAAGATTGACAG 5040  
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QY 5041 CTTCACAGAAAGAGGTCAACAAAGATGTCATGGTGTGTGCTGACCCCAAG 5100  
DB 5041 CTTCACAGAAAGAGGTCAACAAAGATGTCATGGTGTGTGCTGACCCCAAG 5100  
QY 5101 AATTATATGCTCGTGTACAGATTGGCCAGAAAAACACATCATTTTAACTTAATCTTAATTA 5160  
DB 5101 AATTATATGCTCGTGTACAGATTGGCCAGAAAAACACATCATTTTAACTTAATCTTAATTA 5160  
QY 5161 CTGAAGAGACTACTCATGTTGTTATGAAAAACAGATGCTGATGTTGTGTGAACGAGAC 5220  
DB 5161 CTGAAGAGACTACTCATGTTGTTATGAAAAACAGATGCTGATGTTGTGTGAACGAGAC 5220  
QY 5221 TGAATAATATTTCTAGGAATTCGCGAGAGAAATGGGTAGTTACTTCTGCGTGAACCC 5280  
DB 5221 TGAATAATATTTCTAGGAATTCGCGAGAGAAATGGGTAGTTACTTCTGCGTGAACCC 5280  
QY 5281 AGTCTATTAAGAAAGAAAAATGCTGAATGAGATGATTTTGAAGTCAGAGGAGATGTGG 5340  
DB 5281 AGTCTATTAAGAAAGAAAAATGCTGAATGAGATGATTTTGAAGTCAGAGGAGATGTGG 5340

QY 5341 TCAATGGAAGAAACCAACCAAGTCCAAAGCAGAGACAGAAATCCAGACAGAAAGATCT 5400  
DB 5341 TCAATGGAAGAAACCAACCAAGTCCAAAGCAGAGACAGAAATCCAGACAGAAAGATCT 5400  
QY 5401 TCAGGGGGCTAGAAATCTGTTGCTATGAGGCCCTTCAACCAATGCCCAAGATCAACTGG 5460  
DB 5401 TCAGGGGGCTAGAAATCTGTTGCTATGAGGCCCTTCAACCAATGCCCAAGATCAACTGG 5460  
QY 5461 AATGATGATACAGCTGTGTGTGCTCTGTGTGTGAAGAGCTTTCATCATCACTTGC 5520  
DB 5461 AATGATGATACAGCTGTGTGTGCTCTGTGTGTGAAGAGCTTTCATCATCACTTGC 5520  
QY 5521 GCACAGGTGTCACCAATTTGTTGTGTCAGCAGCAGATCTGACAGAGCAATAGCT 5580  
DB 5521 GCACAGGTGTCACCAATTTGTTGTGTCAGCAGCAGATCTGACAGAGCAATAGCT 5580  
QY 5581 TCCATGCAATTTGGGAGATGTGTGAGGACCTGTGTGACCCGAGAGTGGGTGTGACA 5640  
DB 5581 TCCATGCAATTTGGGAGATGTGTGAGGACCTGTGTGACCCGAGAGTGGGTGTGACA 5640  
QY 5641 GTGTAGACTCTTACAGTGCAGAGCTGAGACCTTACTGATPACCCAGATCCCCACA 5700  
DB 5641 GTGTAGACTCTTACAGTGCAGAGCTGAGACCTTACTGATPACCCAGATCCCCACA 5700  
QY 5701 GCCACTACTGA 5711  
DB 5701 GCCACTACTGA 5711

RESULT 5  
US-08-603-753D-1  
Sequence 1, Application US/08603753D  
Patent No. 581857  
GENERAL INFORMATION:  
APPLICANT: HOLT, JEFFREY T.  
APPLICANT: JENSEN, ROY A.  
APPLICANT: PAGE, DAVID L.  
APPLICANT: KING, MARY-CLAIRE  
APPLICANT: SZABO, CELIA I.  
APPLICANT: JETTON, THOMAS L.  
APPLICANT: ROBINSON-BENION, CHERYL L.  
TITLE OF INVENTION: CHARACTERIZED BRCA1 AND BRCA2  
TITLE OF INVENTION: PROTEINS AND SCREENING AND THERAPEUTIC METHODS BASED ON  
TITLE OF INVENTION: CHARACTERIZED BRCA1 AND BRCA2 PROTEINS.  
NUMBER OF SEQUENCES: 29  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ARLES A. TAYLOR, JR.  
STREET: SUITE 1401, UNIVERSITY TOWER, 3100 TOWER  
CITY: DURHAM  
STATE: NORTH CAROLINA  
COUNTRY: USA  
ZIP: 27707  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 800 KB storage  
COMPUTER: IBM PC/XT/AT compatible  
OPERATING SYSTEM: Windows 3.1  
SOFTWARE: WORD PERFECT 6.1 and ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/603,753D  
FILING DATE: 20 FEB 1996  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.S. 08/373,799  
FILING DATE: 17 JAN 1995  
ATTORNEY/AGENT INFORMATION:  
NAME: ARLES A. TAYLOR, JR.  
REGISTRATION NUMBER: 39,395  
REFERENCE/DOCKET NUMBER: 1242/2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919) 493-8000  
TELEFAX: (919) 419-0383

TELEX:  
: INFORMATION FOR SEQ ID NO: 1:  
: SEQUENCE CHARACTERISTICS:  
: LENGTH: 5712  
: TYPE: nucleic acid  
: STRANDEDNESS: double  
: TOPOLOGY: linear  
: MOLECULE TYPE: cDNA to mRNA  
: HYPOTHETICAL: no  
: ANTI-SENSE: no  
: ORIGINAL SOURCE:  
: ORGANISM: Homo sapiens  
: INDIVIDUAL ISOLATE:  
: DEVELOPMENTAL STAGE: adult  
: TISSUE TYPE: female breast  
: CELL TYPE: ductal carcinoma in situ, invasive  
: CELL LINE: breast cancer and normal breast tissue  
: CELL LINE: not derived from a cell line  
: ORGANELLE: no  
: IMMEDIATE SOURCE:  
: LIBRARY: cDNA library derived from human  
: CLONE: obtained using published sequence  
: POSITION IN GENOME:  
: CHROMOSOME/SEGMENT: unknown  
: MAP POSITION: unknown  
: UNITS: unknown  
: FEATURE:  
: NAME/KEY: BRCA1  
: LOCATION: Genbank accession no. U14680  
: IDENTIFICATION METHOD: microscopically directed  
: IDENTIFICATION METHOD: sampling and nuclease protection assay  
: OTHER INFORMATION: gene encoding BRCA1 protein  
: PUBLICATION INFORMATION:  
: AUTHORS: Miki, Y., et. al.  
: TITLE: A strong candidate gene for the breast and  
: TITLE: ovarian cancer susceptibility gene BRCA1.  
: JOURNAL: Science  
: VOLUME: 266  
: PAGES: 66-71  
: DATE: 1994  
: RELEVANT RESIDUES IN SEQ ID NO: 1:  
: US-08-603-753D-1

Query Match 100.0%; Score 5709.4; DB 2; Length 5712;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 5710; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGCTGCTGAGACTTCTGAGACCCGACACAGGCTGGGGTTTCTCAGATACTGGGC 60  
DB 1 AGCTGCTGAGACTTCTGAGACCCGACACAGGCTGGGGTTTCTCAGATACTGGGC 60  
QY 61 CCTGGCTCAGAGAGGCTTCAACCTTCTGCTTGGGTAAGTTATTTGAAACAGAAAGAA 120  
DB 61 CCTGGCTCAGAGAGGCTTCAACCTTCTGCTTGGGTAAGTTATTTGAAACAGAAAGAA 120  
QY 121 TGGATTATCTGCTCTTCCGCTTGAAGAAGTACAAATGTCTATTAATGCTATGAGAAA 180  
DB 121 TGGATTATCTGCTCTTCCGCTTGAAGAAGTACAAATGTCTATTAATGCTATGAGAAA 180  
QY 181 TCTTAGAGTGTCCCATCTGTCTGAGTTGATCAAGAACTGTCTCCACAAATGTGACC 240  
DB 181 TCTTAGAGTGTCCCATCTGTCTGAGTTGATCAAGAACTGTCTCCACAAATGTGACC 240  
QY 241 ACATATTTTTCGAATTTTTCATGCTGAATCTTCTCAACAGAAAGAGGCTTTCACAGT 300  
DB 241 ACATATTTTTCGAATTTTTCATGCTGAATCTTCTCAACAGAAAGAGGCTTTCACAGT 300  
QY 301 GTCTCTTATGTAGAAGATATTAACCAAGAGAGCTTACAAAGAAATGACAGATTAGTC 360  
DB 301 GTCTCTTATGTAGAAGATATTAACCAAGAGAGCTTACAAAGAAATGACAGATTAGTC 360  
QY 361 AACTGTGTGAAGAGCTATTGAAATCATTTGTGCTTTTTCAGCTTGACAGAGTTTGAGT 420  
DB 361 AACTGTGTGAAGAGCTATTGAAATCATTTGTGCTTTTTCAGCTTGACAGAGTTTGAGT 420

DB 361 AACTGTGTGAAGAGCTATTGAAATCATTTGTGCTTTTTCAGCTTGACAGAGTTTGAGT 420  
QY 421 ATGCAAAAGAGCTATAATTTTTCGAAAAAGAAAAATATCTCTCCGACATCTAAAGATG 480  
DB 421 ATGCAAAAGAGCTATAATTTTTCGAAAAAGAAAAATATCTCTCCGACATCTAAAGATG 480  
QY 481 AAGTTTCTATCATCCAAAGTATGGGCTACAGAAACCGTCCCAAAAGACTTTCAGAGATG 540  
DB 481 AAGTTTCTATCATCCAAAGTATGGGCTACAGAAACCGTCCCAAAAGACTTTCAGAGATG 540  
QY 541 AACCAGAAATATCTTCTTTCGAGGAAACCAAGTCTGATGTCCAACTCTTAACCTTGAA 600  
DB 541 AACCAGAAATATCTTCTTTCGAGGAAACCAAGTCTGATGTCCAACTCTTAACCTTGAA 600  
QY 601 CTGTGAGAACTCTGAGCAAAAGAGCGGATACAACTCAAAAGACGCTGTACACTG 660  
DB 601 CTGTGAGAACTCTGAGCAAAAGAGCGGATACAACTCAAAAGACGCTGTCTACACTG 660  
QY 661 AATTGGGATCTGATCTTCTGAGATACCGTTAATAGGCAACTTATTTGAGTGGAG 720  
DB 661 AATTGGGATCTGATCTTCTGAGATACCGTTAATAGGCAACTTATTTGAGTGGAG 720  
QY 721 ATCAAGAAATTTTACAAATCAACCCCTCAAGGACCAAGGATGAATCAGTTGATCTG 780  
DB 721 ATCAAGAAATTTTACAAATCAACCCCTCAAGGACCAAGGATGAATCAGTTGATCTG 780  
QY 781 CAAAAAGAGCTGCTGTAATTTTCTGAGAGGATGTAACAAATACGATCATCAAC 840  
DB 781 CAAAAAGAGCTGCTGTAATTTTCTGAGAGGATGTAACAAATACGATCATCAAC 840  
QY 841 CCAGTAATATGATTTGGAACCACTGAGAGCGTGCAGCTGAGAGGATCCAGAAAGT 900  
DB 841 CCAGTAATATGATTTGGAACCACTGAGAGCGTGCAGCTGAGAGGATCCAGAAAGT 900  
QY 901 ATCAGGGATGTTCTGTTTCAAACTTGCACTGAGAGCCATGTGGCAAAATCTATGCCA 960  
DB 901 ATCAGGGATGTTCTGTTTCAAACTTGCACTGAGAGCCATGTGGCAAAATCTATGCCA 960  
QY 961 GGTCAATTACAGATAGAGAACGAGTTAATTAATCACTAAGAGACGAATGATGAGAA 1020  
DB 961 GGTCAATTACAGATAGAGAACGAGTTAATTAATCACTAAGAGACGAATGATGAGAA 1020  
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DB 1021 AGGCTGAATTCGTATATAAAGCAAAACAGCTGCTTACGAAAGAGCCAACTAATACAT 1080  
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DB 1081 GGGCTGGAATGAGAAACATGTAATGATAGCCGATCTCCAGACACAGAAAAAGGTAG 1140  
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DB 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAGATGGAATGACAGAAATGTCATGCT 1200  
QY 1201 CAGAGAACTCAGAGATACGTAAGTGTCTTGGATTAACACTAATAGCAGACTTACA 1260  
DB 1201 CAGAGAACTCAGAGATACGTAAGTGTCTTGGATTAACACTAATAGCAGACTTACA 1260  
QY 1261 AAGTTAATGAGTGTCTTTCAGAGATGAATCTTTAGTTTCTGATGATCAATGATG 1320  
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QY 1321 GGGAGTCTGAATCAAAATCCAAAGAGTGAATGATGAGAGCTTCTAATAGGTAGATG 1380  
DB 1321 GGGAGTCTGAATCAAAATCCAAAGAGTGAATGATGAGAGCTTCTAATAGGTAGATG 1380  
QY 1381 AATATTCGTGTTCTTTCAGAGAAATAGACTTACTGCGCAGATCTCATGAGCTTTAA 1440  
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QY 1441 TATGTAAAGTGAAGAGTCACTCCAAATCAGTAGAGAGTAAATTTGAGAACAAATAT 1500  
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Db 5701 GCCACTACTGA 5711

RESULT 6  
US-09-099-753-1  
; Sequence 1, Application US/0909753  
; Patent No. 6149903  
; GENERAL INFORMATION:  
; APPLICANT: HOLT, JEFFREY T.

APPLICANT: JENSEN, ROY A.  
 APPLICANT: PAGE, DAVID L.  
 APPLICANT: KING, MARY-CLAIRE  
 APPLICANT: SZABO, CSILLA I.  
 APPLICANT: JETTON, THOMAS L.  
 APPLICANT: ROBINSON-BENION, CHERYL L.  
 APPLICANT: THOMPSON, MARILYN E.  
 TITLE OF INVENTION: CHARACTERIZED BRCA1 AND BRCA2  
 TITLE OF INVENTION: PROTEINS AND SCREENING AND THERAPEUTIC METHODS BASED ON  
 TITLE OF INVENTION: CHARACTERIZED BRCA1 AND BRCA2 PROTEINS.  
 NUMBER OF SEQUENCES: 29  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: ARLES A. TAYLOR, JR.  
 STREET: SUITE 1401, UNIVERSITY TOWER, 3100 TOWER  
 STREET: BOULEVARD  
 CITY: DURHAM  
 STATE: NORTH CAROLINA  
 COUNTRY: USA  
 ZIP: 27707  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette, 3.50 inch, 800 KB storage  
 COMPUTER: IBM PC/XT/AT compatible  
 OPERATING SYSTEM: Windows 3.1  
 SOFTWARE: WORD PERFECT 6.1 and ASCII  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/099,753  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/603,753  
 FILING DATE: 20 FEB 1996  
 APPLICATION NUMBER: U.S. 08/373,799  
 FILING DATE: 17 JAN 1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: ARLES A. TAYLOR, JR.  
 REGISTRATION NUMBER: 39,395  
 REFERENCE/DOCKET NUMBER: 1242/2  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (919) 493-8000  
 TELEFAX: (919) 419-0383  
 TELETYPE:  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 5712  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA to mRNA  
 HYPOTHEICAL: no  
 ANTI-SENSE: no  
 ORIGINAL SOURCE:  
 ORGANISM: Homo sapiens  
 INDIVIDUAL ISOLATE:  
 DEVELOPMENTAL STAGE: adult  
 TISSUE TYPE: female breast  
 CELL TYPE: ductal carcinoma in situ, invasive  
 CELL LINE: breast cancer and normal breast tissue  
 CELL LINE: not derived from a cell line  
 ORGANELLER: no  
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 LIBRARY: cDNA library derived from human  
 CLONE: obtained using published sequence  
 POSITION IN GENOME:  
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 MAP POSITION: unknown  
 UNITS: unknown  
 FEATURE:  
 NAME/KEY: BRCA1  
 LOCATION: GenBank accession no. U14680  
 IDENTIFICATION METHOD: microscopically directed  
 IDENTIFICATION METHOD: sampling and nuclease protection assay  
 OTHER INFORMATION: gene encoding BRCA1 protein  
 PUBLICATION INFORMATION:

AUTHORS: Miki, Y., et. al.  
 TITLE: A strong candidate gene for the breast and  
 TITLE: ovarian cancer susceptibility gene BRCA1.  
 JOURNAL: Science  
 VOLUME: 266  
 PAGES: 66-71  
 DATE: 1994  
 RELEVANT RESIDUES IN SEQ ID NO: 1:  
 US-09-099-753-1  
 Query Match 100.0%; Score 5709.4; DB 3; Length 5712;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 5710; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
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# RESULT 7 US-08-986-106-1

Sequence 1, Application US/08986106  
Patent No. 6,177,410

GENERAL INFORMATION:

APPLICANT: HOLT, JEFFREY T.  
APPLICANT: JENSEN, ROY A.  
APPLICANT: KING, MARY-CLAIRE  
APPLICANT: STEINER, MITCHELL S.  
APPLICANT: ROBINSON-BENION, CHERYL L.  
APPLICANT: THOMPSON, MARILYN E.  
TITLE OF INVENTION: THERAPEUTIC METHODS FOR  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ARLES A. TAYLOR, JR.  
STREET: SUITE 1401, UNIVERSITY TOWER, 3100 TOWER  
STREET: BOULEVARD  
CITY: DURHAM  
STATE: NORTH CAROLINA  
COUNTRY: USA  
ZIP: 27707

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.44MB storage  
COMPUTER: IBM PC/XT/AT compatible  
OPERATING SYSTEM: Windows 3.1  
SOFTWARE: WORD PERFECT 6.1 and ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/986,106  
FILING DATE:

CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/603,753  
FILING DATE: 20 FEB 1996  
ATTORNEY/AGENT INFORMATION:  
NAME: ARLES A. TAYLOR, JR.  
REGISTRATION NUMBER: 39,395  
REFERENCE/DOCKET NUMBER: 1242/3  
TELECOMMUNICATION INFORMATION:

```

TELEPHONE: (919) 493-8000
TELEFAX: (919) 419-0383
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5712
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: BRCA1
LOCATION: Genbank accession no. U14680
PUBLICATION INFORMATION:
AUTHORS: Miki, Y., et. al.
TITLE: A strong candidate gene for the breast and
        ovarian cancer susceptibility gene BRCA1.
JOURNAL: Science
VOLUME: 266
PAGES: 66-71
DATE: 1994
US-08-986-106-1

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Query Match 100.0%; Score 5709.4; DB 4; Length 5712;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 5710; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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## RESULT 8

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US-09-007-678B-47
; Sequence 47, Application US/09007678B
; Patent No. 6342483
; GENERAL INFORMATION:
; APPLICANT: HOLT, JEFFREY T.
; APPLICANT: JENSEN, ROY A.
; APPLICANT: PAGE, DAVID L.
; APPLICANT: OBERMILLER, PATRICE S.
; APPLICANT: ROBINSON-BENION, CHERYL L.
; APPLICANT: THOMPSON, MARILYN E.
; TITLE OF INVENTION: METHOD FOR DETECTION AND TREATMENT OF BREAST CANCER
; FILE REFERENCE: Attorney Docket No. 6342483 1242-1-2-2
; CURRENT APPLICATION NUMBER: US/09/007,678B
; PRIOR FILING DATE: 1998-01-15
; PRIOR APPLICATION NUMBER: 08/373,799
; PRIOR FILING DATE: 1995-01-17
; PRIOR APPLICATION NUMBER: 08/182,961
; PRIOR FILING DATE: 1994-01-14
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: Microsoft Wordpad
; SEQ ID NO 47
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (120)..(5708)

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; NAME/KEY: misc feature
; LOCATION: (4532)..(4535)
; OTHER INFORMATION: Xaa=any amino acid
US-09-007-678B-47

Query Match      100.0%; Score 5709.4; DB 4; Length 5712;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5710; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 841 CAGTATATATGATTTGAACACCACTGAGAGCGTGCAGCTGAGAGGATCCAGAAAGT 900
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Db 3661 TCCGAAGAGAGAGAGCTTAAGAGAGTCTTACCTTTCACCCATACATTTGGCTCAGG 3720  
Qy 3721 GTTACCGAAGAGAGAGAGTAAAGTCTCAGAGAGAGAGCTTAATCTAGTGAAGATG 3780  
Db 3721 GTTACCGAAGAGAGAGAGTAAAGTCTCAGAGAGAGAGCTTAATCTAGTGAAGATG 3780  
Qy 3781 AAGAGCTTCCCTGCTTCCAAACATTTGTTATTTGTTAAAGTAAACATATATCTTCTCAGT 3840  
Db 3781 AAGAGCTTCCCTGCTTCCAAACATTTGTTATTTGTTAAAGTAAACATATATCTTCTCAGT 3840  
Qy 3841 CTACTAGGCAATAGACCGGTTGCTACCGAGTCTCTGTCTAAGAACACAGAGAGATTTAT 3900  
Db 3841 CTACTAGGCAATAGACCGGTTGCTACCGAGTCTCTGTCTAAGAACACAGAGAGATTTAT 3900  
Qy 3901 TATCATTTGAAGATTAAGCTTAATATGATGAGTAAACAGGTAATTTGSCAAAGGCACTCTC 3960  
Db 3901 TATCATTTGAAGATTAAGCTTAATATGATGAGTAAACAGGTAATTTGSCAAAGGCACTCTC 3960  
Qy 3961 AGGAACATCACTTAGTGAAGAAACAAATGTTCTGCTAGCTTTCTTCTCAAGTGA 4020  
Db 3961 AGGAACATCACTTAGTGAAGAAACAAATGTTCTGCTAGCTTTCTTCTCAAGTGA 4020  
Qy 4021 GTGAATTGGAAGATTAAGCTCAAAATACCAACCCAGAGTCTTTCTTAATGGTCTT 4080  
Db 4021 GTGAATTGGAAGATTAAGCTCAAAATACCAACCCAGAGTCTTTCTTAATGGTCTT 4080  
Qy 4081 CCAAAACAATGAGGATCACTGTAAGAGCCAGGAGTTGGTCTGAGTGAAGAGAAATTTGG 4140  
Db 4081 CCAAAACAATGAGGATCACTGTAAGAGCCAGGAGTTGGTCTGAGTGAAGAGAAATTTGG 4140  
Qy 4141 TTTCAATGATGAAGAAAGAGAAACGGGCTTGAAGAAATTAATCAAGAGAGCAAGCA 4200  
Db 4141 TTTCAATGATGAAGAAAGAGAAACGGGCTTGAAGAAATTAATCAAGAGAGCAAGCA 4200  
Qy 4201 TGAATTTAACTTAAGTGAAGAGAGATCTGGGTTGAGATGAAGAAACAGGCTCTGAG 4260  
Db 4201 TGAATTTAACTTAAGTGAAGAGAGATCTGGGTTGAGATGAAGAAACAGGCTCTGAG 4260

Qy 4261 ACTGCTCAGGAGCTATCTCTCAGAGTGAATTTTAACTCAGCAGAGGATACCAATGC 4320  
Db 4261 ACTGCTCAGGAGCTATCTCTCAGAGTGAATTTTAACTCAGCAGAGGATACCAATGC 4320  
Qy 4321 AACATTAACCTGATTAAGCTTCCAGAGAAATGGCTGAATTAAGAGCTGTTTGAACAGC 4380  
Db 4321 AACATTAACCTGATTAAGCTTCCAGAGAAATGGCTGAATTAAGAGCTGTTTGAACAGC 4380  
Qy 4381 ATGGAGCCAGGCTTCTTAAGAGTACCTTCAATCAATGAGTCTTCTGCCCCCTGAG 4440  
Db 4381 ATGGAGCCAGGCTTCTTAAGAGTACCTTCAATCAATGAGTCTTCTGCCCCCTGAG 4440  
Qy 4441 ACCGCGAAATTCAGAAACAAAGCAATCAGAAAAAGCAGTATTAATCTCAGAAAAAGTA 4500  
Db 4441 ACCGCGAAATTCAGAAACAAAGCAATCAGAAAAAGCAGTATTAATCTCAGAAAAAGTA 4500  
Qy 4501 GTGAATACCTTAATAGCCAGAAATCCAGAAAGGCTTTCTGCTGACAAAGTTGAGGTCTG 4560  
Db 4501 GTGAATACCTTAATAGCCAGAAATCCAGAAAGGCTTTCTGCTGACAAAGTTGAGGTCTG 4560  
Qy 4561 CAGATGTTCTACAGTAAATTAAGAAACAGAGTGAAGTCAATCCCTTCTAAT 4620  
Db 4561 CAGATGTTCTACAGTAAATTAAGAAACAGAGTGAAGTCAATCCCTTCTAAT 4620  
Qy 4621 GCCCATCATTAATGATGATGAGTGAATGACAGAGTTCCTGAGGAGTCTTCAAGATGA 4680  
Db 4621 GCCCATCATTAATGATGATGAGTGAATGACAGAGTTCCTGAGGAGTCTTCAAGATGA 4680  
Qy 4681 ACTAACCATCTCAAGAGAGCTCATTAAGGTTGTAATGAGAGCAACAGCTGAG 4740  
Db 4681 ACTAACCATCTCAAGAGAGCTCATTAAGGTTGTAATGAGAGCAACAGCTGAG 4740  
Qy 4741 AGTCTGGGCCACAGATTTGAAGGAAACATCTTAATCTGCAAGCAAGATCTAGAGGAA 4800  
Db 4741 AGTCTGGGCCACAGATTTGAAGGAAACATCTTAATCTGCAAGCAAGATCTAGAGGAA 4800  
Qy 4801 CCCCTTAACCTGAATCTGAATCAGCTCTTCTCTGATGACCTGAAATCTGATCTTCTG 4860  
Db 4801 CCCCTTAACCTGAATCTGAATCAGCTCTTCTCTGATGACCTGAAATCTGATCTTCTG 4860  
Qy 4861 AAGACAGAGCCAGAGATGAGTCTGTTGGCAACATACCATCTTCAACCTCTGCAATGA 4920  
Db 4861 AAGACAGAGCCAGAGATGAGTCTGTTGGCAACATACCATCTTCAACCTCTGCAATGA 4920  
Qy 4921 AAGTTCCTCAATTTGAAGTGAAGATCTGCCAGAGTCCAGGCTGCTCATATCACTG 4980  
Db 4921 AAGTTCCTCAATTTGAAGTGAAGATCTGCCAGAGTCCAGGCTGCTCATATCACTG 4980  
Qy 4981 ATACTGCTGGGATTAATGCAATGGAAGAAAGTGAAGAGAGGAGAGCCAGAAATTTGAG 5040  
Db 4981 ATACTGCTGGGATTAATGCAATGGAAGAAAGTGAAGAGAGGAGAGCCAGAAATTTGAG 5040  
Qy 5041 CTTCAACAGAAAGGATCAACAAAGAGATGTCATGAGTGTGCTGCTGAGCCAGAAAG 5100  
Db 5041 CTTCAACAGAAAGGATCAACAAAGAGATGTCATGAGTGTGCTGCTGAGCCAGAAAG 5100  
Qy 5101 AATTTATGCTCGTGTCAAGTTCGCAAGAAACACACATCACTTTAATCTAATTA 5160  
Db 5101 AATTTATGCTCGTGTCAAGTTCGCAAGAAACACACATCACTTTAATCTAATTA 5160  
Qy 5161 CTGAAGAGACTACTCATGTTGTTATGAAGAAACAGATGCTGAGTGTGTTGAACGGGAC 5220  
Db 5161 CTGAAGAGACTACTCATGTTGTTATGAAGAAACAGATGCTGAGTGTGTTGAACGGGAC 5220  
Qy 5221 TGAATATTTTCTAGGAATTTGCGGAGAGAAATGGGTAGTTAGCTATTTCTGGGTGACC 5280  
Db 5221 TGAATATTTTCTAGGAATTTGCGGAGAGAAATGGGTAGTTAGCTATTTCTGGGTGACC 5280  
Qy 5281 AGTCTATTAAGAAAGAAATGCTGAATGAAGATTTTGAAGTCAAGAGAGATGTGG 5340  
Db 5281 AGTCTATTAAGAAAGAAATGCTGAATGAAGATTTTGAAGTCAAGAGAGATGTGG 5340

|    |      |  |      |
|----|------|--|------|
| OY | 5341 | CCAAATGGAAGAAACACCAACAGGTCCAAAGCCGACAAGAAATCCACAGACAGAAAGATCT  | 5400 |
| Db | 5341 | TCATGGAAGAAACCAACCAAGGTCCAAAGCCGACAAGAAATCCACAGACAGAAAGATCT    | 5400 |
| OY | 5401 | TCAGGGGGCTAGAAATCTGTGCTATGGGCCCTTTCACCAACATGCCCCAGATCAACTGG    | 5460 |
| Db | 5401 | TCAGGGGGCTAGAAATCTGTGCTATGGGGCCCTTTCACCAACATGCCCCAGATCAACTGG   | 5460 |
| OY | 5461 | AATGATGCTACAGCTGTGTGTGCTTCTGTGTGTGAAGAGCTTTCATCATTCACCCCTTG    | 5520 |
| Db | 5461 | AATGATGCTACAGCTGTGTGTGCTTCTGTGTGTGAAGAGCTTTCATCATTCACCCCTTG    | 5520 |
| OY | 5521 | GCACAGGTGTCCACCAATGTGTGTTGTGACCCAGATGCTTCGACAGAGCAATGSGCT      | 5580 |
| Db | 5521 | GCACAGGTGTCCACCAATGTGTGTTGTGACCCAGATGCTTCGACAGAGCAATGSGCT      | 5580 |
| OY | 5581 | TCATATGCAATTGGGACAGATGTGTGAGGCACTCTGTGTGTGACCCGAGAGTGGGTGTGACA | 5640 |
| Db | 5581 | TCATATGCAATTGGGACAGATGTGTGAGGCACTCTGTGTGTGACCCGAGAGTGGGTGTGACA | 5640 |
| OY | 5641 | GTTGTGCACTCTACCAAGTGTGAGAGCTGTGACACTACTGATATACCCAGATCCCCCAACA  | 5700 |
| Db | 5641 | GTTGTGCACTCTACCAAGTGTGAGAGCTGTGACACTACTGATATACCCAGATCCCCCAACA  | 5700 |
| OY | 5701 | GGCACTACTGA 5711   |      |
| Db | 5701 | GGCACTACTGA 5711   |      |

RESULT 9  
 US-08-480-784-1  
 Sequence 1, Application US/08480784  
 Patent No. 5693473  
 GENERAL INFORMATION:  
 APPLICANT: Skolnick, Mark H.  
 APPLICANT: Goldgar, David E.  
 APPLICANT: Miki, Yoshio  
 APPLICANT: Swenson, Jeff  
 APPLICANT: Kamb, Alexander  
 APPLICANT: Harbman, Keith D.  
 APPLICANT: Shattuck-Eidens, Donna M.  
 APPLICANT: Tavliglian, Sean V.  
 APPLICANT: Wiseman, Roger W.  
 TITLE OF INVENTION: Futreal, P. Andrew  
 TITLE OF INVENTION: 17q-Linked Breast and Ovarian Cancer  
 TITLE OF INVENTION: Susceptibility Gene  
 NUMBER OF SEQUENCES: 85  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP  
 STREET: 1201 New York Avenue, N.W., Suite 1000  
 CITY: Washington  
 STATE: DC  
 COUNTRY: USA  
 ZIP: 20005  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/480,784  
 FILING DATE:  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/409,305  
 FILING DATE: 24-MAR-1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/348,824  
 FILING DATE: 29-NOV-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/308,104  
 FILING DATE: 16-SEP-1994  
 PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/300,266  
 FILING DATE: 02-SEP-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/289,221  
 FILING DATE: 12-AUG-1994  
 ATTORNEY/AGENT INFORMATION:  
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 TELEPHONE: 202-962-4810  
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 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 5914 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 ORIGINAL SOURCE:  
 ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 120..5711  
 US-08-480-784-1

|    | Query Marcell  | 100.0%         | Score 5709.4 | DB 1     | Length 5914 |  |
|----|--|----------------|--------------|----------|-------------|--|
|    | Best Local Similarity  | 100.0%         | Pred. No. 0  |          |             |  |
|    | Matches 5710   | Conservative 0 | Mismatches 1 | Indels 0 | Gaps 0      |  |
| Qy | 1 AGCTGCTGAGACTTCTCTGGACCCCGCACACAGCTGTGGGGTTTCTCAGATACATCGGCC   | 60             |              |          |             |  |
| Db | 1 AGCTCGCTGAGACTTCTCTGGACCCCGCACACAGCTGTGGGGTTTCTCAGATACATCGGCC  | 60             |              |          |             |  |
| Qy | 61 CCGGGCTCAGAGAGGCTTCAACCCCTGCTGGGTAAATTATTTGAGAACAGAAAGAA      | 120            |              |          |             |  |
| Db | 61 CCGGGCTCAGAGAGGCTTCAACCCCTGCTGGGTAAATTATTTGAGAACAGAAAGAA      | 120            |              |          |             |  |
| Qy | 121 TGGATTTATCTGCTCTTGGCGTTGAGAGAGTACAAAATGTCAATTAATGCTATGCGAGAA | 180            |              |          |             |  |
| Db | 121 TGGATTTATCTGCTCTTGGCGTTGAGAGAGTACAAAATGTCAATTAATGCTATGCGAGAA | 180            |              |          |             |  |
| Qy | 181 TCTTAAGTGTCCCATCTGTCTGGAGTGTACAGAAACCTGTCTCCACAAGGTGAC       | 240            |              |          |             |  |
| Db | 181 TCTTAAGTGTCCCATCTGTCTGGAGTGTACAGAAACCTGTCTCCACAAGGTGAC       | 240            |              |          |             |  |
| Qy | 241 ACATATTTTGGCAATTTTGGCATGTGCAAACTTCCAAACGAGAAAGGGCTTCCAGT     | 300            |              |          |             |  |
| Db | 241 ACATATTTTGGCAATTTTGGCATGTGCAAACTTCCAAACGAGAAAGGGCTTCCAGT     | 300            |              |          |             |  |
| Qy | 301 GTTCCTTATGTGAAGATGATATACCAAAAGAGCTTACAAAGAAAGTACGATTTAGTC    | 360            |              |          |             |  |
| Db | 301 GTTCCTTATGTGAAGATGATATACCAAAAGAGCTTACAAAGAAAGTACGATTTAGTC    | 360            |              |          |             |  |
| Qy | 361 AACCTGTGAAGAGCTATTGAAAATCATTTGTGCTTTACGTTGACACAGGTTTGAGT     | 420            |              |          |             |  |
| Db | 361 AACCTGTGAAGAGCTATTGAAAATCATTTGTGCTTTACGTTGACACAGGTTTGAGT     | 420            |              |          |             |  |
| Qy | 421 ATGCAAAACGCTATATTTTGGCAAAAAGAAAAATTAATCTCTGGAACATCTTAAAAGATG | 480            |              |          |             |  |
| Db | 421 ATGCAAAACGCTATATTTTGGCAAAAAGAAAAATTAATCTCTGGAACATCTTAAAAGATG | 480            |              |          |             |  |
| Qy | 481 AAGTTCTATCATCCAAAGTATGGCTACAGAAACCTGCCAAAAGACTTTCACAGAGTG    | 540            |              |          |             |  |
| Db | 481 AAGTTCTATCATCCAAAGTATGGCTACAGAAACCTGCCAAAAGACTTTCACAGAGTG    | 540            |              |          |             |  |
| Qy | 541 AACCGAAAATCTTCTCTTGACAGAAACCAAGTCTCAAGTGTCAACCTCTTAACCTTGGAA | 600            |              |          |             |  |
| Db | 541 AACCGAAAATCTTCTCTTGACAGAAACCAAGTCTCAAGTGTCAACCTCTTAACCTTGGAA | 600            |              |          |             |  |
| Qy | 601 CTGTGGAACCTGTGAGACAAAGCAGCGGATACAACTCAAAAGAGCTGTGTACATTG     | 660            |              |          |             |  |



Db 601 CTGAGAACTCTGAGAGCAAGACGCGATACAACTCAAAAGACCTGCTACATG 660  
Qy 661 AATTGGATCTGATCTCTTGAAGATCCGTTAATATAGCACTATGAGTGGAG 720  
Db 661 AATTGGATCTGATCTCTTGAAGATCCGTTAATATAGCACTATGAGTGGAG 720  
Qy 721 ATCAAGATTTGTTACAAATCAACCCCTCAAGAAACAGAGATGAATCATGTTGGATCTG 780  
Db 721 ATCAAGATTTGTTACAAATCAACCCCTCAAGAAACAGAGATGAATCATGTTGGATCTG 780  
Qy 781 CAAAAAGGCTGCTGTTGAAATTTTCTGAGACGATGTAACAAATCTGAACATCATCAC 840  
Db 781 CAAAAAGGCTGCTGTTGAAATTTTCTGAGACGATGTAACAAATCTGAACATCATCAC 840  
Qy 841 CCAATTAATGATTTGAACACCACTGAGAGGCTGAGAGGCAATCCAGAAAGT 900  
Db 841 CCAATTAATGATTTGAACACCACTGAGAGGCTGAGAGGCAATCCAGAAAGT 900  
Qy 901 ATCAGGATGTTCTGTTCAAACTTGATGATGAGCATGAGCAAAATCATCTCA 960  
Db 901 ATCAGGATGTTCTGTTCAAACTTGATGATGAGCATGAGCAAAATCATCTCA 960  
Qy 961 GCTCATTAACAGATGAGAACAGAGTTTATTACTCACTAAAGACAGATGATGAAA 1020  
Db 961 GCTCATTAACAGATGAGAACAGAGTTTATTACTCACTAAAGACAGATGATGAAA 1020  
Qy 1021 AGGCTGAATCTGTAATTAAGCAAAAGCGCTGGCTTACAGAGAGCCATTAACAT 1080  
Db 1021 AGGCTGAATCTGTAATTAAGCAAAAGCGCTGGCTTACAGAGAGCCATTAACAT 1080  
Qy 1081 GGGCTGGAAGTAAAGAAACATGTAATGAGCGGATCCCAAGCAAGAAAAAGTAG 1140  
Db 1081 GGGCTGGAAGTAAAGAAACATGTAATGAGCGGATCCCAAGCAAGAAAAAGTAG 1140  
Qy 1141 ATCTGAATGCTGATCCCTGTGTGAGAAAGAAAGATGAATTAAGCAGAAATCGCATGCT 1200  
Db 1141 ATCTGAATGCTGATCCCTGTGTGAGAAAGAAAGATGAATTAAGCAGAAATCGCATGCT 1200  
Qy 1201 CAGAGATCTTAAGATTAAGATGATGCTTCTGATGAACATTAATAGCAATTCAGA 1260  
Db 1201 CAGAGATCTTAAGATTAAGATGATGCTTCTGATGAACATTAATAGCAATTCAGA 1260  
Qy 1261 AAGTTAATGATGATGTTTCCAGAAAGTATGATGATGATGATGATGATGATGATG 1320  
Db 1261 AAGTTAATGATGATGTTTCCAGAAAGTATGATGATGATGATGATGATGATGATG 1320  
Qy 1321 GGGAGCTGAATCAAAATGCAAAAGTATGATGATGATGATGATGATGATGATGATG 1380  
Db 1321 GGGAGCTGAATCAAAATGCAAAAGTATGATGATGATGATGATGATGATGATGATG 1380  
Qy 1381 AATATTTGCTGTTCTTCAAGAAATGATGATGATGATGATGATGATGATGATGATG 1440  
Db 1381 AATATTTGCTGTTCTTCAAGAAATGATGATGATGATGATGATGATGATGATGATG 1440  
Qy 1441 TATGTAAGATGAAGAGTCACTCCAAATCAGTAGAGATTAATTAAGAGCAAAATAT 1500  
Db 1441 TATGTAAGATGAAGAGTCACTCCAAATCAGTAGAGATTAATTAAGAGCAAAATAT 1500  
Qy 1501 TTGGAGAAACCTATCGAGAGAGGCAAGCTCCCACTTAAGCATGTAATGAAATATC 1560  
Db 1501 TTGGAGAAACCTATCGAGAGAGGCAAGCTCCCACTTAAGCATGTAATGAAATATC 1560  
Qy 1561 TAAATATAGAGATTTGTTACTGAGCACAAGATTAATCAAGAGCGTCCCTCAAAATA 1620  
Db 1561 TAAATATAGAGATTTGTTACTGAGCACAAGATTAATCAAGAGCGTCCCTCAAAATA 1620  
Qy 1621 AATTAAAGCGTAAAGAGAGATCATCAGAGCTTCACTCGAGATTTTATCAAGAAAG 1680  
Db 1621 AATTAAAGCGTAAAGAGAGATCATCAGAGCTTCACTCGAGATTTTATCAAGAAAG 1680  
Qy 1681 CAGATTTGGAGTTCAAAAGACTCTGAAATGATTAATCAGGAACTTAACCAAGCGAGC 1740  
Db 1681 CAGATTTGGAGTTCAAAAGACTCTGAAATGATTAATCAGGAACTTAACCAAGCGAGC 1740  
Db 1741 AGAATGCTCAAGTATGATTAATTAATGATGATGATGATGATGATGATGATGATGATG 1800  
Qy 1741 AGAATGCTCAAGTATGATTAATTAATGATGATGATGATGATGATGATGATGATGATG 1800  
Db 1801 CTATTCAGATGAGAAAAATCTTAACCAATAGATCACTCGAAAAAGATCTGCTTTCA 1860  
Qy 1801 CTATTCAGATGAGAAAAATCTTAACCAATAGATCACTCGAAAAAGATCTGCTTTCA 1860  
Db 1861 AAACGAAGCTGAACCTTAATAGAGAGATTAAGCAATATGAACTCGAATTAATATCC 1920  
Qy 1861 AAACGAAGCTGAACCTTAATAGAGAGATTAAGCAATATGAACTCGAATTAATATCC 1920  
Db 1921 ACAATTCAAAAGACCTTAAGAAATAGGCTGAGAGAGTCTTCAACAGGATATTC 1980  
Qy 1921 ACAATTCAAAAGACCTTAAGAAATAGGCTGAGAGAGTCTTCAACAGGATATTC 1980  
Db 1981 ATGCGCTTGAATAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2040  
Qy 1981 ATGCGCTTGAATAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2040  
Db 2041 TTGATGTTGTTCTTACAGTGAAGAGATTAAGCAAAAGATTAAGCAAAAGATTAAGCA 2100  
Qy 2041 TTGATGTTGTTCTTACAGTGAAGAGATTAAGCAAAAGATTAAGCAAAAGATTAAGCA 2100  
Db 2101 GGCAGAGCAAAACCTTAAGAACTCATGAAAGTAAAGACCTGCACTGAGCGCAAGAGA 2160  
Qy 2101 GGCAGAGCAAAACCTTAAGAACTCATGAAAGTAAAGACCTGCACTGAGCGCAAGAGA 2160  
Db 2161 GTAAACAGCAAAATGAAAGAGAGATTAAGCAAAAGATTAAGCAAAAGATTAAGCAAAAG 2220  
Qy 2161 GTAAACAGCAAAATGAAAGAGAGATTAAGCAAAAGATTAAGCAAAAGATTAAGCAAAAG 2220  
Db 2221 AGTTAACAATGCACTGCTGTTCTTAACTGATGATGATGATGATGATGATGATGATG 2280  
Qy 2221 AGTTAACAATGCACTGCTGTTCTTAACTGATGATGATGATGATGATGATGATGATG 2280  
Db 2281 TTGTCATCTGCTGCTTCAAGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 2340  
Qy 2281 TTGTCATCTGCTGCTTCAAGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 2340  
Db 2341 CTAAATATGCTGAAGACCCCAAGATCTCATGTTAAAGTGAAGAGGTTTTCAGAACTG 2400  
Qy 2341 CTAAATATGCTGAAGACCCCAAGATCTCATGTTAAAGTGAAGAGGTTTTCAGAACTG 2400  
Db 2401 AAAAGATCTGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2460  
Qy 2401 AAAAGATCTGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2460  
Db 2461 AAAAGATCTGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2460  
Qy 2461 AAAAGATCTGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2460  
Db 2461 AAAAGATCTGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2460  
Qy 2521 GTGTGAGTCAAGTGTGAGATTTGAAAGACCCCAAGAGGATTAATCTATGTTTTCAGAG 2580  
Db 2521 GTGTGAGTCAAGTGTGAGATTTGAAAGACCCCAAGAGGATTAATCTATGTTTTCAGAG 2580  
Qy 2581 ATTAATGAAATGACACAGAAAGCTTAATGATGATGATGATGATGATGATGATGATGATG 2640  
Db 2581 ATTAATGAAATGACACAGAAAGCTTAATGATGATGATGATGATGATGATGATGATGATG 2640  
Qy 2641 GGGAAACAGAGCTTAAGAAATGAGAAAGTGAATGATGATGATGATGATGATGATGATGATG 2700  
Db 2641 GGGAAACAGAGCTTAAGAAATGAGAAAGTGAATGATGATGATGATGATGATGATGATGATG 2700  
Qy 2701 TCAAGGTTTCAAGAGCGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2760  
Db 2701 TCAAGGTTTCAAGAGCGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2760  
Qy 2761 AATGTCACATTTCTGCTCCACTGCTGCTTAAAGAAACAAATGCAAAAGTCACTT 2820  
Db 2761 AATGTCACATTTCTGCTCCACTGCTGCTTAAAGAAACAAATGCAAAAGTCACTT 2820

|    |      |  |      |
|----|------|--|------|
| OY | 2821 | TTGAAATGTCGAACAAAAGAGAAATAACAAGAAAAGATGAGCTTAATCTCAAGCTGTAC    | 2880 |
| Db | 2821 | TTGAATGTGAAACAAAAGAGAAATAACAAGAAAAGATGAGCTTAATCTCAAGCTGTAC     | 2880 |
| OY | 2881 | AGACAGTTAAATATCACTGACAGGCTTCCGTGTGGTACAGAAAGATTAAGCAGTTGATA    | 2940 |
| Db | 2881 | AGACAGTTAAATATCACTGACAGGCTTCCGTGTGGTACAGAAAGATTAAGCAGTTGATA    | 2940 |
| OY | 2941 | ATGCCAAATGTATGATCAAAAGAGGCTCTAGGTTTGTCTATCATCTCAGTTCAAGAGCA    | 3000 |
| Db | 2941 | ATGCCAAATGTATGATCAAAAGAGGCTCTAGGTTTGTCTATCATCTCAGTTCAAGAGCA    | 3000 |
| OY | 3001 | ACGAATCTGGACTCATTTACTCCAAATTAACATGACCTTTTCAAAACCATATGTATAC     | 3060 |
| Db | 3001 | ACGAATCTGGACTCATTTACTCCAAATTAACATGACCTTTTCAAAACCATATGTATAC     | 3060 |
| OY | 3061 | CACCACTTTTCCCATCAAGTCATTTGTTAAAACTAAATGTAGAAAAATCTGTAGAGG      | 3120 |
| Db | 3061 | CACCACTTTTCCCATCAAGTCATTTGTTAAAACTAAATGTAGAAAAATCTGTAGAGG      | 3120 |
| OY | 3121 | AAAACCTTGGAGAACATTTCAATGTCACTGAAAAGAAATGGGAAATGAAACATTTCCA     | 3180 |
| Db | 3121 | AAAACCTTGGAGAACATTTCAATGTCACTGAAAAGAAATGGGAAATGAAACATTTCCA     | 3180 |
| OY | 3181 | GTACAGTAGACAAATTAAGCCGTATTAACATTAGAGAAAATGTTTTTAAAGAACAGCT     | 3240 |
| Db | 3181 | GTACAGTAGACAAATTAAGCCGTATTAACATTAGAGAAAATGTTTTTAAAGAACAGCT     | 3240 |
| OY | 3241 | CAGCAATATTATAGAGTAGTTCACAGTAAATGAAGTGGGCTCCAGTATTAATGAA        | 3300 |
| Db | 3241 | CAGCAATATTATAGAGTAGTTCACAGTAAATGAAGTGGGCTCCAGTATTAATGAA        | 3300 |
| OY | 3301 | TAGGTTCCAGTAGATGAAAAATTCAGAGGAACTGTATGAGAAACAGAGGCCCCAAATTGA   | 3360 |
| Db | 3301 | TAGGTTCCAGTAGATGAAAAATTCAGAGGAACTGTATGAGAAACAGAGGCCCCAAATTGA   | 3360 |
| OY | 3361 | ATGCTATGCTTAGATTAGGGGTTTTTGCAACCTGAGGCTATTAACAAGTCTTCTGGAA     | 3420 |
| Db | 3361 | ATGCTATGCTTAGATTAGGGGTTTTTGCAACCTGAGGCTATTAACAAGTCTTCTGGAA     | 3420 |
| OY | 3421 | GTAATTGTAGAGATCTCTAAATTAATAAAGCAAAATAGAAAGATTAATTAGACTGTTA     | 3480 |
| Db | 3421 | GTAATTGTAGAGATCTCTAAATTAATAAAGCAAAATAGAAAGATTAATTAGACTGTTA     | 3480 |
| OY | 3481 | ATACAGATTTCTCTCCATATCTGATTTAGATTAAGTAAACAGCTTAATGGGAATGTC      | 3540 |
| Db | 3481 | ATACAGATTTCTCTCCATATCTGATTTAGATTAAGTAAACAGCTTAATGGGAATGTC      | 3540 |
| OY | 3541 | ATGCATCTCAGGTTTGTCTGAGACACTGATGACCTGTATGATGATGTGAAATTAAGG      | 3600 |
| Db | 3541 | ATGCATCTCAGGTTTGTCTGAGACACTGATGACCTGTATGATGATGTGAAATTAAGG      | 3600 |
| OY | 3601 | AAGATACTAGTTTCTGCTGAAAAATGACATTAAGGAAAGTTTGCCTTTTGAACAAACGC    | 3660 |
| Db | 3601 | AAGATACTAGTTTCTGCTGAAAAATGACATTAAGGAAAGTTTGCCTTTTGAACAAACGC    | 3660 |
| OY | 3661 | TCACAGAAAGAGAGCTTAGACAGAGTCTTAGGCCCTTTACACCATACACATTTGGCTCAGG  | 3720 |
| Db | 3661 | TCACAGAAAGAGAGCTTAGACAGAGTCTTAGGCCCTTTACACCATACACATTTGGCTCAGG  | 3720 |
| OY | 3721 | GTTACCGAAGAGGGGCCAAAGAAATTAGAGTCTCTGAGAGACAACTTAATCTGTAGAGATG  | 3780 |
| Db | 3721 | GTTACCGAAGAGGGGCCAAAGAAATTAGAGTCTCTGAGAGACAACTTAATCTGTAGAGATG  | 3780 |
| OY | 3781 | AAGAGCTTCCCTGCTTCCAAACAACCTGTTATTTGTATTAAGTAAACAAATTAACCTTCAGT | 3840 |
| Db | 3781 | AAGAGCTTCCCTGCTTCCAAACAACCTGTTATTTGTATTAAGTAAACAAATTAACCTTCAGT | 3840 |
| OY | 3841 | CTACTAGGCATAGCACCGTGTGTTACCGAGTGTCTGTCTTAAGAACACAGAGAGAAATTAAT | 3900 |
| Db | 3841 | CTACTAGGCATAGCACCGTGTGTTACCGAGTGTCTGTCTTAAGAACACAGAGAGAAATTAAT | 3900 |

|    |      |  |      |
|----|------|--|------|
| QY | 3901 | TATCATTTGAAGATATGCTTAATATGACTGACGTAACACAGTAAATATTTGGCAAAAGCATCTC | 3960 |
| Db | 3901 | TATCATTTGAAGATATGCTTAATATGACTGACGTAACACAGTAAATATTTGGCAAAAGCATCTC | 3960 |
| QY | 3961 | AGGAACATCACCTTAGTAGAGGAAACAAATGTTCTGTAGCTGTGTTTCTTCACAGTGC       | 4020 |
| Db | 3961 | AGGAACATCACCTTAGTAGAGGAAACAAATGTTCTGTAGCTGTGTTTCTTCACAGTGC       | 4020 |
| QY | 4021 | GTGAATTTGAAAGACTGACTGCAAAATACAAACCCACAGATCTTTCTTGATTTGGTCTT      | 4080 |
| Db | 4021 | GTGAATTTGAAAGACTGACTGCAAAATACAAACCCACAGATCTTTCTTGATTTGGTCTT      | 4080 |
| QY | 4081 | CCAAACAAATAGAGCATATGCTCTGAAGACCAGGAGTTGTGCTAGTACAAAGAAATGG       | 4140 |
| Db | 4081 | CCAAACAAATAGAGCATATGCTCTGAAGACCAGGAGTTGTGCTAGTACAAAGAAATGG       | 4140 |
| QY | 4141 | TTTCGATGATGAAAGAAAGAGAAACGGGCTTGAAAGAAATATATCAAGCAAGCAAAACA      | 4200 |
| Db | 4141 | TTTCGATGATGAAAGAAAGAGAAACGGGCTTGAAAGAAATATATCAAGCAAGCAAAACA      | 4200 |
| QY | 4201 | TGGAATTCAAACTTAGTGTAAGCAGCATCTGGGTGTGAGAGTGAACAACAGCTCTGTAG      | 4260 |
| Db | 4201 | TGGAATTCAAACTTAGTGTAAGCAGCATCTGGGTGTGAGAGTGAACAACAGCTCTGTAG      | 4260 |
| QY | 4261 | ACTGCTCAGGGCTATCTCTCTCAGAGTGACATTTTAACCACTCACAGAGGATACATATGC     | 4320 |
| Db | 4261 | ACTGCTCAGGGCTATCTCTCTCAGAGTGACATTTTAACCACTCACAGAGGATACATATGC     | 4320 |
| QY | 4321 | AAACAATACCTGATTAAGAGCTCCAGAGGAAATGGCGTAACCTGAAGCTGTGTAAACAGC     | 4380 |
| Db | 4321 | AAACAATACCTGATTAAGAGCTCCAGAGGAAATGGCGTAACCTGAAGCTGTGTAAACAGC     | 4380 |
| QY | 4381 | ATGGAGCAGACCTCTTCAACAGTAAACCTTCATCATTAAGTACTCTTCTGCCCCTTGAG      | 4440 |
| Db | 4381 | ATGGAGCAGACCTCTTCAACAGTAAACCTTCATCATTAAGTACTCTTCTGCCCCTTGAG      | 4440 |
| QY | 4441 | ACCTGCGAATTCAGAACAAAGCAATCAGAAAAAGCATTTAACTTACACGAAAAAGTA        | 4500 |
| Db | 4441 | ACCTGCGAATTCAGAACAAAGCAATCAGAAAAAGCATTTAACTTACACGAAAAAGTA        | 4500 |
| QY | 4501 | GTGAATTCCTGATTAAGCAGAAATCCAGAGGCTTTCTGCTGACAAAGTTGAGGTGCTG       | 4560 |
| Db | 4501 | GTGAATTCCTGATTAAGCAGAAATCCAGAGGCTTTCTGCTGACAAAGTTGAGGTGCTG       | 4560 |
| QY | 4561 | CAGATAGTCTTACCAAGTAAAAATAAAGAACAGGAGTGAAGGTCAATCCCTCTCTAAAT      | 4620 |
| Db | 4561 | CAGATAGTCTTACCAAGTAAAAATAAAGAACAGGAGTGAAGGTCAATCCCTCTCTAAAT      | 4620 |
| QY | 4621 | GCCCATCATTAAGATGATAGTGTGTACATGACAGTGTCTCTGGAGTCTTCAGAAATGAA      | 4680 |
| Db | 4621 | GCCCATCATTAAGATGATAGTGTGTACATGACAGTGTCTCTGGAGTCTTCAGAAATGAA      | 4680 |
| QY | 4681 | ACTTACCATCTTCAAGAGAGCTCATTTAAGTGTGTTGATGTGGAGAGCAACAGCTGGAAG     | 4740 |
| Db | 4681 | ACTTACCATCTTCAAGAGAGCTCATTTAAGTGTGTTGATGTGGAGAGCAACAGCTGGAAG     | 4740 |
| QY | 4741 | AGTCTGGGCCCACAGATTTGAACGAAACATTTTCTTGCCAAAGCAAGTATTAAGGGA        | 4800 |
| Db | 4741 | AGTCTGGGCCCACAGATTTGAACGAAACATTTTCTTGCCAAAGCAAGTATTAAGGGA        | 4800 |
| QY | 4801 | CCCCTTACTTGGAATCTTGGAATCAGCCTCTTCTCTGTATGACCTTGAAATCTGATCTTCTG   | 4860 |
| Db | 4801 | CCCCTTACTTGGAATCTTGGAATCAGCCTCTTCTCTGTATGACCTTGAAATCTGATCTTCTG   | 4860 |
| QY | 4861 | AAAGACAGAGCCCCAGAGTCAAGTCTGTGTGGCAACATACATCTTCAACCTCTGCAATTTGA   | 4920 |
| Db | 4861 | AAAGACAGAGCCCCAGAGTCAAGTCTGTGTGGCAACATACATCTTCAACCTCTGCAATTTGA   | 4920 |
| QY | 4921 | AAAGTTCGCCAATTAAGAAAGTTGCAAAATCTGCCCCAGAGTCCAGAGCTGCTCATACTG     | 4980 |
| Db | 4921 | AAAGTTCGCCAATTAAGAAAGTTGCAAAATCTGCCCCAGAGTCCAGAGCTGCTCATACTG     | 4980 |
| QY | 4981 | ATACTGCTGGTATATATGCAATGGAACAAAGTGTGACAGGAGAAAGCCAGAAATTTGACG     | 5040 |

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Db      4981 ATACTGCTGGGTATTAATGCAATGAGAAAGTGTGACAGAGGAGAAACCGAATTTGACAG 5040
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Db      5041 CTTCAACAGAAAGGGCTCAACAAAGATGTCATGAGTGTCTGGGCTGACCCCAAG 5100
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QY      5221 TGAATTTTTCATGAGAAATGCGGAGAGAAATGGGTAGTTAGTATTTCTGGGTGACC 5280
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QY      5281 AGTCTATTAAAGAAAGAAATGCTGATGAGCATGATTTTGAAGTCAGAGAGATG 5340
Db      5281 AGTCTATTAAAGAAAGAAATGCTGATGAGCATGATTTTGAAGTCAGAGAGATG 5340
QY      5341 TCAATGAGAAACCAACCAAGTCCAAAGCGAGCAGAGAAATCCAGAGCAAAAGATCT 5400
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QY      5401 TCAGGGGGCTAGAAATGTTGTCATGAGGCTTCAACCAATGCCCAAGATCAATG 5460
Db      5401 TCAGGGGGCTAGAAATGTTGTCATGAGGCTTCAACCAATGCCCAAGATCAATG 5460
QY      5461 AATGATGATGACAGCTGTGTGCTCTCTGATGAGAGAGCTTTCATCATTCACCTTG 5520
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QY      5521 GCACAGGTGTCACCCCAATTTGTGTTGTGACCCAGATGCTGACAGAGCAATGCT 5580
Db      5521 GCACAGGTGTCACCCCAATTTGTGTTGTGACCCAGATGCTGACAGAGCAATGCT 5580
QY      5581 TCCATGCAATTTGGGCAATGTGTGAGCACCCTGTGTGACCCGAGATGGGTGTGACA 5640
Db      5581 TCCATGCAATTTGGGCAATGTGTGAGCACCCTGTGTGACCCGAGATGGGTGTGACA 5640
QY      5641 GTGTAGACCTCTACCACTGCGAGAGCTGTGACCTTCTGATACCTGATACCTGAT 5700
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QY      5701 GCCACTACTGA 5711
Db      5701 GCCACTACTGA 5711

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RESULT 10
US-08-483-553-1
; Sequence 1, Application US/08483553
; Patent No. 5709999
; GENERAL INFORMATION:
; APPLICANT: Skolnick, Mark H.
; APPLICANT: Goldfar, David E.
; APPLICANT: Miki, Yoshio
; APPLICANT: Swenson, Jeff
; APPLICANT: Kamb, Alexander
; APPLICANT: Harshe, Keith D.
; APPLICANT: Shattuck-Eidens, Donna M.
; APPLICANT: Tavelian, Sean V.
; APPLICANT: Wiseman, Roger W.
; APPLICANT: Futreal, P. Andrew
; TITLE OF INVENTION: 17q-Linked Breast and Ovarian Cancer
; TITLE OF INVENTION: Susceptibility Gene
; NUMBER OF SEQUENCES: 85
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, N.W., Suite 1000

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? CITY: Washington
? STATE: DC
? COUNTRY: USA
? ZIP: 20005
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patent Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/483,553
? FILING DATE:
? CLASSIFICATION: 435
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 08/409,305
? FILING DATE: 24-MAR-1995
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 08/348,824
? FILING DATE: 29-NOV-1994
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 08/308,104
? FILING DATE: 16-SEP-1994
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 08/300,266
? FILING DATE: 02-SEP-1994
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 08/289,221
? FILING DATE: 12-AUG-1994
? ATTORNEY/AGENT INFORMATION:
? NAME: Ihnen, Jeffrey L.
? REGISTRATION NUMBER: 28,957
? REFERENCE/DOCKET NUMBER: 24884-109347
? TELEPHONE: 202-962-4810
? TELEFAX: 202-962-8300
? INFORMATION FOR SEQ ID NO: 1:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 5914 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: double
? TOPOLOGY: linear
? MOLECULE TYPE: cDNA
? HYPOTHETICAL: NO
? ANTI-SENSE: NO
? ORIGINAL SOURCE:
? ORGANISM: Homo sapiens
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 120..5711
?
US-08-483-553-1

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Query Match 100.0%; Score 5709.4; DB 1; Length 5914;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5710; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 361 AACTGTGGAAGAGCATTTGAAATATCTTTGCTTTTCACTTGAACAGGTTTGGAGT 420  
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Db 541 AACCAGAAAATCTCTCTGAGAAACAGCTCAGTGTCAACTCTCTAACCTTGGAA 600  
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Db 601 CTGTGAGAACTGTGAGAGCAAAAGCAGCGATACACTCTCAAAAGAGTGTCTTACATG 660  
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QY 1261 AAGTTAATAGTGTGTTTCCAGAAAGTGAATCTGTAGTCTGATGATCACTCAATGATG 1320  
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Db 1501 TTGGGAAAACTTATGGAAGAAAGGCAAGCTCCCAATTTAAGCATGTAAGTAAATC 1560  
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Db 1621 AATTAAAGCTTAAAGAGACCTCATCATGAGCTTATCTGAGATTTTATCAAGAAAG 1680  
QY 1681 CAGATTTGGCAGTTCAAAAAGACTCCTGAAATGATTAATCAGGGAATTAACCAAGGAGC 1740  
Db 1681 CAGATTTGGCAGTTCAAAAAGACTCCTGAAATGATTAATCAGGGAATTAACCAAGGAGC 1740  
QY 1741 AGAATGTCAGATGATGAATATTAATTAATGATGTCATGAGATTAACCAAGGAGT 1800  
Db 1741 AGAATGTCAGATGATGAATATTAATTAATGATGTCATGAGATTAACCAAGGAGT 1800  
QY 1801 CTATTCAGATGAGAAAAATCTTAACCAATGAAATCACTGAAAAAGATCTGTTTCA 1860  
Db 1801 CTATTCAGATGAGAAAAATCTTAACCAATGAAATCACTGAAAAAGATCTGTTTCA 1860  
QY 1861 AAACGAAAGCTGAACCTTAACAGACAGATTAAGCAATGGAATCTGAATTAATATCC 1920  
Db 1861 AAACGAAAGCTGAACCTTAACAGACAGATTAAGCAATGGAATCTGAATTAATATCC 1920  
QY 1921 ACAATTCAAAACACCTTAAAGAAATAGGCTGAGAGGAGTCTTCAACGAGCATATTC 1980  
Db 1921 ACAATTCAAAACACCTTAAAGAAATAGGCTGAGAGGAGTCTTCAACGAGCATATTC 1980  
QY 1981 ATGCGCTTGAATAGTATGATGAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 2040  
Db 1981 ATGCGCTTGAATAGTATGATGAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 2040  
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Db 2041 TTGATATGTTCTTGAAGTGAAGATTAAGAAAAAAGTAAACCAAAATGCGACATCA 2100  
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Db 2161 GTTAAAGCAGAAATGAAACAGCAAGTAAAGACATGACAGGATTCCTTCCAGAGCTGA 2220  
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Db 2341 CTAAATATGCTGAAGACCCCAAGATCTCATGTTAAGTGAAGAAAGGCTTTTGGCAACTG 2400  
QY 2401 AAAAGTCTGTAAAGATGAGCAATTTTCAATGTTGATCTGATGATTAATGAGCACTCAGG 2460  
Db 2401 AAAAGTCTGTAAAGATGAGCAATTTTCAATGTTGATCTGATGATTAATGAGCACTCAGG 2460

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|----|------|---|------|
| QY | 2461 | AAAGATCTCGTTACTGGAGTTTGACATCTAGGGAAAGGCAAAAACGAACCAATTAAT         | 2520 |
| Db | 2461 | AAAGATCTCGTTACTGGAGTTTGACATCTAGGGAAAGGCAAAAACGAACCAATTAAT         | 2520 |
| QY | 2521 | GTGTGAGTCAGTCGTGACAGCATTTTGAAAAACCCCAAGGGAGCTAATTCAATGTTGTTCCAAAG | 2580 |
| Db | 2521 | GTGTGAGTCAGTCGTGACAGCATTTTGAAAAACCCCAAGGGAGCTAATTCAATGTTGTTCCAAAG | 2580 |
| QY | 2581 | ATTAATAGAAATGACACAGAGAGCTTTAAGTATCCATTGGGACATGAAGTTAACCAAGTC      | 2640 |
| Db | 2581 | ATTAATAGAAATGACACAGAGAGCTTTAAGTATCCATTGGGACATGAAGTTAACCAAGTC      | 2640 |
| QY | 2661 | GGGAAACAGAGATGAAATGGAGAAAGTGAATTCAGTCAAGTATTTGGCAAAATCAT          | 2700 |
| Db | 2661 | GGGAAACAGAGATGAAATGGAGAAAGTGAATTCAGTCAAGTATTTGGCAAAATCAT          | 2700 |
| QY | 2701 | TCAAGGTTTCAAAAGGCGCAGTCATTGGTCTGTTTTCAATCCAGGAAATGCAGAAAGG        | 2760 |
| Db | 2701 | TCAAGGTTTCAAAAGGCGCAGTCATTGGTCTGTTTTCAATCCAGGAAATGCAGAAAGG        | 2760 |
| QY | 2761 | AATGTGCAACATTCCTGCGCCACTCTGGGTCCTTAAAGAAACAAAGTCCAAAGTCACTT       | 2820 |
| Db | 2761 | AATGTGCAACATTCCTGCGCCACTCTGGGTCCTTAAAGAAACAAAGTCCAAAGTCACTT       | 2820 |
| QY | 2821 | TTGAATGTGAACAAAGGAAGAAATACAGAAAGATGAGTCTAATATCAAGCTGTAC           | 2880 |
| Db | 2821 | TTGAATGTGAACAAAGGAAGAAATACAGAAAGATGAGTCTAATATCAAGCTGTAC           | 2880 |
| QY | 2881 | AGACAGTTAATATCACTGACAGGCTTCCGTGGTGGGCACAAAGATTAAGCAATGTATA        | 2940 |
| Db | 2881 | AGACAGTTAATATCACTGACAGGCTTCCGTGGTGGGCACAAAGATTAAGCAATGTATA        | 2940 |
| QY | 2941 | ATGCCAAATGTAGTATCAAGAGAGGCTCTAGGTTTTGTCTATCATCTCAGTTCAGAGGCA      | 3000 |
| Db | 2941 | ATGCCAAATGTAGTATCAAGAGAGGCTCTAGGTTTTGTCTATCATCTCAGTTCAGAGGCA      | 3000 |
| QY | 3001 | ACGAAATCGCACTCATTACTCCAAATPAACATGGACTTTTACAAACCATATCGTATAC        | 3060 |
| Db | 3001 | ACGAAATCGCACTCATTACTCCAAATPAACATGGACTTTTACAAACCATATCGTATAC        | 3060 |
| QY | 3061 | CACACACTTTTCCCATCAAGTCATTTGTTAAACTTAAATGTAAAGAAAAATCTGCTAAGG      | 3120 |
| Db | 3061 | CACACACTTTTCCCATCAAGTCATTTGTTAAACTTAAATGTAAAGAAAAATCTGCTAAGG      | 3120 |
| QY | 3121 | AAAACTTTGAGGAACATTCAATGTCACCTGAAAGAAATGGGAAATGAGAACATTCGAA        | 3180 |
| Db | 3121 | AAAACTTTGAGGAACATTCAATGTCACCTGAAAGAAATGGGAAATGAGAACATTCGAA        | 3180 |
| QY | 3181 | GTACAGTGAGCACAATTAGCCGTAAATACATTAGAGAAATGTTTTTAAAGAACCCAGCT       | 3240 |
| Db | 3181 | GTACAGTGAGCACAATTAGCCGTAAATACATTAGAGAAATGTTTTTAAAGAACCCAGCT       | 3240 |
| QY | 3241 | CAACCAATATTAAGAAGTAGTCCAGTACTAATGAAATGGGCTCCAGTATTAATGAA          | 3300 |
| Db | 3241 | CAACCAATATTAAGAAGTAGTCCAGTACTAATGAAATGGGCTCCAGTATTAATGAA          | 3300 |
| QY | 3301 | TAGGTTCCAGTGATGAAAAACATTCAGACAGAACTAGGTAGAAACAGAGGGCCAAATTTGA     | 3360 |
| Db | 3301 | TAGGTTCCAGTGATGAAAAACATTCAGACAGAACTAGGTAGAAACAGAGGGCCAAATTTGA     | 3360 |
| QY | 3361 | ATGCTATGCTTAGATTAGGGGGTTTTGCAACCTGAGGTCTATPAACAAAGTCTTCTTGAA      | 3420 |
| Db | 3361 | ATGCTATGCTTAGATTAGGGGGTTTTGCAACCTGAGGTCTATPAACAAAGTCTTCTTGAA      | 3420 |
| QY | 3421 | GTAATTGGAAGCATCCCTGAAATTAAGAAAGCAAGATATGAAAGATGTTCAACCTGTTA       | 3480 |
| Db | 3421 | GTAATTGGAAGCATCCCTGAAATTAAGAAAGCAAGATATGAAAGATGTTCAACCTGTTA       | 3480 |
| QY | 3481 | ATACAGATTTCTCTCCATATCTGAATTCAGATTACTTAGAAACAGCCATATGGAAAGTAGTC    | 3540 |
| Db | 3481 | ATACAGATTTCTCTCCATATCTGAATTCAGATTACTTAGAAACAGCCATATGGAAAGTAGTC    | 3540 |
| QY | 3541 | ATGCATCTCAGGTTTGTTCGTGAGACACCTGATGACCTGTTAGATGATGTGAAATPAAGG      | 3600 |

|    |      |   |      |
|----|------|---|------|
| Db | 3541 | ATGCATCTCAGGTTGTGTTGTGAGACCCGTAATGACCTGTAGATGATGGAAATAAAGG        | 3600 |
| Qy | 3601 | AAGATACTAGTATTGCTGAAAAATGACATTAAAGAAAGTTCTGCTGTTTTATGCAAAAGCG     | 3660 |
| Db | 3601 | AAGATACTAGTATTGCTGAAAAATGACATTAAAGAAAGTTCTGCTGTTTTATGCAAAAGCG     | 3660 |
| Qy | 3661 | TCCAGAAAGAGAGCTTACAGAGAGTCTGAGCCCTTTACCCATPACATTTGGCTCAGG         | 3720 |
| Db | 3661 | TCCAGAAAGAGAGCTTACAGAGAGTCTGAGCCCTTTACCCATPACATTTGGCTCAGG         | 3720 |
| Qy | 3721 | GTTACCGAAGAGGGGCCAAGAAATTAAGACTCCTCABAAGAACTTATCTAGAGAGATG        | 3780 |
| Db | 3721 | GTTACCGAAGAGGGGCCAAGAAATTAAGACTCCTCABAAGAACTTATCTAGAGAGATG        | 3780 |
| Qy | 3781 | AAGAGCTTCCCTGCTTCCCAACACTGTGTTATTTGGTAAAGTAAACAATPACCTTCAGT       | 3840 |
| Db | 3781 | AAGAGCTTCCCTGCTTCCCAACACTGTGTTATTTGGTAAAGTAAACAATPACCTTCAGT       | 3840 |
| Qy | 3841 | CTACTAGGATATGACACCGTTGCTACCGAGTGTCTGTAAAGACACAGAGAGAAATTTAT       | 3900 |
| Db | 3841 | CTACTAGGATATGACACCGTTGCTACCGAGTGTCTGTAAAGACACAGAGAGAAATTTAT       | 3900 |
| Qy | 3901 | TATCATTTGAAGATATGCTTAAATGACTGCAATPACAGGTAAATTTGGCAAGGCATCTC       | 3960 |
| Db | 3901 | TATCATTTGAAGATATGCTTAAATGACTGCAATPACAGGTAAATTTGGCAAGGCATCTC       | 3960 |
| Qy | 3961 | AGGAATCATCCTTGTAGAGAGAAACAAATGTTGCTGAGCTGTTTCTTCACAGTGA           | 4020 |
| Db | 3961 | AGGAATCATCCTTGTAGAGAGAAACAAATGTTGCTGAGCTGTTTCTTCACAGTGA           | 4020 |
| Qy | 4021 | GTTGAATTTGGAAGACTTGACTGCAAAATACAAACACCAGAGATCCTTTCTTGATTTGTTCTT   | 4080 |
| Db | 4021 | GTTGAATTTGGAAGACTTGACTGCAAAATACAAACACCAGAGATCCTTTCTTGATTTGTTCTT   | 4080 |
| Qy | 4081 | CCAAACAATGAGGCATCAGTCTGAAAGCCAGGGATTTGGTCTGAGTGAACAAAGAAATTTGG    | 4140 |
| Db | 4081 | CCAAACAATGAGGCATCAGTCTGAAAGCCAGGGATTTGGTCTGAGTGAACAAAGAAATTTGG    | 4140 |
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| Db | 4141 | TTTCAGATGATGAAGAAAGAGAAAGGGGCTTGGAAAGAAATTAATCAAGAAAGCAAAAGCA     | 4200 |
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| Db | 4321 | AAACATAACCTGATTAAGCTCCAGCAGAGAAATGGCGTAATAAGCTGTGTTAAGAACAG       | 4380 |
| Qy | 4381 | ATGGAGCAGAGCTTCTAACAAGCTACCTTCATATAAGTACTCTTCTGCCCCCTTGAGG        | 4440 |
| Db | 4381 | ATGGAGCAGAGCTTCTAACAAGCTACCTTCATATAAGTACTCTTCTGCCCCCTTGAGG        | 4440 |
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| Db | 4501 | GTTGAATTAACCTATTAAGCCAGAAATCCAGAAAGGCTTTTCTGCTGACAAAGTTTGAGTGTCTG | 4560 |
| Qy | 4561 | CAGATAGTCTTACACAGTAAATAAAGAACACAGAGTGGAAAGTCAATCCCTCTTAAT         | 4620 |
| Db | 4561 | CAGATAGTCTTACACAGTAAATAAAGAACACAGAGTGGAAAGTCAATCCCTCTTAAT         | 4620 |
| Qy | 4621 | GCCCATCTTAAGATGATAGTGTGATCATGCAAGTTGCTCTGGAGTCTTCAGAAATAGAA       | 4680 |

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1      RESULT 11
2      US-08-487-002-1
3      : Sequence 1, Application US/08487002
4      : Patent No. 5710001
5      :
6      : GENERAL INFORMATION:
7      : APPLICANT: Shatuck-Eidens, Donna M.
8      : APPLICANT: Shatuck-Eidens, Jacques
9      : APPLICANT: Emi, Mitsuru
10     : APPLICANT: Nakamura, Yutake
11     : APPLICANT: Durocher, Francine
12     : TITLE OF INVENTION: 17q-Linked Breast and Ovarian Cancer
13     : TITLE OF INVENTION: Susceptibility Gene
14     : NUMBER OF SEQUENCES: 85
15     :
16     : CORRESPONDENCE ADDRESS:
17     : ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
18     : STREET: 1201 New York Avenue, N.W., Suite 1000
19     : City: Washington
20     : STATE: DC
21     : COUNTRY: USA
22     : ZIP: 20005
23     :
24     : COMPUTER READABLE FORM:
25     : MEDIUM TYPE: Floppy disk
26     : COMPUTER: IBM PC compatible
27     : OPERATING SYSTEM: PC-DOS/MS-DOS
28     : SOFTWARE: Patentin Release #1.0, Version #1.30
29     : CURRENT APPLICATION DATA:
30     : APPLICATION NUMBER: US/08/487,002
31     : FILING DATE:
32     : CLASSIFICATION: 424
33     : PRIOR APPLICATION DATA:
34     : APPLICATION NUMBER: US 08/409,305
35     : FILING DATE: 24-MAR-1995
36     : PRIOR APPLICATION DATA:
37     : APPLICATION NUMBER: US 08/348,824
38     : FILING DATE: 29-NOV-1994
39     : PRIOR APPLICATION DATA:
40     : APPLICATION NUMBER: US 08/308,104
41     : FILING DATE: 16-SEP-1994
42     : PRIOR APPLICATION DATA:
43     : APPLICATION NUMBER: US 08/300,266
44     : FILING DATE: 02-SEP-1994
45     : PRIOR APPLICATION DATA:
46     : APPLICATION NUMBER: US 08/289,221
47     : FILING DATE: 12-AUG-1994
48     : ATTORNEY/AGENT INFORMATION:
49     : NAME: Ihnen, Jeffrey L.
50     : REGISTRATION NUMBER: 28,957
51     : REFERENCE/DOCKET NUMBER: 24884-109347
52     : TELECOMMUNICATION INFORMATION:
53     : TELEPHONE: 202-962-4810
54     : TELEFAX: 202-962-8300
55     : INFORMATION FOR SEQ ID NO: 1:
56     : SEQUENCE CHARACTERISTICS:
57     : LENGTH: 5914 base pairs
58     : TYPE: nucleic acid
59     : STRANDEDNESS: double
60     : TOPOLOGY: linear
61     : MOLECULE TYPE: cDNA
62     : HYPOTHEetical: NO
63     : ANTI-SENSE: NO
64     : ORIGINAL SOURCE:
65     : ORGANISM: Homo sapiens
66     : FEATURE:
67     : NAME/KEY: CDS
68     : LOCATION: 120..5711
69     :
70     : US-08-487-002-1
71     :
72     : Query Match 100.0%; Score 5709.4; DB 1; Length 5914;
73     : Best Local Similarity 100.0%; Pred. No. 0;
74     : Matches 5710; Conservative 0; Mismatches 1; Indels 0; Gaps 0

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 Db 5641 GTGTAGACTCTTACAGTCCAGAGCTGACACCTTACTGATTAACCCAGATCCCCACA 5700  
 QY 5701 GCCACTACTGA 5711  
 Db 5701 GCCACTACTGA 5711

RESULT 12  
 US-08-483-554B-1  
 Sequence 1, Application US/0848354B  
 Patent No. 5747282  
 GENERAL INFORMATION:  
 APPLICANT: Skolnick, Mark H.  
 APPLICANT: Goldger, David E.  
 APPLICANT: Miki, Yoshio  
 APPLICANT: Swenson, Jeff  
 APPLICANT: Kamb, Alexander  
 APPLICANT: Harshman, Keith D.  
 APPLICANT: Shattuck-Eidens, Donna M.  
 APPLICANT: Tavlijan, Sean V.  
 APPLICANT: Wiseman, Roger W.  
 APPLICANT: Fureal, P. Andrew  
 TITLE OF INVENTION: 17q-Linked Breast and Ovarian Cancer  
 NUMBER OF SEQUENCES: 85  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP  
 STREET: 1201 New York Avenue, N.W., Suite 1000  
 CITY: Washington  
 STATE: DC  
 COUNTRY: USA  
 ZIP: 20005  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/483,554B  
 FILING DATE: 07-JUN-1995  
 CLASSIFICATION: 514  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/409,305  
 FILING DATE: 24-MAR-1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/348,824  
 FILING DATE: 29-NOV-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/308,104  
 FILING DATE: 16-SEP-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/300,266  
 FILING DATE: 02-SEP-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 06/289,221  
 FILING DATE: 12-AUG-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Ihnen, Jeffrey L.  
 REGISTRATION NUMBER: 28,957  
 REFERENCE/DOCKET NUMBER: 24884-109347

## TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-962-4810

TELEFAX: 202-962-8300

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 5914 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: 120..5708

US-08-483-554B-1

Query Match

Best Local Similarity 100.0%; Score 5709.4; DB 1; Length 5914;

Matches 5710; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db      4081 CCAACCAATGAGCATCTGCTGAAAGCCAGGAGTTGGTCTGAGTACAGAAATGG 4140
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Qy      4201 TGGATTCAAACCTTAGGTGAGAGCATCTGGGTGTGAGAGTGAACAGAGCTCTGAA 4260
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Db      5581 TCATGATCAATGAGGAGATGTGTGAGGACCTGTGTGTCAGAGGCTTCAACCAATGCTCCAGATCACTGG 5640
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Qy      5701 GCCACTACTGA 5711
Db      5701 GCCACTACTGA 5711

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RESULT 13
US-08-488-011B-1
; Sequence 1, Application US/08488011B
; Patent No. 5753441
; GENERAL INFORMATION:
; APPLICANT: Skolnick, Mark H.
; APPLICANT: Goldgar, David E.
; APPLICANT: Miki, Yoshio
; APPLICANT: Swenson, Jeff
; APPLICANT: Kamb, Alexander
; APPLICANT: Harshman, Keith D.
; APPLICANT: Shatluck-Eldens, Donna M.
; APPLICANT: Tavligian, Sean V.
; APPLICANT: Wiseman, Roger W.
; APPLICANT: Ruteal, P. Andrew
; TITLE OF INVENTION: 17q-Linked Breast and Ovarian Cancer
; NUMBER OF SEQUENCES: 85
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
; STREET: 1201 New York Avenue, N.W., Suite 1000
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

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CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/488,011B  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/409,305  
FILING DATE: 24-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/348,824  
FILING DATE: 29-NOV-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/308,104  
FILING DATE: 16-SEP-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/300,266  
FILING DATE: 02-SEP-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/289,221  
FILING DATE: 12-AUG-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Ihnen, Jeffrey L.  
REGISTRATION NUMBER: 28,957  
REFERENCE/DOCKET NUMBER: 24884-109347-09  
TELEPHONE: 202-962-4810  
TELEFAX: 202-962-8300  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5914 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 120..5708  
US-08-488-011B-1

Query Match 100.0%; Score 5709.4; DB 1; Length 5914;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 5710; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGCTCGCTGAGACTTCTCTGACCCCGACACAGGCTGTGGGGTTTCTCAGATACTGGGCC 60  
DB 1 AGCTCGCTGAGACTTCTCTGACCCCGACACAGGCTGTGGGGTTTCTCAGATACTGGGCC 60  
QY 61 CTTGCGCTCAGAGAGGCTTCACTCTGCTGTGGGTAAAGTTCAATTGGAACAGAAAGAA 120  
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QY 121 TGAATTTATCTGCTCTTGGGTTGAGAGATGACAAATGTCATTAATGATGAGAGAA 180  
DB 121 TGAATTTATCTGCTCTTGGGTTGAGAGATGACAAATGTCATTAATGATGAGAGAA 180  
QY 181 TCTTAAGTGTCCCATCTGTCTGAGATTGATCAAGAACTGTCTCCAAAGTGTGACC 240  
DB 181 TCTTAAGTGTCCCATCTGTCTGAGATTGATCAAGAACTGTCTCCAAAGTGTGACC 240  
QY 241 ACATATTTTGAATTTTGCATGCTGAACTTCTCAACAGAAAGAGGCTTTCACAGT 300  
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DB 301 GTCTTTATGTAAAGATGATATAACAAAGAGAGCTTCAAGAAAGTACAGATTTAGTC 360  
QY 361 AACTGTGTGAAGAGCTATTGAAATCACTTTGTGCTTTTCACTTGAACAGGTTTGAGT 420  
DB 361 AACTGTGTGAAGAGCTATTGAAATCACTTTGTGCTTTTCACTTGAACAGGTTTGAGT 420

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DB 481 AAGTTTCTATCTCAAAAGATGAGGCTACAGAAACCGTGCCAAAAGACTTTCAGAGTG 540  
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DB 541 AATCCGAAATCTCTCTTTCAGAGAAACAGGCTCATGTGTCACCTCTTAACCTTGGA 600  
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DB 601 CTGTGAGAACTCTGAGACAAAGAGGAGATACAACTCAAAAGAGCTGTCTACATTTG 660  
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DB 781 CAAAAAAGGCTGCTTGTGAATTTTCTGAGACGAGTGAACAAATACGAAATCATCATAC 840  
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DB 841 CCAAGTAATTAATGATTTGAACACCACTGAGAAAGCGTGACGTGAGAGGATCCAGAAAAGT 900  
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Db 1741 AGAATGCTCAGTGAATATTTACTAATATGCTGATGAGATTAACCAAAAGTGAT 1800  
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 Db 5701 GCCCATCTGA 5711

RESULT 14  
 US-08-850-727-1  
 ; Sequence 1, Application US/08850727  
 ; Patent No. 6162897  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Skolnick, Mark H.  
 ; APPLICANT: Goldgar, David E.

APPLICANT: Miki, Yoshio  
APPLICANT: Swenson, Jeff  
APPLICANT: Kamb, Alexander  
APPLICANT: Harshman, Keith D.  
APPLICANT: Shatuck-Eldens, Donna M.  
APPLICANT: Tavtigian, Sean V.  
APPLICANT: Wiseman, Roger W.  
APPLICANT: Futreal, P. Andrew  
TITLE OF INVENTION: 17q-Linked Breast and Ovarian Cancer  
TITLE OF INVENTION: Suseptibility Gene  
NUMBER OF SEQUENCES: 85  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP  
STREET: 1201 New York Avenue, N.W., Suite 1000  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/850,727  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/483,554  
FILING DATE: 07-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/348,824  
FILING DATE: 29-NOV-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/308,104  
FILING DATE: 16-SEP-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/300,266  
FILING DATE: 02-SEP-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/289,221  
FILING DATE: 12-AUG-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Innen, Jeffrey L.  
REGISTRATION NUMBER: 28,957  
REFERENCE/DOCKET NUMBER: 24884-109347  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-962-4810  
TELEFAX: 202-962-8300  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5914 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 120..5708  
US-08-850-727-1

Query Match 100.0%; Score 5709.4; DB 4; Length 5914;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 5710; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AACTGGCTGAGACTTCTGAGACCCCGACACAGGCTGTGGGTTTTCAGATACTGGCC 60  
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 RESULT 15  
 PCT-US95-10202-1  
 Sequence 1, Application PC/TUS9510202  
 GENERAL INFORMATION:  
 APPLICANT: Shattuck-Bidens, Donna M.  
 APPLICANT: Simard, Jacques  
 APPLICANT: EMI, Mitsuru  
 APPLICANT: Nakamura, Yusuke  
 APPLICANT: Durocher, Francine  
 TITLE OF INVENTION: In vivo Mutations and Polymorphisms  
 TITLE OF INVENTION: in the 17q-linked Breast and Ovarian Cancer  
 TITLE OF INVENTION: Susceptibility Gene  
 NUMBER OF SEQUENCES: 85  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP  
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 CITY: Washington  
 STATE: DC  
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 ZIP: 20005  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentln Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
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 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US  
 FILING DATE: 07-JUN-1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/409,305  
 FILING DATE: 24-MAR-1995  
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 APPLICATION NUMBER: US 08/348,824  
 FILING DATE: 29-NOV-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08-308,104  
 FILING DATE: 16-SEP-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/300,266  
 FILING DATE: 02-SEP-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/289,221  
 FILING DATE: 12-AUG-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Ihnen, Jeffrey L.  
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 TELEFAX: 202-962-8300  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 5914 base pairs

TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 ORIGINAL SOURCE:  
 ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 120..5711  
 PCT-US95-10202-1  
 Query Match 100.0%; Score 5709.4; DB 5; Length 5914;  
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1681 CAGATTTGGCAGTTCAAAAGAGCTCTGAATGATTAATCAGGAGCTTAACCAAGGAG 1740  
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1741 AGAATGCTCAAGTGAATATTAATTAATGATGATGATGATGATGATGATGATGATG 1800  
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1801 CTAATCAGATGAGAAAAATCTTAACCAATAGAACTACGAAAAAGATCTGCTTCA 1860  
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1861 AAAAGAAAGCTGAACCTTAATGAGAGAGTAATGAGCAATTAAGCACTGAAATTAATTC 1920  
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2041 TTGATAGTGTCTGAGAGTGAAGATTAAGAAAAAATGATACCAACCAATGCGAGTCA 2100  
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2701 TGAAGTTTCAAGAGGCGCACTATTTGCTGTTTCAAAATCCAGGAAATCAGAAAGG 2760  
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2881 AGACAGTTAATTCATGAGGCTTCTGAGTGTGTCAGAAAGATTAAGCCAGTGAATA 2940  
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2941 ATGCCAAATGATGATCAAAAGAGGCTCTAGATTTTGTCTAATCTCAGTTCAAGAGCA 3000  
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Db 3001 ACGAACTGCACTACTCCAAATPAACGTGACTTTTCAAAACCATATCTGTATAC 3060  
QY 3061 CACCACCTTTTCCCATCAAGTCATTTGTTAAATGAAGAAAATCTGCTAGAG 3120  
Db 3061 CACCACCTTTTCCCATCAAGTCATTTGTTAAATGAAGAAAATCTGCTAGAG 3120  
QY 3121 AAAACCTTTGAGAACCTTCAATGTCACCTGAAAGAGAAATGGGAAATGAGACATTCGA 3180  
Db 3121 AAAACCTTTGAGAACCTTCAATGTCACCTGAAAGAGAAATGGGAAATGAGACATTCGA 3180  
QY 3181 GTACAGTGAAGCAATTAAGCCGTAATTAACAATTAGAAAATGTTTTAAAGAGCCAGCT 3240  
Db 3181 GTACAGTGAAGCAATTAAGCCGTAATTAACAATTAGAAAATGTTTTAAAGAGCCAGCT 3240  
QY 3241 CAAGCAATATTAATGAAGTAGTTCAGTACTAATGAAGTGGGCTCAGATTAATGA 3300  
Db 3241 CAAGCAATATTAATGAAGTAGTTCAGTACTAATGAAGTGGGCTCAGATTAATGA 3300  
QY 3301 TAGGTTCCAGTGAATGAACATTCAGACAGAACTAGGTGAAACAGAGGCCAAATTTGA 3360  
Db 3301 TAGGTTCCAGTGAATGAACATTCAGACAGAACTAGGTGAAACAGAGGCCAAATTTGA 3360  
QY 3361 ATGCTATGCTATGAATTAAGGGGTTTTGCAACCTGAGCTTATAACAAAGCTTCTGGA 3420  
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Db 3421 GTAAATGTGAAGCATCTCTGAAATTAAGAAAGCAAGATATGAAGAGTAGTTCAAGCTGTA 3480  
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QY 3541 ATGCAATCTCAGGTTTGTCTGAGACACCTGATACCTGTTAGTAGATGGAATTAAG 3600  
Db 3541 ATGCAATCTCAGGTTTGTCTGAGACACCTGATACCTGTTAGTAGATGGAATTAAG 3600  
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Db 3661 TCCAGAAAGAGAGCTTGAAGAGAGTCTAGCCCTTTCAACCAATACATTTGGCTCAG 3720  
QY 3721 GTTACCGAAGAGGGGCCAAGAAATTAAGATCTCAGAAAGAACTTATCTAGAGAGATG 3780  
Db 3721 GTTACCGAAGAGGGGCCAAGAAATTAAGATCTCAGAAAGAACTTATCTAGAGAGATG 3780  
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QY 4141 TTTCAATGATGAGAAAGAGGACCGGCTTGGAAAGAAAATATCAAGAAAGCAAGCA 4200  
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Db 4201 TGGATTTCAAACTTGAAGTGAAGCATCTGGGTGTGAAGTGAACAAAGCTTCTGAAG 4260  
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QY 4321 AACATTAACCTGATTAAGCTCCAGAGAAATGCTGAACTAGAGCTGTGTTGAACAGC 4380  
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QY 4561 CAGATATGTTCTACAGTAAATTAAGAAACAGAGTGAAGAGTCAATCCCTTCTTAAT 4620  
Db 4561 CAGATATGTTCTACAGTAAATTAAGAAACAGAGTGAAGAGTCAATCCCTTCTTAAT 4620  
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Db 4621 GGCATCATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4680  
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Db 4681 ACTACCATCTCAAGAGAGCTCATTAAGGTTGTTGATGATGAGAGCAACAGCTGGAAG 4740  
QY 4741 AGTCTGGGCAACGATTTGACGGAACATCTTAATCTTCCAAAGCAAGATCTAGAGGAA 4800  
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QY 4801 CCCCTTACTGGAATCTGGAATCAGGCTTCTCTGATGAACCTGGAATCTGATCTTCTG 4860  
Db 4801 CCCCTTACTGGAATCTGGAATCAGGCTTCTCTGATGAACCTGGAATCTGATCTTCTG 4860  
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Db 4861 AAGACAGAGCCCGAGAGTCAAGTCTGTTGGCAACATACATCTTCAACCTGCAATGA 4920  
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Db 4921 AAGTTCCCAATTTGAAGTTGCAAGATCTGCCAGAGTCCAGCTGCTGCTACTACTG 4980  
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Db 4981 ATACTGCTGGGTATTAATGAAATGAAGAAAGTGTGAGCAGGAGAAAGCAGAAATGACAG 5040  
QY 5041 CTTCAACAGAAAGGCTCAACAAAGAAATGCTCATGATGATGATGATGATGATGATGAT 5100  
Db 5041 CTTCAACAGAAAGGCTCAACAAAGAAATGCTCATGATGATGATGATGATGATGATGAT 5100  
QY 5101 AATTTATGCTGCTGATCAAGTTTGCAGAAACACCAATCACTTAATTAATTAATTAAT 5160  
Db 5101 AATTTATGCTGCTGATCAAGTTTGCAGAAACACCAATCACTTAATTAATTAATTAAT 5160  
QY 5161 CTGAAGAGCTACTATGTTTATGAAGAAAGAGATGCTGAGTTGTGTGAACGAGCAGC 5220  
Db 5161 CTGAAGAGCTACTATGTTTATGAAGAAAGAGATGCTGAGTTGTGTGAACGAGCAGC 5220

|    |      |  |      |
|----|------|--|------|
| Qy | 5221 | TGAATATTTTCTAGAAATGGGAGGAGAAATGGGTAGTATTTCTGGGTGACCC       | 5280 |
| Db | 5221 | TGAATATTTTCTAGAAATGGGAGGAGAAATGGGTAGTATTTCTGGGTGACCC       | 5280 |
| Qy | 5281 | AGTCTATTAAAGAAAGAAATGCTGAATGACATGATTTTGAAGTCAGAGAGATGTGG   | 5340 |
| Db | 5281 | AGTCTATTAAAGAAAGAAATGCTGAATGACATGATTTTGAAGTCAGAGAGATGTGG   | 5340 |
| Qy | 5341 | TCATGGAAGAAACCCAGAGTCCAAAGCGAGCAAGAAATCCGAGACAGAAAGATCT    | 5400 |
| Db | 5341 | TCATGGAAGAAACCCAGAGTCCAAAGCGAGCAAGAAATCCGAGACAGAAAGATCT    | 5400 |
| Qy | 5401 | TCAGGGGGCTAGAAATCTGTGCTATGGGCCCTTCACCAATGCCACAGATCAACTGG   | 5460 |
| Db | 5401 | TCAGGGGGCTAGAAATCTGTGCTATGGGCCCTTCACCAATGCCACAGATCAACTGG   | 5460 |
| Qy | 5461 | AATGATGTACAGCTGTGTGCTTCTGTGTGAGAGAGCTTTCATCATTCACCCCTTG    | 5520 |
| Db | 5461 | AATGATGTACAGCTGTGTGCTTCTGTGTGAGAGAGCTTTCATCATTCACCCCTTG    | 5520 |
| Qy | 5521 | GCAAGGTGTCACCCAAATTGTTGTTGTCAGCCAGATGCCCTGACAGAGCAATGGCT   | 5580 |
| Db | 5521 | GCAAGGTGTCACCCAAATTGTTGTTGTCAGCCAGATGCCCTGACAGAGCAATGGCT   | 5580 |
| Qy | 5581 | TCCATGCAATTGGGAGATGTGTAGGCACTGTGTGACCCGAGAGTGGTGTGGACA     | 5640 |
| Db | 5581 | TCCATGCAATTGGGAGATGTGTAGGCACTGTGTGACCCGAGAGTGGTGTGGACA     | 5640 |
| Qy | 5641 | GTGTAGCACTCTACCAAGTCCAGAGCTGAGACACTACTGATATCCCAAGATCCCCACA | 5700 |
| Db | 5641 | GTGTAGCACTCTACCAAGTCCAGAGCTGAGACACTACTGATATCCCAAGATCCCCACA | 5700 |
| Qy | 5701 | GCCACTACTGA 5711   |      |
| Db | 5701 | GCCACTACTGA 5711   |      |

Search completed: June 13, 2003, 12:21:43  
 Job time : 298 secs

|          |   |
|----------|---|
| RESULT 1 |   |
| AAT87085 |   |
| ID       | AAT87085 standard; cDNA; 5711 BP.                                 |
| XX       | AAT87085;   |
| AC       |   |
| XX       | 06-JAN-1998 (first entry)   |
| DT       |   |
| XX       |   |
| DE       | Human BRCA1 gene consensus.                                       |
| XX       |   |
| KW       | BRCA1 gene; BRCA1(om1); breast cancer; ovary cancer; polymorphism |
| XX       | genetic testing; diagnosis; gene therapy; ss.                     |
| XX       |   |
| OS       |   |
| XX       | Homo sapiens.   |
| XX       |   |
| Key      | Location/Qualifiers   |
| FH       | 120..5711   |
| FT       | /*tag= a  |
| FT       | 2201  |
| FT       | /*tag= b  |
| FT       | /note= "AGC (40%) and AGT (55-65%) polymorphism                   |
| FT       | at position 2201"   |
| FT       |   |
| FT       | 2430  |
| FT       | /*tag= c  |
| FT       | /*note= "35-45% TTG (Leu) and 55-65% CTG (Leu)                    |
| FT       | polymorphism at position 2430"                                    |
| FT       |   |
| FT       | 2731  |
| FT       | /*tag= d  |
| FT       | /*note= "25-35% CCG (Pro) and 65-75% CTG (Leu)                    |
| FT       | polymorphism at position 2731"                                    |
| FT       |   |
| FT       | 3232  |
| FT       | /*tag= e  |

| Query Match  | 100.0%   | Score 5711   | DB 18    | Length 5711 |
|--|--|--------------|----------|-------------|
| Best Local Similarity                                      | 100.0%   | Pred. No. 0  |          |             |
| Matches 5711   | Conservative 0   | Mismatches 0 | Indels 0 | Gaps 0      |
| Sequence 5711 BP; 1953 A; 1099 C; 1277 G; 1382 T; 0 other; |  |              |          |             |
| 1  | ACTCGCTGAGACTTCTCTGAGACCCCGCACCAGGCTGTGGGGTTCTCAGATACACTGGCC | 60           |          |             |
| 1  | AGCTGCTGAGACTTCTCTGAGACCCCGCACCAGGCTGTGGGGTTCTCAGATACACTGGCC | 60           |          |             |
| 61   | CCTGCGCTGAGAGGAGCTTCAACCTCTGCTGGTGGTAAAGTTGATTGGAAACAAGAA    | 120          |          |             |
| 61   | CCTGCGCTGAGAGGAGCTTCAACCTCTGCTGGTGGTAAAGTTGATTGGAAACAAGAA    | 120          |          |             |
| 121  | TGAGATTATCTGCTCTCTGGGTTGAAGAAATGATCATTAATGCTATGACAGAAA       | 180          |          |             |
| 121  | TGAGATTATCTGCTCTCTGGGTTGAAGAAATGATCATTAATGCTATGACAGAAA       | 180          |          |             |
| 181  | TCTTAGAGTGTCCCATCTGTCTGAGTTGATCAAGAACTGTCTCCACAAGGTGACC      | 240          |          |             |
| 181  | TCTTAGAGTGTCCCATCTGTCTGAGTTGATCAAGAACTGTCTCCACAAGGTGACC      | 240          |          |             |

|    |      |             |                  |                 |                      |               |            |           |      |      |
|----|------|-------------|------------------|-----------------|----------------------|---------------|------------|-----------|------|------|
| QY | 241  | ACATATTTTGC | AATTTTGCATGCTG   | GAACCTTTCTCAAC  | CAGAAAGAGGGCTTCA     | CAGT          | 300        |           |      |      |
| Db | 241  | ACATATTTTGG | CAAAATTTTGGCAATG | CTGCAAACTTCTC   | MACCAAGAAAGGGCTTCA   | CAGT          | 300        |           |      |      |
| QY | 301  | GTCCTTTATG  | TAAAGATATATTA    | CCAAAGAGGCTCTCA | AGAAAGTACGAGATT      | TAGTC         | 360        |           |      |      |
| Db | 301  | GTCCTTTATG  | TAAAGATATATTA    | CCAAAGAGGCTCTCA | AGAAAGTACGAGATT      | TAGTC         | 360        |           |      |      |
| QY | 361  | AACTTGTGA   | AGAGCTATTTGA     | AAATCATTTGCTTT  | CAGCTTGACACAGGTT     | TGAGT         | 420        |           |      |      |
| Db | 361  | AACTTGTGA   | AGAGCTATTTGA     | AAATCATTTGCTTT  | CAGCTTGACACAGGTT     | TGAGT         | 420        |           |      |      |
| QY | 421  | ATGCAACAG   | CAATATTTTGG      | CAAAAAAGAAATTA  | CTCTCTGTAACAT        | CTAAAGATG     | 480        |           |      |      |
| Db | 421  | ATGCAACAG   | CAATATTTTGG      | CAAAAAAGAAATTA  | CTCTCTGTAACAT        | CTAAAGATG     | 480        |           |      |      |
| QY | 481  | AAGTTTCTA   | TCATCCAAAGTA     | TGGGCTACAGAA    | CCGTGCCAAAAGACTT     | CTACAGAGT     | 540        |           |      |      |
| Db | 481  | AAGTTTCTA   | TCATCCAAAGTA     | TGGGCTACAGAA    | CCGTGCCAAAAGACTT     | CTACAGAGT     | 540        |           |      |      |
| QY | 541  | AACCCGAA    | AATCTCTTCTTG     | CAGGGAACCA      | CGTCCAGTCCCACTCTCTA  | ACCTTGGA      | 600        |           |      |      |
| Db | 541  | AACCCGAA    | AATCTCTTCTTG     | CAGGGAACCA      | CGTCCAGTCCCACTCTCTA  | ACCTTGGA      | 600        |           |      |      |
| QY | 601  | CTGTGAG     | AACTCTGAG        | CAAAAGCGCGAT    | ACAACCTCAAAAGACGTCTG | CTACATTG      | 660        |           |      |      |
| Db | 601  | CTGTGAG     | AACTCTGAG        | CAAAAGCGCGAT    | ACAACCTCAAAAGACGTCTG | CTACATTG      | 660        |           |      |      |
| QY | 661  | AATTGGAT    | CTGATCTTCT       | CTGAGATAC       | CCGTTAATAGGCA        | CTTATTGCA     | GTGGAG     | 720       |      |      |
| Db | 661  | AATTGGAT    | CTGATCTTCT       | CTGAGATAC       | CCGTTAATAGGCA        | CTTATTGCA     | GTGGAG     | 720       |      |      |
| QY | 721  | ATCAGAAT    | TGTTTACAA        | TCAACCCCTCA     | AGAAACAAGGATGA       | AAATCAGTTGGAT | CTG        | 780       |      |      |
| Db | 721  | ATCAGAAT    | TGTTTACAA        | TCAACCCCTCA     | AGAAACAAGGATGA       | AAATCAGTTGGAT | CTG        | 780       |      |      |
| QY | 781  | CAAAAAGG    | CTGCTTGTGA       | ATTTTCTG        | AGACGAGATTA          | CAAAATCTGA    | CATCTAC    | 840       |      |      |
| Db | 781  | CAAAAAGG    | CTGCTTGTGA       | ATTTTCTG        | AGACGAGATTA          | CAAAATCTGA    | CATCTAC    | 840       |      |      |
| QY | 841  | CCAGTAAT    | TAATGATTTG       | GAACCACTG       | GAAGCGCGACG          | CTGAGAGGAT    | CTCAGAAAGT | 900       |      |      |
| Db | 841  | CCAGTAAT    | TAATGATTTG       | GAACCACTG       | GAAGCGCGACG          | CTGAGAGGAT    | CTCAGAAAGT | 900       |      |      |
| QY | 901  | ATCAGGG     | TAGTCTGT         | TTCAAACTTG      | CACTGTGAC            | CCATGTGGCA    | CAAAATCTCA | TGCCA     | 960  |      |
| Db | 901  | ATCAGGG     | TAGTCTGT         | TTCAAACTTG      | CACTGTGAC            | CCATGTGGCA    | CAAAATCTCA | TGCCA     | 960  |      |
| QY | 961  | GCTCAT      | TACAGATAG        | AAACAGCACTT     | ATATACCTAA           | AGACAGATG     | ATATATG    | AA        | 1020 |      |
| Db | 961  | GCTCAT      | TACAGATAG        | AAACAGCACTT     | ATATACCTAA           | AGACAGATG     | ATATATG    | AA        | 1020 |      |
| QY | 1021 | AGGCTGA     | ATTCGTATAT       | AAAAAGCAAC      | CGCTTGCTT            | AGCAAGAGCC    | MAATTA     | CAGAT     | 1080 |      |
| Db | 1021 | AGGCTGA     | ATTCGTATAT       | AAAAAGCAAC      | CGCTTGCTT            | AGCAAGAGCC    | MAATTA     | CAGAT     | 1080 |      |
| QY | 1081 | GGGCTGA     | AGTAAAGAA        | CATGTAATG       | ATAGCGCGA            | CTCCAGC       | ACAGAAAAA  | AGGTA     | 1140 |      |
| Db | 1081 | GGGCTGA     | AGTAAAGAA        | CATGTAATG       | ATAGCGCGA            | CTCCAGC       | ACAGAAAAA  | AGGTA     | 1140 |      |
| QY | 1141 | ATCTGAAT    | GTGATCCCT        | GTGTGTAG        | AGAAAAAGAA           | TGGAAT        | TAGCAGAA   | ATCGCATCT | 1200 |      |
| Db | 1141 | ATCTGAAT    | GTGATCCCT        | GTGTGTAG        | AGAAAAAGAA           | TGGAAT        | TAGCAGAA   | ATCGCATCT | 1200 |      |
| QY | 1201 | CAGAGAA     | TCTTAGAG         | ATCTAG          | TAAGTGT              | CTTGGAT       | TACA       | CTAAAT    | TG   | 1260 |
| Db | 1201 | CAGAGAA     | TCTTAGAG         | ATCTAG          | TAAGTGT              | CTTGGAT       | TACA       | CTAAAT    | TG   | 1260 |
| QY | 1261 | AAAGTTA     | TAGATG           | GTGTTT          | CCAGAA               | GTATGA        | AACTTT     | AGTTT     | AG   | 1320 |
| Db | 1261 | AAAGTTA     | TAGATG           | GTGTTT          | CCAGAA               | GTATGA        | AACTTT     | AGTTT     | AG   | 1320 |



QY 1321 GGGAGTCTGAATCAAAATGCCAAAGTAGCTGATGTATTGGACGTTCTAAATGAGTAGATG 1380  
Db 1321 GGGAGTCTGAATCAAAATGCCAAAGTAGCTGATGTATTGGACGTTCTAAATGAGTAGATG 1380  
QY 1381 AATATTCTGGTCTTCAAGAAAATGACTTACTGCGCAGTGATCTCTCATGAGGCTTTAA 1440  
Db 1381 AATATTCTGGTCTTCAAGAAAATGACTTACTGCGCAGTGATCTCTCATGAGGCTTTAA 1440  
QY 1441 TATGTAAAGTGAAGAGTTCACTCCAAATCAGTAGAGTAAATATTGTAAGCAAAATAT 1500  
Db 1441 TATGTAAAGTGAAGAGTTCACTCCAAATCAGTAGAGTAAATATTGTAAGCAAAATAT 1500  
QY 1501 TTGGGAAAACCTATCGGAAGAAAGGCAAGCCTCCCACTTAAAGCCATGTAAGTAAATC 1560  
Db 1501 TTGGGAAAACCTATCGGAAGAAAGGCAAGCCTCCCACTTAAAGCCATGTAAGTAAATC 1560  
QY 1561 TAAATTAGAGAGATTTGTTACTGAGCCACAGATTAATACAGAGCGTCCCTCACAATA 1620  
Db 1561 TAAATTAGAGAGATTTGTTACTGAGCCACAGATTAATACAGAGCGTCCCTCACAATA 1620  
QY 1621 AATTAAGGTTAAAGAGACCTACATCAGGCTTATCTGAGATTTTATCAAGAAAG 1680  
Db 1621 AATTAAGGTTAAAGAGACCTACATCAGGCTTATCTGAGATTTTATCAAGAAAG 1680  
QY 1681 CAGATTGGCAGTTCAAAAGACTCTGAATGATTAATCAGGAACTAAACCAACGAGAC 1740  
Db 1681 CAGATTGGCAGTTCAAAAGACTCTGAATGATTAATCAGGAACTAAACCAACGAGAC 1740  
QY 1741 AGAATGTCAGAGTGAATATTACTTAATAGTGTATGATGAATTAATAAAGAGTATT 1800  
Db 1741 AGAATGTCAGAGTGAATATTACTTAATAGTGTATGATGAATTAATAAAGAGTATT 1800  
QY 1801 CTATTGAGATGAGAAAATCTTAACCCAAATGAAATCACTCGAAAAGAAATCTGCTTTA 1860  
Db 1801 CTATTGAGATGAGAAAATCTTAACCCAAATGAAATCACTCGAAAAGAAATCTGCTTTA 1860  
QY 1861 AAACGAAGCTGAACCTATAGCAGAGATTAAGCAATATGAAATCGAATTAATATATCC 1920  
Db 1861 AAACGAAGCTGAACCTATAGCAGAGATTAAGCAATATGAAATCGAATTAATATATCC 1920  
QY 1921 ACAATTCAAAAGCACTTAAGAAATAGGCTGAGGAGAAAGTCTTACAGAGCATATTC 1980  
Db 1921 ACAATTCAAAAGCACTTAAGAAATAGGCTGAGGAGAAAGTCTTACAGAGCATATTC 1980  
QY 1981 ATGCGCTTGAACCTAGTACAGTGAAGATCTAAAGCCACCTAATGTAATGTAATGCCAA 2040  
Db 1981 ATGCGCTTGAACCTAGTACAGTGAAGATCTAAAGCCACCTAATGTAATGTAATGCCAA 2040  
QY 2041 TTGATAGTGTCTAGCAGTGAAGATTAAGAAAAGTAAAGCAACCAATGCGAGTCA 2100  
Db 2041 TTGATAGTGTCTAGCAGTGAAGATTAAGAAAAGTAAAGCAACCAATGCGAGTCA 2100  
QY 2101 GGCACGCGAAGAACTTACAACTCATGAAAGTAAACCTGCAATCGAGCCAGAGAA 2160  
Db 2101 GGCACGCGAAGAACTTACAACTCATGAAAGTAAACCTGCAATCGAGCCAGAGAA 2160  
QY 2161 GTAAACAGGCAATGAAAGCAAGTAAAGAGATGACAGTAACTTTCCAGAGCTGA 2220  
Db 2161 GTAAACAGGCAATGAAAGCAAGTAAAGAGATGACAGTAACTTTCCAGAGCTGA 2220  
QY 2221 AGTTAAACAATGACCTGCTTTCTTACTAAGTTCCTAATACAGTGAATCTTAAGAAAT 2280  
Db 2221 AGTTAAACAATGACCTGCTTTCTTACTAAGTTCCTAATACAGTGAATCTTAAGAAAT 2280  
QY 2281 TTGTCAATCTTACCTTCCAGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGTAAAGTGT 2340  
Db 2281 TTGTCAATCTTACCTTCCAGAGAAAGAAAGAAAGAAAGAAAGAAAGTAAAGTGT 2340  
QY 2341 CTAAATATGCTGAAGCCCAAGATCTCATGTTAAGTGAAGAAAGGTTTGGCAACAG 2400  
Db 2341 CTAAATATGCTGAAGCCCAAGATCTCATGTTAAGTGAAGAAAGGTTTGGCAACAG 2400  
QY 2401 AAAGATCTGAGAGTAGAGTATTTCACTGCTGTAAGTATTTGCACTGAG 2460

Db 2401 AAAGATCTGAGAGTAGAGTATTTCACTGCTGTAAGTATTTGCACTGAG 2460  
QY 2461 AAAGATCTGCTTACTGGAAGTATGACATCTTGAAGGAAAGGCAAAACCAATTAAT 2520  
Db 2461 AAAGATCTGCTTACTGGAAGTATGACATCTTGAAGGAAAGGCAAAACCAATTAAT 2520  
QY 2521 GTGTAGTCAAGTGTGACGATTTGAAAACCCCAAGGACTAATTCATGAGTGTCCAAAG 2580  
Db 2521 GTGTAGTCAAGTGTGACGATTTGAAAACCCCAAGGACTAATTCATGAGTGTCCAAAG 2580  
QY 2581 AATAATGAAATGACACAGAGGCTTTAAGTATCAATGGAGATGAAGTTAAACAAGTC 2640  
Db 2581 AATAATGAAATGACACAGAGGCTTTAAGTATCAATGGAGATGAAGTTAAACAAGTC 2640  
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Db 2641 GGGAAACAAGCATTAATAATGGAAGAAAGTGAAGTGAATGCTTCAATTTGCAAGTACT 2700  
QY 2701 TCAAGGTTTCAAAAGGCGCAGTATTTGCTGTTTCAAAATCAGGAAATGCAAGAGAG 2760  
Db 2701 TCAAGGTTTCAAAAGGCGCAGTATTTGCTGTTTCAAAATCAGGAAATGCAAGAGAG 2760  
QY 2761 AATGTGCAACATTTCTGCCCCCTCTGGGCTCTTAAGAAACAAAGTCCAAAGTCACTT 2820  
Db 2761 AATGTGCAACATTTCTGCCCCCTCTGGGCTCTTAAGAAACAAAGTCCAAAGTCACTT 2820  
QY 2821 TTGAATGTGAACAAAGAAAGAAATCAAGAAAGAAAGTGAATATCAAGCTGTAC 2880  
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QY 2941 ATGCCAAATGTAATGATCAAGAGGCTCTAGGTTTGTCTATCATCTCAGTCAAGAGCA 3000  
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QY 3001 ACGAAATGGAATCTTACTCCAAATTAACATGAGACTTTTACAAACCATATGCTATAC 3060  
Db 3001 ACGAAATGGAATCTTACTCCAAATTAACATGAGACTTTTACAAACCATATGCTATAC 3060  
QY 3061 CACCACTTTTCCATCAAGTCAATTTGTTAAATGTAAGAAATCTGCTAGAG 3120  
Db 3061 CACCACTTTTCCATCAAGTCAATTTGTTAAATGTAAGAAATCTGCTAGAG 3120  
QY 3121 AAACTTTGAGGAACATTCATGTCACTGAAAGAAATGGAATGAAACATTCGA 3180  
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QY 3301 TAGGTTCCAGTATGAAACATTCAGAGCAAGTAAAGTGAAGAAAGAGGCAAAATGGA 3360  
Db 3301 TAGGTTCCAGTATGAAACATTCAGAGCAAGTAAAGTGAAGAAAGAGGCAAAATGGA 3360  
QY 3361 ATGCTATGCTTAAGTGAAGGTTTGAACCTGAGAGTCTAATAAAGAGTCTTCTGGA 3420  
Db 3361 ATGCTATGCTTAAGTGAAGGTTTGAACCTGAGAGTCTAATAAAGAGTCTTCTGGA 3420  
QY 3421 GTAAATGTAAGATCTGAAATTAATAAAGCAAGATTAAGAAAGTGAAGTGAAGTCACTGTA 3480  
Db 3421 GTAAATGTAAGATCTGAAATTAATAAAGCAAGATTAAGAAAGTGAAGTGAAGTCACTGTA 3480  
QY 3481 ATACAGATTTCTTCATATCTGATTTGAGTAACTTAAGAACGCTATGGAAGTATGTC 3540

3481 ATACAGATTTCTCTCATATCTGATTTGATTAACCTAGAACAGCCTATGGAGATGATC 3540  
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3541 ATGATCTCAGGTTGTTCTTGAGACACCTGATGACCTGTATATATATGTTGTAATAAAG 3600  
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3661 TCCAGAGAGAGAGAGCTTAGCAGAGAGTCTAGCCCTTTCACCCATACACATTGGCTCAG 3720  
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3721 GTTACCGAG 3780  
3721 GTTACCGAG 3780  
3781 AAGAGCTTCCCTGCTTCCAACTGTTATTTGTTAAAGTAACAATATACCTTCTCAGT 3840  
3781 AAGAGCTTCCCTGCTTCCAACTGTTATTTGTTAAAGTAACAATATACCTTCTCAGT 3840  
3841 CTACTAGGATAGACACCGTTGCTACCGAGTGTCTGTCTAAGAACACAGAGAGAAATTA 3900  
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3961 AGGAACATCACTTAGTAG 4020  
3961 AGGAACATCACTTAGTAG 4020  
4021 GTGAATTTGGAAGACTTGAATGCAATTAACAACCCAGAGATCTTTCTTGAATGTTCTT 4080  
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4081 CCAAAACAAATGAGGATCATGCTGTAAGCAGGAGTGTGCTGAGTGACAGAAATGG 4140  
4081 CCAAAACAAATGAGGATCATGCTGTAAGCAGGAGTGTGCTGAGTGACAGAAATGG 4140  
4141 TTTGAGATGATGAAG 4200  
4141 TTTGAGATGATGAAG 4200  
4201 TGAATTTCAAATCTTAGTGAGAGAGATCTGGGTGTGAGAGTGAACCAAGCTCTGAG 4260  
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4261 ACTGCTCAGGAGTATCTCTGAGAGTGAATTTAAACCACTGAGAGAGAGAGATGAGC 4320  
4261 ACTGCTCAGGAGTATCTCTGAGAGTGAATTTAAACCACTGAGAGAGAGAGATGAGC 4320  
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4381 ATGGAGGACAGCTTCTTAACAGCTACCTTCCATATAGTACCTCTCTGCTGAGG 4440  
4381 ATGGAGGACAGCTTCTTAACAGCTACCTTCCATATAGTACCTCTCTGCTGAGG 4440  
4441 ACCGCGAGAAATCCAGAGCAATGACATGAGAAAGAGATTAATCTTACAGAGAAAGTA 4500  
4441 ACCGCGAGAAATCCAGAGCAATGACATGAGAAAGAGATTAATCTTACAGAGAAAGTA 4500  
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4501 GTGAATACCTTAATAGCCAGAAATCCAGAGAGGCTTTCTGCTGACAAATTTGAAGTCTG 4560  
4561 CAGATAGTTCTTACCGTAAAAATTAAGAACACAGAGTGGAAAGTCACTCCCTTCTAAAT 4620  
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4621 GCCCATCTTAGATGATAGTGTGATACATGACAGTGTCTGGAGTCTTCAGATAGAA 4680  
4621 GCCCATCTTAGATGATAGTGTGATACATGACAGTGTCTCTGGAGTCTTCAGATAGAA 4680  
4681 ACTACCATCTCAAGAGAGAGTCAATTAAGTTGTTGATGAGAGAGCAACAGCTGAG 4740  
4681 ACTACCATCTCAAGAGAGAGTCAATTAAGTTGTTGATGAGAGAGCAACAGCTGAG 4740  
4741 AGTCTGGGCGACAGATTTGACGGAACATCTTCTGCAAGGACAGAGATCTAGAGGAA 4800  
4741 AGTCTGGGCGACAGATTTGACGGAACATCTTCTGCAAGGACAGAGATCTAGAGGAA 4800  
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4801 CCCCTTACCTGGAATTCGGAATTCAGCTCTCTGATGACCCCTGAATCTGATCTCTG 4860  
4861 AAGACAGAGCCCAAGAGTCAAGCTGCTGTGAGCAATACCATCTTCAACCTCTGATGA 4920  
4861 AAGACAGAGCCCAAGAGTCAAGCTGCTGTGAGCAATACCATCTTCAACCTCTGATGA 4920  
4921 AAGTTCCCAATTTGAAGTTGACAGAAATCTGCCCAGGCTCCAGCTGCTCATATCTG 4980  
4921 AAGTTCCCAATTTGAAGTTGACAGAAATCTGCCCAGGCTCCAGCTGCTCATATCTG 4980  
4981 ATACTGCTGGGTATATGCAATGGAAGAAAGTGAACAGAGAGAGAGAGAGAGAGAG 5040  
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5041 CTTCAACAGAAAGGCTCAACAAAGAAATGTCATGATGATGATGATGATGATGATGATG 5100  
5041 CTTCAACAGAAAGGCTCAACAAAGAAATGTCATGATGATGATGATGATGATGATGATG 5100  
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5101 AATTATGCTGCTTATCAAGTTTCCAGAAACCAACATCACTTCAATCAATCAATTA 5160  
5161 CTGAAGAGACTACTCATGTTGTTATGAAGACAGATGCTGATGTTGTTGTTGTTGTTG 5220  
5161 CTGAAGAGACTACTCATGTTGTTATGAAGACAGATGCTGATGTTGTTGTTGTTGTTG 5220  
5221 TGAATATTTTCTAGAAATTCGGGAGAGAAATGGTATGTAATTTCTGAGTACCC 5280  
5221 TGAATATTTTCTAGAAATTCGGGAGAGAAATGGTATGTAATTTCTGAGTACCC 5280  
5281 AGTCTATTAAGAAAGAAATTCGTAATGATGATGATGATGATGATGATGATGATG 5340  
5281 AGTCTATTAAGAAAGAAATTCGTAATGATGATGATGATGATGATGATGATGATGATG 5340  
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5401 TCAGGGGCTAGAAATCTGTTGCTATAGGCTTACCAATGAGGAGAGAGAGAGAGAG 5460  
5401 TCAGGGGCTAGAAATCTGTTGCTATAGGCTTACCAATGAGGAGAGAGAGAGAGAGAG 5460  
5461 AATGAGTGTACAGCTGTGTGTGCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5520  
5461 AATGAGTGTACAGCTGTGTGTGCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5520  
5521 GCACAGGTGTCAACCAATTTGTTGTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5580  
5521 GCACAGGTGTCAACCAATTTGTTGTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5580  
5581 TCATGCAATTTGGCAGATGTGTGAGGACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5640  
5581 TCATGCAATTTGGCAGATGTGTGAGGACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5640  
5641 GTGTAGCACTTACAG 5700  
5641 GTGTAGCACTTACAG 5700

QY 5701 GCCACTACTGA 5711  
DB 5701 GCCACTACTGA 5711

RESULT 2  
AAV62180  
ID AAV62180 standard; DNA; 5711 BP.

AAV62180;

11-FEB-1999 (first entry)

BRCA1 (omil) coding sequence.

BRCA1: mutation detection; disease screening; multiple allele variation;  
breast cancer; ovarian cancer; cystic fibrosis; Li-Fraumeni syndrome;  
Duchenne muscular dystrophy; Becker muscular dystrophy; ss.

Homo sapiens.

Key Location/Qualifiers  
CDS 120..5711  
/\*tag= a

W09844157-A2.

08-OCT-1998.

26-MAR-1998; 98WO-US06002.

28-MAR-1997; 97US-0825487.

(ONCO-) ONCOMED INC.

Murphy PD, White MB;

WPI; 1998-542713/46.

P-PSDB; AAW79665.

Identifying variations in polynucleotide sequences - using allele  
specific hybridisation assay, sequence variation locating assay, and  
direct sequencing, in a stepwise procedure

Disclosure; Fig 1a-j; 62pp; English.

This sequence encodes the human BRCA (omil) protein, and was used to test  
the method of the invention. The method is for determining the presence  
or absence of a sequence variation in a gene sample, and comprises:  
(a) performing an allele specific hybridisation assay for one or more  
pre-determined sequence variations; (b) if no pre-determined sequence  
variation found in step (a) then performing a sequence variation location  
assay; (c) if no sequence variation found in step (b) then sequencing  
the gene sample; (c1) if sequence variation is found in step (b) then  
targeted confirmatory sequencing is performed; and (d) determining the  
presence of a sequence variation by analysing the sequence(s) obtained in  
step (c) or step (c1) against a reference sample. Alternatively, step  
(a) or step (b) is omitted from the method. The invention provides a step  
stepwise and integrated method for the efficient and accurate detection  
of variations in polynucleotide sequences, being directed towards  
screening for diseases associated with multiple allele variations,  
including breast and ovarian cancer, cystic fibrosis, Duchenne and Becker  
muscular dystrophy, and Li-Fraumeni syndrome.

Sequence 5711 BP; 1953 A; 1099 C; 1277 G; 1382 T; 0 other;

Query Match 100.0%; Score 5711; DB 19; Length 5711;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 5711; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACTGCGTGAAGCTTCTCTGAGACCCGACACAGAGCTGTGGGTTTCTCAATTAACCTGGGCC 60  
DB 1 AACTGCGTGAAGCTTCTCTGAGACCCGACACAGAGCTGTGGGTTTCTCAATTAACCTGGGCC 60

QY 61 CCTGCGCTCAGAGAGCCTTCAACCTCTGCTCTGGGTAAAGTTCATTGGAACAGAAAGAAA 120  
DB 61 CCTGCGCTCAGAGAGCCTTCAACCTCTGCTCTGGGTAAAGTTCATTGGAACAGAAAGAAA 120

QY 121 TGGATTATCTGCTCTTGGCGGTTGAAGAGTACAAATATGCTATTAATGCTATGACAGAAA 180  
DB 121 TGGATTATCTGCTCTTGGCGGTTGAAGAGTACAAATATGCTATTAATGCTATGACAGAAA 180

QY 181 TCTTAGAGTTCGCCATCTGCTGAGTGTATCAAGAAACCTGTCGCCAAGAGTGTAGC 240  
DB 181 TCTTAGAGTTCGCCATCTGCTGAGTGTATCAAGAAACCTGTCGCCAAGAGTGTAGC 240

QY 241 ACATATTTTGGCAATTTTGGCATGCGAAATCTCTCAACAGAGAAAGAGGCTTCAACAGT 300  
DB 241 ACATATTTTGGCAATTTTGGCATGCGAAATCTCTCAACAGAGAAAGAGGCTTCAACAGT 300

QY 301 GTCTTTATGTGAAGATATATACCAAAAGAGGCTTCAAGAAAGTACGAGATTAGTC 360  
DB 301 GTCTTTATGTGAAGATATATACCAAAAGAGGCTTCAAGAAAGTACGAGATTAGTC 360

QY 361 AACTGTTGAAGAGCTATGAAAATCATTTGCTTTTCAAGTTCACAGGTTTGAGT 420  
DB 361 AACTGTTGAAGAGCTATGAAAATCATTTGCTTTTCAAGTTCACAGGTTTGAGT 420

QY 421 ATGCAAAAGCTATTAATTTTGGCAAAAAGAAAATTAATCTCTCTGAAACATCTAAAGATG 480  
DB 421 ATGCAAAAGCTATTAATTTTGGCAAAAAGAAAATTAATCTCTCTGAAACATCTAAAGATG 480

QY 481 AAGTTTCTATCATCCAAAGATGAGGCTTACAGAAACCTGTCACAAAGACTTCTACAGAGT 540  
DB 481 AAGTTTCTATCATCCAAAGATGAGGCTTACAGAAACCTGTCACAAAGACTTCTACAGAGT 540

QY 541 AACCCGAAATTCCTTCTCTGAGGAAACCAAGTCTAGTCTCAACTCTTCACTTGA 600  
DB 541 AACCCGAAATTCCTTCTCTGAGGAAACCAAGTCTAGTCTCAACTCTTCACTTGA 600

QY 601 CTGTGAGAACTCTGAGACCAAAAGCAGGATCAACCTCAAAAAGAGCTGTCTCATTTG 660  
DB 601 CTGTGAGAACTCTGAGACCAAAAGCAGGATCAACCTCAAAAAGAGCTGTCTCATTTG 660

QY 661 AATTGGAGTCTGATTTCTTCTGAAGATACCGTTAATAGGCAACTTATTTGACGTGGAG 720  
DB 661 AATTGGAGTCTGATTTCTTCTGAAGATACCGTTAATAGGCAACTTATTTGACGTGGAG 720

QY 721 ATCAAGATTTGTAAATCAACCTCTCAAGAAACCAAGGATGAATTCAGTTTGAATTCG 780  
DB 721 ATCAAGATTTGTAAATCAACCTCTCAAGAAACCAAGGATGAATTCAGTTTGAATTCG 780

QY 781 CAAAAGAGGCTGCTGTGAATTTTCTGAGACGAGATGAACAAATCTGAACATCATCAAC 840  
DB 781 CAAAAGAGGCTGCTGTGAATTTTCTGAGACGAGATGAACAAATCTGAACATCATCAAC 840

QY 841 CCAAGTAATATGATTTTGAACCACTGAGAAACGCTGACGCTGAGAGGATCCAGAAAGT 900  
DB 841 CCAAGTAATATGATTTTGAACCACTGAGAAACGCTGACGCTGAGAGGATCCAGAAAGT 900

QY 901 ATCAGGATGTTCTGTTTCAAACTTGCATGTGAGACCATGTGGCAAAATCTATGCA 960  
DB 901 ATCAGGATGTTCTGTTTCAAACTTGCATGTGAGACCATGTGGCAAAATCTATGCA 960

QY 961 GCTCATTCACAGATGAGAAACAGCACTTTATTAATCACTTAAGACAGAAATGATGAAA 1020  
DB 961 GCTCATTCACAGATGAGAAACAGCACTTTATTAATCACTTAAGACAGAAATGATGAAA 1020

QY 1021 AGGCTGAATTTGTAAATTAAGCAAAAGAGGCTTGAAGAGGCAACATTAACAGAT 1080  
DB 1021 AGGCTGAATTTGTAAATTAAGCAAAAGAGGCTTGAAGAGGCAACATTAACAGAT 1080

QY 1081 GGGCTGGAAGTAAAGAAACATGTAATGATAGGCGGACTCCAGACACAGAAAAAGGTAG 1140  
DB 1081 GGGCTGGAAGTAAAGAAACATGTAATGATAGGCGGACTCCAGACACAGAAAAAGGTAG 1140

1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAAAAGTAATGGAATTAAGCAGAAAATGTCATGCT 1200  
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1201 CAGAGAAATCTAGAGATCTGAAAGATGTTCTTGGATAACACTAAATATAGCAGCATTTGAGA 1260  
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1261 AAGTAATAGAGTGGTTTCCAGAAATGGAATCTGTTAGGTTCTGATGATCTGATGATGATG 1320  
1261 AAGTAATAGAGTGGTTTCCAGAAATGGAATCTGTTAGGTTCTGATGATCTGATGATGATG 1320  
1321 GGGAGTCTGAATCAAAATGCCAAAGTAGCTGATGATGTTGGACGTTCTTAAATGAGTAGATG 1380  
1321 GGGAGTCTGAATCAAAATGCCAAAGTAGCTGATGATGTTGGACGTTCTTAAATGAGTAGATG 1380  
1381 AATATCTGTTCTTCAAGAGAAATAGACTTACGAGCAATGATCTGATCTGATGAGCTTTAA 1440  
1381 AATATCTGTTCTTCAAGAGAAATAGACTTACGAGCAATGATCTGATCTGATGAGCTTTAA 1440  
1441 TATGTAAAGTGAAGAGTTTCACTGCAAAATCACTGAGAGATTAATTTGAGACAAATAT 1500  
1441 TATGTAAAGTGAAGAGTTTCACTGCAAAATCACTGAGAGATTAATTTGAGACAAATAT 1500  
1501 TTGGGAAAACTTATCGAAGAAAGGCAAGCTCCCAACTTAAGCATGTAATCTGAAAAATC 1560  
1501 TTGGGAAAACTTATCGAAGAAAGGCAAGCTCCCAACTTAAGCATGTAATCTGAAAAATC 1560  
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1621 AATTTAAAGCGTAAAGAGAGACTCATGAGCGCTTCACTGAGAGATTTTATCAAGAAAG 1680  
1621 AATTTAAAGCGTAAAGAGAGACTCATGAGCGCTTCACTGAGAGATTTTATCAAGAAAG 1680  
1681 CAGATTTGGCAGTTCAAAAAGACTCCTGAAATGATTAATCAGGAACTAACCAAGAGAGC 1740  
1681 CAGATTTGGCAGTTCAAAAAGACTCCTGAAATGATTAATCAGGAACTAACCAAGAGAGC 1740  
1741 AGAATGGTCAAGTGAATTAATTAATTAATGATGATGATGATGATGATGATGATGATGATG 1800  
1741 AGAATGGTCAAGTGAATTAATTAATTAATGATGATGATGATGATGATGATGATGATGATG 1800  
1801 CTAATTCAGAAATGAGAAAAATCTTAACCCAAATGAAATCACTGAAAAAGAAATGCTTTCA 1860  
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1861 AAACGAAAGCTGAACCTTAATGACAGCAGATTAAGCAATATGAGAACTGAAATTAATCC 1920  
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1921 ACAATTTCAAAAGCAGCTTAAGAAATAGAGCTGAGAGAGAAAGCTTTCTACAGAGCAATATC 1980  
1921 ACAATTTCAAAAGCAGCTTAAGAAATAGAGCTGAGAGAGAAAGCTTTCTACAGAGCAATATC 1980  
1981 ATGGGCTTGAAGTCTAGTACAGTAAGAAATCTTAAGCCACTTAATTTGATGATGATGATG 2040  
1981 ATGGGCTTGAAGTCTAGTACAGTAAGAAATCTTAAGCCACTTAATTTGATGATGATGATG 2040  
1981 ATGGGCTTGAAGTCTAGTACAGTAAGAAATCTTAAGCCACTTAATTTGATGATGATGATG 2040  
2041 TTGATAGTGTCTTACAGCAGTGAAGATTAAGAAAAAAGTAAACCAAAATGCCAGTCA 2100  
2041 TTGATAGTGTCTTACAGCAGTGAAGATTAAGAAAAAAGTAAACCAAAATGCCAGTCA 2100  
2101 GGGCAGAGAGAACTTACAACTCATGAGAGGTAAGAAAGCTGCAACTGAGCAGAGAGAA 2160  
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2161 GTAAACAAGCCAAATGAGACAGCAAGTAAGAAAGCATGAGAGTACTTTCCAGAGCTGA 2220  
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2221 AGTTAAACAATGACCTGTTCTTTACTAAGTGTCAAAATTAACAGTGAATTTAAAGAT 2280  
2221 AGTTAAACAATGACCTGTTCTTTACTAAGTGTCAAAATTAACAGTGAATTTAAAGAT 2280

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2281 TTGTCAATCTTACGCTTCCAAAGAGAGAAAAAGAAAGAACTTAAGAAACGTTAAAGT 2340  
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2341 CTAATTAATGCTGAAGAGACCCCAAGATCTCATGTTAAGTGAAGAAAGGTTTTCAAACTG 2400  
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2461 AAAGATCTGAGAGAGTGAAGATTTCACTGTAACCTGTAATGATGATGATGATGATGATG 2520  
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2521 GTGTGAGTCAAGTGAAGAGTGAAGATTTCACTGTAACCTGTAATGATGATGATGATGATG 2580  
2581 AATTAAGAAATGACACAGAAAGCTTTAAGTATCCATTGGACATGAAGTTAACACAGTC 2640  
2581 AATTAAGAAATGACACAGAAAGCTTTAAGTATCCATTGGACATGAAGTTAACACAGTC 2640  
2641 GGGAAACAGAGATGAAGATGAAGAAAGTGAATGATGATGATGATGATGATGATGATGATG 2700  
2641 GGGAAACAGAGATGAAGATGAAGAAAGTGAATGATGATGATGATGATGATGATGATGATG 2700  
2701 TCAAGGTTTCAAAAGCGCAGTCAATTTCTGTTTCAATTCAGGAAATGAGAGAGG 2760  
2701 TCAAGGTTTCAAAAGCGCAGTCAATTTCTGTTTCAATTCAGGAAATGAGAGAGG 2760  
2761 AATGTGCAACATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2820  
2761 AATGTGCAACATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2820  
2821 TTGAATGGAACAAAGAGAGAAATCAAGAGAAAGTGAATGATGATGATGATGATGATGATG 2880  
2821 TTGAATGGAACAAAGAGAGAAATCAAGAGAAAGTGAATGATGATGATGATGATGATGATG 2880  
2881 AGACAGTTAATATACCTGAGAGCTTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 2940  
2881 AGACAGTTAATATACCTGAGAGCTTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 2940  
2941 ATGCCAAATGATATCAAGAGAGCTTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 3000  
2941 ATGCCAAATGATATCAAGAGAGCTTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 3000  
3001 ACGAAACCTGAGCTCAATTAATCCAAATGAAGAGCTTTTAAACAAACCCATTCGATATAC 3060  
3001 ACGAAACCTGAGCTCAATTAATCCAAATGAAGAGCTTTTAAACAAACCCATTCGATATAC 3060  
3061 CACCACTTTTCCATCAAGTCAATTTGTTTAAATGATTAAGAAAAATCTCTAGAGG 3120  
3061 CACCACTTTTCCATCAAGTCAATTTGTTTAAATGATTAAGAAAAATCTCTAGAGG 3120  
3121 AAAAATTTGAGAAATTTCAATGTCACCTGAAGAAAGTGAAGAAATGAGAAATTTCA 3180  
3121 AAAAATTTGAGAAATTTCAATGTCACCTGAAGAAAGTGAAGAAATGAGAAATTTCA 3180  
3121 AAAAATTTGAGAAATTTCAATGTCACCTGAAGAAAGTGAAGAAATGAGAAATTTCA 3180  
3181 GTACAGTGAAGCAATTAAGCCGTAATTAATTAAGAAATGTTTAAAGAGAGCAAGCT 3240  
3181 GTACAGTGAAGCAATTAAGCCGTAATTAATTAAGAAATGTTTAAAGAGAGCAAGCT 3240  
3241 CAACCAATTAATTAAGAGTGAAGTCCAGTCTAATGAAGAGGCTCAGATTAATGA 3300  
3241 CAACCAATTAATTAAGAGTGAAGTCCAGTCTAATGAAGAGGCTCAGATTAATGA 3300  
3241 CAACCAATTAATTAAGAGTGAAGTCCAGTCTAATGAAGAGGCTCAGATTAATGA 3300  
3301 TAGGTTCAAGTGAAGAAATTTCAAGCAAGCTAGTGAAGAAAGAGGCTCAAAATTTGA 3360  
3301 TAGGTTCAAGTGAAGAAATTTCAAGCAAGCTAGTGAAGAAAGAGGCTCAAAATTTGA 3360

Db 3301 TAGGTTCCAGTAGTAAACATTCAAGCAGACTAGTAGAAAAGAGGGCCAAATGTA 3360  
QY 3361 ATGCTATGCTTAATTAGGGGTTTTGCAACCTGAGGCTATAACAAAGCTTCCGAGAA 3420  
Db 3361 ATGCTATGCTTAATTAGGGGTTTTGCAACCTGAGGCTATAACAAAGCTTCCGAGAA 3420  
QY 3421 GTAATGTAGCATCTCGTAATTAATAAGCAGAAATATGAGAAGTAGTTCAAGCTGTA 3480  
Db 3421 GTAATGTAGCATCTCGTAATTAATAAGCAGAAATATGAGAAGTAGTTCAAGCTGTA 3480  
QY 3481 ATACAGATTTCTCTCCATATCTGATTTAGATACTTAGAACGCTATGGAAGTAGTC 3540  
Db 3481 ATACAGATTTCTCTCCATATCTGATTTAGATACTTAGAACGCTATGGAAGTAGTC 3540  
QY 3541 ATGATCTCAGGTTGTTGTTGAGACACCTGATGACCTGTTAGTAGTGGGAAATGAAG 3600  
Db 3541 ATGATCTCAGGTTGTTGTTGAGACACCTGATGACCTGTTAGTAGTGGGAAATGAAG 3600  
QY 3601 AAGATACTAGTTTGTGTAATAATGACATTAGGAAAGTTCTGCTGTTTTAGCAAAAGCG 3660  
Db 3601 AAGATACTAGTTTGTGTAATAATGACATTAGGAAAGTTCTGCTGTTTTAGCAAAAGCG 3660  
QY 3661 TCCAGAGAGAGGCTTAGCAGAGAGTCTAGCCCTTTACCCATACATTTGGCTCAGG 3720  
Db 3661 TCCAGAGAGAGGCTTAGCAGAGAGTCTAGCCCTTTACCCATACATTTGGCTCAGG 3720  
QY 3721 GTTACCGAAGAGGGCCAAAGAAATTAAGTCTCAGAAAGAACTTATCTAGTAGAAGTG 3780  
Db 3721 GTTACCGAAGAGGGCCAAAGAAATTAAGTCTCAGAAAGAACTTATCTAGTAGAAGTG 3780  
QY 3781 AAGAGCTTCCCTGCTTCCAAACCTGTTATTTGGTAAAGTAAACAATATACCTTCTCAGT 3840  
Db 3781 AAGAGCTTCCCTGCTTCCAAACCTGTTATTTGGTAAAGTAAACAATATACCTTCTCAGT 3840  
QY 3841 CTACTGAGCATAGCACCGTTGCTACCGAGTGTCTGTCTAAGAACACAGAGAGAAATTAT 3900  
Db 3841 CTACTGAGCATAGCACCGTTGCTACCGAGTGTCTGTCTAAGAACACAGAGAGAAATTAT 3900  
QY 3901 TATCATTTGAAGAAATAGCTTAATGATGATGATGATGATGATGATGATGATGATGATG 3960  
Db 3901 TATCATTTGAAGAAATAGCTTAATGATGATGATGATGATGATGATGATGATGATGATG 3960  
QY 3961 AGGAACTACCTTATGAGGAAACAAATGTTCTGCTAGCTGTTTCTTCACTGCA 4020  
Db 3961 AGGAACTACCTTATGAGGAAACAAATGTTCTGCTAGCTGTTTCTTCACTGCA 4020  
QY 4021 GTGAATTTGGAAGCTGAGCTGCAATACAAACCCAGAGATCTTCTTGTGATGTTGTT 4080  
Db 4021 GTGAATTTGGAAGCTGAGCTGCAATACAAACCCAGAGATCTTCTTGTGATGTTGTT 4080  
QY 4081 CCMAACAAATAGGAGCATGAGTGAAGAGCAGGAGATGCTGAGTGAACAAGAAATGG 4140  
Db 4081 CCMAACAAATAGGAGCATGAGTGAAGAGCAGGAGATGCTGAGTGAACAAGAAATGG 4140  
QY 4141 TTTTCAGATGATGAAGAAAGAGAAACGGGCTTGGAAAGAAATATATCAAGAAAGCAAGCA 4200  
Db 4141 TTTTCAGATGATGAAGAAAGAGAAACGGGCTTGGAAAGAAATATATCAAGAAAGCAAGCA 4200  
QY 4201 TGGATTTCAAACTTAAAGTGAAGAGCATCTGGGCTGAGAGTGAAGAAACAGCTCTGGAAG 4260  
Db 4201 TGGATTTCAAACTTAAAGTGAAGAGCATCTGGGCTGAGAGTGAAGAAACAGCTCTGGAAG 4260  
QY 4261 ACTGCTCAGAGGCTATCTCTCAGAGTGAAGATTTTAAACAAGAGAGAGATGATGATG 4320  
Db 4261 ACTGCTCAGAGGCTATCTCTCAGAGTGAAGATTTTAAACAAGAGAGAGATGATGATG 4320  
QY 4321 AACATTAAGCTGAATTAAGCTCAGCAGAGAAATGCTGTAAGTGAAGCTGTTGTAAGCAAGC 4380  
Db 4321 AACATTAAGCTGAATTAAGCTCAGCAGAGAAATGCTGTAAGTGAAGCTGTTGTAAGCAAGC 4380  
QY 4381 ATGGAGCCAGAGCTTTTAAAGCTTCAAGCTTCAATCAATGAAGCTCTGCTGCTTGAAG 4440  
Db 4381 ATGGAGCCAGAGCTTTTAAAGCTTCAAGCTTCAATCAATGAAGCTCTGCTGCTTGAAG 4440

QY 4441 ACCGCGAAATCGAGAACAAAGCACATCGAAGAAAGCAGATATTAATTCAAGAAAGTA 4500  
Db 4441 ACCGCGAAATCGAGAACAAAGCACATCGAAGAAAGCAGATATTAATTCAAGAAAGTA 4500  
QY 4501 GTGAATTAAGCTTAAGCCAGAAATCGAAGAGGCTTCTGCTGCAAGATTTGAGTGTCTG 4560  
Db 4501 GTGAATTAAGCTTAAGCCAGAAATCGAAGAGGCTTCTGCTGCAAGATTTGAGTGTCTG 4560  
QY 4561 CAGATAGTTCTACAGTAAATAATTAAGAAACGAGAGTGAAGAGTATCCCTTCTAAT 4620  
Db 4561 CAGATAGTTCTACAGTAAATAATTAAGAAACGAGAGTGAAGAGTATCCCTTCTAAT 4620  
QY 4621 GCCCATCATTAATGATGATGAGTGTATGATGATGATGATGATGATGATGATGATGATG 4680  
Db 4621 GCCCATCATTAATGATGATGAGTGTATGATGATGATGATGATGATGATGATGATGATG 4680  
QY 4681 ACTACCATCTCAGAGAGGCTCATTAAGTGTGATGATGATGATGATGATGATGATGATG 4740  
Db 4681 ACTACCATCTCAGAGAGGCTCATTAAGTGTGATGATGATGATGATGATGATGATGATG 4740  
QY 4741 AGTCTGGGCAACAGATTTGAAGAAACATTTTCTGCAAGGCAAGTCTAGAGGAA 4800  
Db 4741 AGTCTGGGCAACAGATTTGAAGAAACATTTTCTGCAAGGCAAGTCTAGAGGAA 4800  
QY 4801 CCCCTTACCTGGAATCTGGAATCAGGCTCTGCTGATGATGATGATGATGATGATGATG 4860  
Db 4801 CCCCTTACCTGGAATCTGGAATCAGGCTCTGCTGATGATGATGATGATGATGATGATG 4860  
QY 4861 AAGACAGAGCCCAAGAGTACAGTCTGTTGGCAAGATACATCTTCAACCTTGCATTTGA 4920  
Db 4861 AAGACAGAGCCCAAGAGTACAGTCTGTTGGCAAGATACATCTTCAACCTTGCATTTGA 4920  
QY 4921 AAGTCCCAATTTGAAGTGTGCAATCTGCCAGAGTCTCAGCTGCTCATCTACTG 4980  
Db 4921 AAGTCCCAATTTGAAGTGTGCAATCTGCCAGAGTCTCAGCTGCTCATCTACTG 4980  
QY 4981 ATACTGCTGGTATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5040  
Db 4981 ATACTGCTGGTATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5040  
QY 5041 CTTCAACAGAAAGGCTCAACAAAGATGTCATGATGATGATGATGATGATGATGATGATG 5100  
Db 5041 CTTCAACAGAAAGGCTCAACAAAGATGTCATGATGATGATGATGATGATGATGATGATG 5100  
QY 5101 AATTATGCTGCTGATCAAGTGTGCAAGAAACACCATCACTTAACTAATTA 5160  
Db 5101 AATTATGCTGCTGATCAAGTGTGCAAGAAACACCATCACTTAACTAATTA 5160  
QY 5161 CTGAAGAGCTACATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5220  
Db 5161 CTGAAGAGCTACATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5220  
QY 5221 TGAATATTTTCTAGAAATTTGGGAGAGAAATGGGTAGTTAGTATTTCTGGTGACCC 5280  
Db 5221 TGAATATTTTCTAGAAATTTGGGAGAGAAATGGGTAGTTAGTATTTCTGGTGACCC 5280  
QY 5281 AGTCTATTTAAAGAAATGCTGAATGAGCATGATTTGAAGTCTAGAGAGATGTTGG 5340  
Db 5281 AGTCTATTTAAAGAAATGCTGAATGAGCATGATTTGAAGTCTAGAGAGATGTTGG 5340  
QY 5341 TCAATGGAAGAAACCAAGGCTCCAAAGGAGCAAGAGATCCAGAGACGAAGAAATCT 5400  
Db 5341 TCAATGGAAGAAACCAAGGCTCCAAAGGAGCAAGAGATCCAGAGACGAAGAAATCT 5400  
QY 5401 TCAGGGGCTAGAAATCTGTTGCTATGAGGCTTCAACCAAGATGCTCAGATCAACTGG 5460  
Db 5401 TCAGGGGCTAGAAATCTGTTGCTATGAGGCTTCAACCAAGATGCTCAGATCAACTGG 5460  
QY 5461 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5520  
Db 5461 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5520

|          |   |                                |   |       |
|----------|---|--------------------------------|---|-------|
| OY       |   | 5521                           | GCACAGGGTCCACCATTGCGTTGTGACACCCAGATGCCCTGACAGAGGACAATGGCT     | 5580  |
| DB       |   | 5521                           | GCACAGGGTCCACCATTGCGTTGTGACACCCAGATGCCCTGACAGAGGACAATGGCT     | 5580  |
| OY       |   | 5581                           | TCCATGCAATTGGGAGATGTGTGAAGCACCCTGTGTGTGACCCGAGAGTGGGTGTGACA   | 5640  |
| DB       |   | 5581                           | TCCATGCAATTGGGAGATGTGTGAAGCACCCTGTGTGTGACCCGAGAGTGGGTGTGACA   | 5640  |
| OY       |   | 5641                           | GGTGTGCACTCTAACCAAGTCGCGAGAGCTGGAAACTTACTGATTAACCCAGATCCCCACA | 57000 |
| DB       |   | 5641                           | GGTGTGCACTCTAACCAAGTCGCGAGAGCTGGAAACTTACTGATTAACCCAGATCCCCACA | 57000 |
| OY       |   | 5701                           | GCCACTACTGA 5711<br>     <br>                                 |       |
| DB       |   | 5701                           | GCCACTACTGA 5711  |       |
| RESULT 3 |   |                                |   |       |
| ID       | AAV46448  |                                |   |       |
| XX       | AAV46448  | standard; cDNA; 5711 BP.       |   |       |
| AC       | AAV46448;   |                                |   |       |
| DT       | 18-NOV-1998   | (first entry)                  |   |       |
| DE       | Human BRCA1 om1l cDNA.  |                                |   |       |
| KX       | BRCA1; om1l; human; breast and ovarian cancer predisposing gene;          |                                |   |       |
| KM       | polymorphism; susceptibility; anti-oncogene; tumour suppressor;           |                                |   |       |
| KW       | chromosome 17q; ss.   |                                |   |       |
| OS       | Homo sapiens.   |                                |   |       |
| FT       | Key   | Location/Qualifiers            |   |       |
| FH       | CDS   | 120..5711                      |   |       |
| FT       |   | /*tag= a                       |   |       |
| XX       |   | /product= "BRCA1 om1l protein" |   |       |
| PN       | US5750400-A.  |                                |   |       |
| PD       | 12-MAY-1998.  |                                |   |       |
| PF       | 12-FEB-1997;  | 97US-0798691.                  |   |       |
| PR       | 12-FEB-1996;  | 96US-0598591.                  |   |       |
| PR       | 12-FEB-1997;  | 97US-0798691.                  |   |       |
| PA       | (ONCO-) ONCORMED INC.   |                                |   |       |
| PI       | Allien AC, Alvares CP, Critz BS, Murphy PD, Olson SJ,                     |                                |   |       |
| PI       | Schelter DB, Zeng B;  |                                |   |       |
| DR       | MP1: 1998-296774/26.  |                                |   |       |
| DR       | P-PsDB; AAM76098.   |                                |   |       |
| PT       | BRCA1 om1 gene coding sequences - useful for distinguishing between       |                                |   |       |
| PT       | polymorphisms and mutation(s) in the screening for disposition to         |                                |   |       |
| PT       | breast or ovarian cancer  |                                |   |       |
| PS       | Claim 2d; Column 27-32; 54pd; English.                                    |                                |   |       |
| XX       | This sequence encodes the human BRCA1 (breast and ovarian cancer          |                                |   |       |
| XX       | predisposing gene) om1l gene. This sequence and polymorphic variations of |                                |   |       |
| XX       | this sequence are useful for the identification of an individual who may  |                                |   |       |
| XX       | or may not have an increased susceptibility to breast or ovarian cancer.  |                                |   |       |
| XX       | The sequences used identify gene changes which are due to polymorphisms,  |                                |   |       |
| XX       | rather than cancer causing mutations. BRCA1 is an anti-oncogene (tumour   |                                |   |       |
| XX       | suppressor) which is involved in genetic inheritance of cancers,          |                                |   |       |
| XX       | especially breast and ovarian cancer. It is found at human chromosome 17q |                                |   |       |
| XX       | which is known to be linked to cancer susceptibility, especially breast   |                                |   |       |
| XX       | cancer. Cells containing a mutation in this gene lose the wild-type       |                                |   |       |
| XX       | function of BRCA1 and are more susceptible to cancers.                    |                                |   |       |

|                       |                      |   |
|-----------------------|----------------------|---|
| SQ                    | Sequence             | 5711 BP; 1953 A; 1099 C; 1277 G; 1382 T; 0 other;                   |
| Query Match           | 100.0%; Score 5711;  | DB 19; Length 5711;   |
| Best Local Similarity | 100.0%; Pred. No. 0; | Mismatches 0;   |
| Matches 5711;         | Conservative 0;      | Indels 0; Gaps 0;   |
| OY                    | 1                    | AGCTGCGTAGAAGACTTCTGTGAACCCCGCACCGGGCTGTGGGGTTTCTCAGATACTGGGCC 60   |
| Db                    | 1                    | AGCTGCGTAGAAGACTTCTGTGAACCCCGCACCGGGCTGTGGGGTTTCTCAGATACTGGGCC 60   |
| OY                    | 61                   | CCTGGCGTCAGAGAAGCCCTTCAACCCTCTGCTCTGGGTAAAGTTCATTGGAAACAGAAAGAA 120 |
| Db                    | 61                   | CCTGGCGTCAGAGAAGCCCTTCAACCCTCTGCTCTGGGTAAAGTTCATTGGAAACAGAAAGAA 120 |
| OY                    | 121                  | TGGATTTATCTGCTCTTGCGCTTGGAGAGTAACAATGTCATTAAATGCTATGAGAAA 180       |
| Db                    | 121                  | TGGATTTATCTGCTCTTGCGCTTGGAGAGTAACAATGTCATTAAATGCTATGAGAAA 180       |
| OY                    | 181                  | TCTTAGAGTGTCCCATCTGCTGTGAGATTGATCAAGAACCTGTCTCCAACAAGTGTGACC 240    |
| Db                    | 181                  | TCTTAGAGTGTCCCATCTGCTGTGAGATTGATCAAGAACCTGTCTCCAACAAGTGTGACC 240    |
| OY                    | 241                  | ACATTTTTGGAAAAATTTGGACNGCGAAACCTTCCACACAGAAAGAGGCCTTCACAGT 300      |
| Db                    | 241                  | ACATTTTTGGAAAAATTTGGACNGCGAAACCTTCCACACAGAAAGAGGCCTTCACAGT 300      |
| OY                    | 301                  | GTCCTTTATGTAGAATGATATAACCAAAGAGAGCTTCAAGAAAAGTACGAGATTTACTC 360     |
| Db                    | 301                  | GTCCTTTATGTAGAATGATATAACCAAAGAGAGCTTCAAGAAAAGTACGAGATTTACTC 360     |
| OY                    | 361                  | AACCTGTGAAGAGCTATGGAANAATCATTTGCTTTCACTTGAACACAGTTTGAAGT 420        |
| Db                    | 361                  | AACCTGTGAAGAGCTATGGAANAATCATTTGCTTTCACTTGAACACAGTTTGAAGT 420        |
| OY                    | 421                  | ATGCAACAGCTATATTTTGCAAAAAGAAAAATACTCTCTGAAACATCTAAAGATG 480         |
| Db                    | 421                  | ATGCAACAGCTATATTTTGCAAAAAGAAAAATACTCTCTGAAACATCTAAAGATG 480         |
| OY                    | 481                  | AAGTTTCTATCATCCAAAAGTATGGGCTACAGAAAACCGTGCCAAAAGACTTTACAGAGTG 540   |
| Db                    | 481                  | AAGTTTCTATCATCCAAAAGTATGGGCTACAGAAAACCGTGCCAAAAGACTTTACAGAGTG 540   |
| OY                    | 541                  | AAACCGAAAAATCCCTTCTTGACAGGAACACAGTTCAGTGTCCAACCTCTAACCTGGAA 600     |
| Db                    | 541                  | AAACCGAAAAATCCCTTCTTGACAGGAACACAGTTCAGTGTCCAACCTCTAACCTGGAA 600     |
| OY                    | 601                  | CTGTGAGAACTCTGTAGACAAAGCAGCGGATACAACTCAAAAGACGTCCTTCAATTG 660       |
| Db                    | 601                  | CTGTGAGAACTCTGTAGACAAAGCAGCGGATACAACTCAAAAGACGTCCTTCAATTG 660       |
| OY                    | 661                  | AATGGGATCTGATTTCTTCTGAAGTACCGTTAATAGGCAACTATTTGGCAGTGGGAG 720       |
| Db                    | 661                  | AATGGGATCTGATTTCTTCTGAAGTACCGTTAATAGGCAACTATTTGGCAGTGGGAG 720       |
| OY                    | 721                  | ATCAAGAATTTGTTCAAAATCAACCCCTCAAGAACACAGGATGAATACGTTTGAATTCG 780     |
| Db                    | 721                  | ATCAAGAATTTGTTCAAAATCAACCCCTCAAGAACACAGGATGAATACGTTTGAATTCG 780     |
| OY                    | 781                  | CAAAAAAGGCGCTGTGTAATTTCTGTGAGAGGAGTAAACAAATATCTGAACATATCAAC 840     |
| Db                    | 781                  | CAAAAAAGGCGCTGTGTAATTTCTGTGAGAGGAGTAAACAAATATCTGAACATATCAAC 840     |
| OY                    | 841                  | CCAGTAAATATGATTTGAACACCACTGAGAAAGCGTCAGCTGAGAGGATCCAGAAAAGT 900     |
| Db                    | 841                  | CCAGTAAATATGATTTGAACACCACTGAGAAAGCGTCAGCTGAGAGGATCCAGAAAAGT 900     |
| OY                    | 901                  | ATCAGGGTAGTTCGTGTTCAACTTGACGTGTGAGCAATGTGSCACAAATATCTATGCCA 960     |
| Db                    | 901                  | ATCAGGGTAGTTCGTGTTCAACTTGACGTGTGAGCAATGTGSCACAAATATCTATGCCA 960     |
| OY                    | 961                  | GCTCATTTACACATGAGAACAGCAGCTTATTAATCACTAAAGACAGAAATGATATAGAA 1020    |
| Db                    | 961                  | GCTCATTTACACATGAGAACAGCAGCTTATTAATCACTAAAGACAGAAATGATATAGAA 1020    |



QY 1021 AGCGTAATTCGTGAATTAAGCAACAGCCTGGCTTAGCAAGAGCAACATAACAGAT 1080  
DB 1021 AGCGTAATTCGTGAATTAAGCAACAGCCTGGCTTAGCAAGAGCAACATAACAGAT 1080  
QY 1081 GGGCTGGAAGTAGAAGAACTGTAAATAGTAGCGGACCTCCAGACAGAAAAAAGGTAG 1140  
DB 1081 GGGCTGGAAGTAGAAGAACTGTAAATAGTAGCGGACCTCCAGACAGAAAAAAGGTAG 1140  
QY 1141 ATCTGAATGCTGATCCCGCTGTGAGAGAAAGAAATAGCAAGAAATGCCCATGCT 1200  
DB 1141 ATCTGAATGCTGATCCCGCTGTGAGAGAAAGAAATAGCAAGAAATGCCCATGCT 1200  
QY 1201 CAGAGATCCTAGAGATCTAGAGATGTTCTTGATTAACATTAATAGAGCATTCAG 1260  
DB 1201 CAGAGATCCTAGAGATCTAGAGATGTTCTTGATTAACATTAATAGAGCATTCAG 1260  
QY 1261 AAGTTAATGAGTGGTTTTCCAGAAGTAGAAGCTGTAGGTTCTGATGACATGATG 1320  
DB 1261 AAGTTAATGAGTGGTTTTCCAGAAGTAGAAGCTGTAGGTTCTGATGACATGATG 1320  
QY 1321 GGGAGTCTGAATTAATGCAAGTAGCTGATTTGGACGTTCTTAATGAGGTAGTG 1380  
DB 1321 GGGAGTCTGAATTAATGCAAGTAGCTGATTTGGACGTTCTTAATGAGGTAGTG 1380  
QY 1381 AATATTCTGGTCTTCAAGAGAAATAGACTTACCTGGCAGTATCCTCATGAGCTTTTA 1440  
DB 1381 AATATTCTGGTCTTCAAGAGAAATAGACTTACCTGGCAGTATCCTCATGAGCTTTTA 1440  
QY 1441 TATGTAAAGTGAAGAGTTCACTCCAAATCAGTAGAGATTAATTGAAGCAAAATAT 1500  
DB 1441 TATGTAAAGTGAAGAGTTCACTCCAAATCAGTAGAGATTAATTGAAGCAAAATAT 1500  
QY 1501 TTGGGAAACCTATCGGAGAGAGCAAGCCTCCCACTTAAGCCATGTAACGAAATATC 1560  
DB 1501 TTGGGAAACCTATCGGAGAGAGCAAGCCTCCCACTTAAGCCATGTAACGAAATATC 1560  
QY 1561 TAAATATAGGAGATTTGTTACTGAGCCACAGATTAATACAGAGCGCTCCCTCACAATTA 1620  
DB 1561 TAAATATAGGAGATTTGTTACTGAGCCACAGATTAATACAGAGCGCTCCCTCACAATTA 1620  
QY 1621 AATTAAGCGTAAAGAGACCTACATCAGGCTTCATCCTGAGATTTTATCAAGAAAG 1680  
DB 1621 AATTAAGCGTAAAGAGACCTACATCAGGCTTCATCCTGAGATTTTATCAAGAAAG 1680  
QY 1681 CAGATTTGCGAGTTCAAAAAGACTCTCGAAATGATTAATCAGGAGCTAAACGAGAC 1740  
DB 1681 CAGATTTGCGAGTTCAAAAAGACTCTCGAAATGATTAATCAGGAGCTAAACGAGAC 1740  
QY 1741 AGAATGCTCAAGATGAATTAATTAATAGTGTGATGAGATTAAGCAAAAGGTGAT 1800  
DB 1741 AGAATGCTCAAGATGAATTAATTAATAGTGTGATGAGATTAAGCAAAAGGTGAT 1800  
QY 1801 CTATTGAGATGAGAAAAATCTTAACCAATAGAAATCACTCGAAAAAGAAATCTGCTTTCA 1860  
DB 1801 CTATTGAGATGAGAAAAATCTTAACCAATAGAAATCACTCGAAAAAGAAATCTGCTTTCA 1860  
QY 1861 AAAACGAAGCTGAACCTATTAAGAGAGATTAAGCAATATGCAATTCGAAATTAATATCC 1920  
DB 1861 AAAACGAAGCTGAACCTATTAAGAGAGATTAAGCAATATGCAATTCGAAATTAATATCC 1920  
QY 1921 ACAATTCAAAAGCACTTAAGAAATAGGCTGAGAGAAAGTCTTTCACAGCATATATTC 1980  
DB 1921 ACAATTCAAAAGCACTTAAGAAATAGGCTGAGAGAAAGTCTTTCACAGCATATATTC 1980  
QY 1981 ATGCGCTTGAAGTGAAGTGAAGAAATCTAAAGCCACCTAATGTACTGAATTCGAA 2040  
DB 1981 ATGCGCTTGAAGTGAAGTGAAGAAATCTAAAGCCACCTAATGTACTGAATTCGAA 2040  
QY 2041 TTGATATGTTGTTCTAGCAGTGAAGATTAAGAAAAAAGTAAACCAAAATGCGACGTCA 2100  
DB 2041 TTGATATGTTGTTCTAGCAGTGAAGATTAAGAAAAAAGTAAACCAAAATGCGACGTCA 2100

QY 2101 GGCACAGCAAAACCTAACACTATGAGAGTAAAGAACTTCAGCTGAGCCAGAAAGA 2160  
DB 2101 GGCACAGCAAAACCTAACACTATGAGAGTAAAGAACTTCAGCTGAGCCAGAAAGA 2160  
QY 2161 GTTAAACAGCCAAATGAAACAGACAGTAAAGACATGACGTGATCTTCCAGACCTGA 2220  
DB 2161 GTTAAACAGCCAAATGAAACAGACAGTAAAGACATGACGTGATCTTCCAGACCTGA 2220  
QY 2221 AGTTAAACAAATGACCTGGTCTTTTACTAAGGTTCAAATCCAGTGAACCTTAAGAT 2280  
DB 2221 AGTTAAACAAATGACCTGGTCTTTTACTAAGGTTCAAATCCAGTGAACCTTAAGAT 2280  
QY 2281 TTGTCATCTGACCTTCCAGAGAAAGAAAGAGAAAGTAAACAGTTAAAGTGT 2340  
DB 2281 TTGTCATCTGACCTTCCAGAGAAAGAAAGAGAAAGTAAACAGTTAAAGTGT 2340  
QY 2341 CTAAATATGCTGAAGACCCCAAGATCTCATGTTAAGTGAAGAAAGGTTTTGCAAACTG 2400  
DB 2341 CTAAATATGCTGAAGACCCCAAGATCTCATGTTAAGTGAAGAAAGGTTTTGCAAACTG 2400  
QY 2401 AAAAGATCTGTAGAGATGACATATTTCACTGTGACCTGTACTGATTAATGCACTCAG 2460  
DB 2401 AAAAGATCTGTAGAGATGACATATTTCACTGTGACCTGTACTGATTAATGCACTCAG 2460  
QY 2461 AAAAGATCTGTAGAGATGACATATTTCACTGTGACCTGTACTGATTAATGCACTCAG 2520  
DB 2461 AAAAGATCTGTAGAGATGACATATTTCACTGTGACCTGTACTGATTAATGCACTCAG 2520  
QY 2521 GTGTAGTCAAGTGTGACAGATTTGAAAACCCCAAGGACCTAAATTCATGTTGTTCCAAAG 2580  
DB 2521 GTGTAGTCAAGTGTGACAGATTTGAAAACCCCAAGGACCTAAATTCATGTTGTTCCAAAG 2580  
QY 2581 AATAATGAATGACACAGAGAGCTTAAATACCTGGAGATGAAGTAAACCAACAGC 2640  
DB 2581 AATAATGAATGACACAGAGAGCTTAAATACCTGGAGATGAAGTAAACCAACAGC 2640  
QY 2641 GGGAAACAAAGCTAATAAGTGAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2700  
DB 2641 GGGAAACAAAGCTAATAAGTGAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2700  
QY 2701 TCAAGTTTCAAAAGGCGCAGTCAATTTGCTCTGTTTTCAAAATCAGAGAAATGCAAGAG 2760  
DB 2701 TCAAGTTTCAAAAGGCGCAGTCAATTTGCTCTGTTTTCAAAATCAGAGAAATGCAAGAG 2760  
QY 2761 AATGTGCAACATTTCTGCTGCCACTCTGGGTCTTAAAGAAACAAAGTCCAAAGTCACTT 2820  
DB 2761 AATGTGCAACATTTCTGCTGCCACTCTGGGTCTTAAAGAAACAAAGTCCAAAGTCACTT 2820  
QY 2821 TTGAATGTGAACAAAGAGAAAGAAATCAAGAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2880  
DB 2821 TTGAATGTGAACAAAGAGAAAGAAATCAAGAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2880  
QY 2881 AGACAGTTAATATCACTGCAAGCTTTCTGTGTTGTGTCAGAAAGATGAAGCCAGTTGATA 2940  
DB 2881 AGACAGTTAATATCACTGCAAGCTTTCTGTGTTGTGTCAGAAAGATGAAGCCAGTTGATA 2940  
QY 2941 ATGCCAAATGTATGATCAAGAGAGCTTGAAGTTTGTCTATCATCTCAGTTCAAGAGCA 3000  
DB 2941 ATGCCAAATGTATGATCAAGAGAGCTTGAAGTTTGTCTATCATCTCAGTTCAAGAGCA 3000  
QY 3001 ACGAATCTGSACTCAATTAACCAATTAAGCACTTTTCAAAACCAATTAAGCACTTAATC 3060  
DB 3001 ACGAATCTGSACTCAATTAACCAATTAAGCACTTTTCAAAACCAATTAAGCACTTAATC 3060  
QY 3061 CACCACTTTTCCATCAAGTCAATTTGTTAAATCTAAATGTAAGAAATCTGCTAGAGG 3120  
DB 3061 CACCACTTTTCCATCAAGTCAATTTGTTAAATCTAAATGTAAGAAATCTGCTAGAGG 3120  
QY 3121 AAAAATTGAGAGCAATTCATGATGACCTGAAAGAAATGAGAAATGAGAAATGAGAAATGAGAA 3180  
DB 3121 AAAAATTGAGAGCAATTCATGATGACCTGAAAGAAATGAGAAATGAGAAATGAGAAATGAGAA 3180  
QY 3181 GTACAGTAGACCAATTAAGCCGTATTAACATTTAGAGAAAAATGTTTTTAAAGAGCCAGCT 3240

|    |      |   |      |
|----|------|---|------|
| Db | 3181 | GTACAGTAGCAATTAAGCCGTAAATACATTAGAGAAAATGTTTTTAAAGAGCACCT      | 3240 |
| Qy | 3241 | CAAGCAATATTATAGTAAGTAGGTTCCAGTACTAATGAAGTGCGCTCCAGTATTAATGAA  | 3300 |
| Db | 3241 | CAAGCAATATTATAGTAGAGTTCCAGTACTAATGAAGTGCGCTCCAGTATTAATGAA     | 3300 |
| Qy | 3301 | TAGGTTCCAGTATGATGAAAATTCAAGCAGAACTTAGTAAGAACAGAGGCCAAATTTGA   | 3360 |
| Db | 3301 | TAGGTTCCAGTATGATGAAAATTCAAGCAGAACTTAGTAAGAACAGAGGCCAAATTTGA   | 3360 |
| Qy | 3361 | ATGCTATGCTTATAGTAGGCGGTTTTGCAACCTGAGGTCTATTAACAAAGTCTTCTGSA   | 3420 |
| Db | 3361 | ATGCTATGCTTATAGTAGGCGGTTTTGCAACCTGAGGTCTATTAACAAAGTCTTCTGSA   | 3420 |
| Qy | 3421 | GTAATTGTAGACATCTCGAAATTAAGAAAGCAAGAAATATGAAGTAGTTCAGACTGTA    | 3480 |
| Db | 3421 | GTAATTGTAGACATCTCGAAATTAAGAAAGCAAGAAATATGAAGTAGTTCAGACTGTA    | 3480 |
| Qy | 3481 | ATACGATTTCTCTCCATATCTGATTTTCAAGAACTTGAACAGCTTAGGAAAGTATC      | 3540 |
| Db | 3481 | ATACGATTTCTCTCCATATCTGATTTTCAAGAACTTGAACAGCTTAGGAAAGTATC      | 3540 |
| Qy | 3541 | ATGCACTCAGGTTTGCTCTGAGACCTGATGACCTGTAGATAGTGTAATTAAGG         | 3600 |
| Db | 3541 | ATGCACTCAGGTTTGCTCTGAGACCTGATGACCTGTAGATAGTGTAATTAAGG         | 3600 |
| Qy | 3601 | AAGATATCTAGTTTTGCTGAAAATGACATTAAAGAAAGTTCTGCTGTTTTAGCAAAAGC   | 3660 |
| Db | 3601 | AAGATATCTAGTTTTGCTGAAAATGACATTAAAGAAAGTTCTGCTGTTTTAGCAAAAGC   | 3660 |
| Qy | 3661 | TCCAGAGAGAGAGCTTAGACAGAGATCCAGGCTTTACACCATACATTGGCTCAGG       | 3720 |
| Db | 3661 | TCCAGAGAGAGAGCTTAGACAGAGATCCAGGCTTTACACCATACATTGGCTCAGG       | 3720 |
| Qy | 3721 | GTTACCGAAGAGGGGCGAAAGAAATTAGAGTCTCTCAAGAGAACTTATCTAGAGATG     | 3780 |
| Db | 3721 | GTTACCGAAGAGGGGCGAAAGAAATTAGAGTCTCTCAAGAGAACTTATCTAGAGATG     | 3780 |
| Qy | 3781 | AAGAGCTTCCCTGCTTCCAAACCTTGTTATTTGTAAGTAAGAACTATPACCTTCTCAGT   | 3840 |
| Db | 3781 | AAGAGCTTCCCTGCTTCCAAACCTTGTTATTTGTAAGTAAGAACTATPACCTTCTCAGT   | 3840 |
| Qy | 3841 | CTACTAGGATAGCAACCGTTGCTACCGAGTGTCTGTCAAGAACACAGAGAGAAATTAAT   | 3900 |
| Db | 3841 | CTACTAGGATAGCAACCGTTGCTACCGAGTGTCTGTCAAGAACACAGAGAGAAATTAAT   | 3900 |
| Qy | 3901 | TATCATTTGAAGATAGCTTAATATGACTCGAGTAACCAAGATATATGGCAAAAGCATTC   | 3960 |
| Db | 3901 | TATCATTTGAAGATAGCTTAATATGACTCGAGTAACCAAGATATATGGCAAAAGCATTC   | 3960 |
| Qy | 3961 | AGGAACATCACCTTAGTAGAGAAACAAATGTTCTGTAAGTGTGTTCTTCAACAGTCA     | 4020 |
| Db | 3961 | AGGAACATCACCTTAGTAGAGAAACAAATGTTCTGTAAGTGTGTTCTTCAACAGTCA     | 4020 |
| Qy | 4021 | GTGAATTGGAGACTTGAATGCAAAATATCAAAACACCAGAGATCCTTTCTTGATTGGTCTT | 4080 |
| Db | 4021 | GTGAATTGGAGACTTGAATGCAAAATATCAAAACACCAGAGATCCTTTCTTGATTGGTCTT | 4080 |
| Qy | 4081 | CCAAACCAATGAGGATCAGTCTGAAAGCAGAGAGTTGCTGTGATACAGAGAAATGG      | 4140 |
| Db | 4081 | CCAAACCAATGAGGATCAGTCTGAAAGCAGAGAGTTGCTGTGATACAGAGAAATGG      | 4140 |
| Qy | 4141 | TTTCAGATGATGAAGAAAGAGAACCGGCTTGGAAAGAAATATCAAGAGCAAAACA       | 4200 |
| Db | 4141 | TTTCAGATGATGAAGAAAGAGAACCGGCTTGGAAAGAAATATCAAGAGCAAAACA       | 4200 |
| Qy | 4201 | TGGATTCAAACTTAGTGAAGAGCATCTGGGTGTGAAGTAACAAGCGTCTCTAGAG       | 4260 |
| Db | 4201 | TGGATTCAAACTTAGTGAAGAGCATCTGGGTGTGAAGTAACAAGCGTCTCTAGAG       | 4260 |
| Qy | 4261 | ACTGCTCAGGCGTATCTCTCAGAGTGAATTATTAACACTCAGCAGAGGATACATGC      | 4320 |

|    |      |  |      |
|----|------|--|------|
| Db | 4261 | ACTGCTCAGGGCTACTCTCTAGAGTGACATTTTAAACCACTCAGACAGGATACCATGC       | 4320 |
| Qy | 4321 | AACATTAACCTGATAAAGCTCCAGCAGGAAATGGCTGAACTAGAAGCTGTGTTAGACAGC     | 4380 |
| Db | 4321 | AACATTAACCTGATAAAGCTCCAGCAGGAAATGGCTGAACTAGAAGCTGTGTTAGACAGC     | 4380 |
| Qy | 4381 | ATGGAGGACACCTTCTAAGCAGTAACTTCATCATTAAGGACTCCTCGCCCTBAGG          | 4440 |
| Db | 4381 | ATGGAGGACACCTTCTAAGCAGTAACTTCATCATTAAGGACTCCTCGCCCTBAGG          | 4440 |
| Qy | 4441 | ACCTGCGAAATCCAGAACAAAGCACAATCAGAAAAAGAGTATTAACTTCCACAGAAAAATA    | 4500 |
| Db | 4441 | ACCTGCGAAATCCAGAACAAAGCACAATCAGAAAAAGAGTATTAACTTCCACAGAAAAATA    | 4500 |
| Qy | 4501 | GTGAATATCCCTATATAAGCCAGAAATCCAGAGGCCCTTTCTGTGACAAAGTTTGAGGTGTCTG | 4560 |
| Db | 4501 | GTGAATATCCCTATATAAGCCAGAAATCCAGAGGCCCTTTCTGTGACAAAGTTTGAGGTGTCTG | 4560 |
| Qy | 4561 | CAGATAGTCTTACACAGTAAATAATAAAGAACAGAGTGAAGAAAGGTCAATCCCTCTTAAT    | 4620 |
| Db | 4561 | CAGATAGTCTTACACAGTAAATAATAAAGAACAGAGTGAAGAAAGGTCAATCCCTCTTAAT    | 4620 |
| Qy | 4621 | GCCCATCATTAAGATATAGTGTGTAATGCAAGTTGCTCTGGAGTCTTCAGATAAGAA        | 4680 |
| Db | 4621 | GCCCATCATTAAGATATAGTGTGTAATGCAAGTTGCTCTGGAGTCTTCAGATAAGAA        | 4680 |
| Qy | 4681 | ACTACCCATCTCAAGAGAGGCTCAATTAAGTTGTGAATGTGGAGAGACCAAGCTGGAG       | 4740 |
| Db | 4681 | ACTACCCATCTCAAGAGAGGCTCAATTAAGTTGTGAATGTGGAGAGACCAAGCTGGAG       | 4740 |
| Qy | 4741 | AGCTGGGCGCACAGGATTTGAACGGAAACATCTTACTTCCAAAGGCAAGATCTAGAGGAA     | 4800 |
| Db | 4741 | AGCTGGGCGCACAGGATTTGAACGGAAACATCTTACTTCCAAAGGCAAGATCTAGAGGAA     | 4800 |
| Qy | 4801 | CCCCCTTACCTGGAATCTGGAATCAGCCTCTTCTGTGATGACCTCGAATCTGAATCCTTCTG   | 4860 |
| Db | 4801 | CCCCCTTACCTGGAATCTGGAATCAGCCTCTTCTGTGATGACCTCGAATCTGAATCCTTCTG   | 4860 |
| Qy | 4861 | AAGACAGAGCCCCCAGAGTCAAGCTGTGTGGCAACATAACATCTTCAACCTCTGCAATGA     | 4920 |
| Db | 4861 | AAGACAGAGCCCCCAGAGTCAAGCTGTGTGGCAACATAACATCTTCAACCTCTGCAATGA     | 4920 |
| Qy | 4921 | AAAGTCCCAATTGAAGTTGCAGAAATCTGCCAGGGTCCAGCTGCTCATCTACTG           | 4980 |
| Db | 4921 | AAAGTCCCAATTGAAGTTGCAGAAATCTGCCAGGGTCCAGCTGCTCATCTACTG           | 4980 |
| Qy | 4981 | ATATCGCTGGGATATAAGTGAATGGAAGAAATGTGACAGAGGAAAGCCAGAAATTTGACAG    | 5040 |
| Db | 4981 | ATATCGCTGGGATATAAGTGAATGGAAGAAATGTGACAGAGGAAAGCCAGAAATTTGACAG    | 5040 |
| Qy | 5041 | CTTCAACAGAAAGGTCACAAAGAAATGTCCATGTGTGTCTGAGCTGACCCACAGAG         | 5100 |
| Db | 5041 | CTTCAACAGAAAGGTCACAAAGAAATGTCCATGTGTGTCTGAGCTGACCCACAGAG         | 5100 |
| Qy | 5101 | AATTTATGCTGTGTACAAAGTTTCCGAGAAAACCAATCATTAACTTAATTAATTA          | 5160 |
| Db | 5101 | AATTTATGCTGTGTACAAAGTTTCCGAGAAAACCAATCATTAACTTAATTAATTA          | 5160 |
| Qy | 5161 | CTGAAGAGACTACTCATGTTGTATGAAAACAGATGCTGAGTTGTGTGTAACGAGCAC        | 5220 |
| Db | 5161 | CTGAAGAGACTACTCATGTTGTATGAAAACAGATGCTGAGTTGTGTGTAACGAGCAC        | 5220 |
| Qy | 5221 | TGAAATATTTTCTAGGAATTCGGGAGGAAATGGATGTAGCTATTTCTGGGTGACCC         | 5280 |
| Db | 5221 | TGAAATATTTTCTAGGAATTCGGGAGGAAATGGATGTAGCTATTTCTGGGTGACCC         | 5280 |
| Qy | 5281 | AGCTATTTAAAGAAAGAAAAATGCTGATGATGACATGATTTTGAAGTCAAGAGGAGATGTGG   | 5340 |
| Db | 5281 | AGCTATTTAAAGAAAGAAAAATGCTGATGATGACATGATTTTGAAGTCAAGAGGAGATGTGG   | 5340 |
| Qy | 5341 | TCAATGGAAGAACACCCAGGTCCAAAGCAGACAGAGATCCACAGACAGAAAGATCT         | 5400 |
| Db | 5341 | TCAATGGAAGAACACCCAGGTCCAAAGCAGACAGAGATCCACAGACAGAAAGATCT         | 5400 |



QY 841 CCAGTAATTAATGATTTGAACCACTGAGAGCCGTCAGTGAAGGATCCAGAAAAGT 900  
DB 841 CCAGTAATTAATGATTTGAACCACTGAGAGCCGTCAGTGAAGGATCCAGAAAAGT 900  
QY 901 ATCAGGGTAGTCTGTTTCAAACTTGATGAGACCCTATGCGCAAAATACTCATGCGCA 960  
DB 901 ATCAGGGTAGTCTGTTTCAAACTTGATGAGACCCTATGCGCAAAATACTCATGCGCA 960  
QY 961 GCTCATTAACAGCATGAGAACAGCATGTTTATTACTCACTAAGACAGAAATGATGAGAAA 1020  
DB 961 GCTCATTAACAGCATGAGAACAGCATGTTTATTACTCACTAAGACAGAAATGATGAGAAA 1020  
QY 1021 AGGCTGATTTCTGTAATTAAGCAAAACAGCCGTCGTTGCAAGAGGCCCAATACAGAT 1080  
DB 1021 AGGCTGATTTCTGTAATTAAGCAAAACAGCCGTCGTTGCAAGAGGCCCAATACAGAT 1080  
QY 1081 GGGCTGGAAGTGAAGAAACATGTAATGATAGCGGAGCTCCAGCACAGAAAAAGGTAG 1140  
DB 1081 GGGCTGGAAGTGAAGAAACATGTAATGATAGCGGAGCTCCAGCACAGAAAAAGGTAG 1140  
QY 1141 ATCTGAATGCTGATCCCTGCTGTGAGAGAAAAAGAAATGGAATAGCAGAAATCTGCTGCT 1200  
DB 1141 ATCTGAATGCTGATCCCTGCTGTGAGAGAAAAAGAAATGGAATAGCAGAAATCTGCTGCT 1200  
QY 1201 CAGAGAACTCTAGAGATCTGAGATGTTCTTGATTAACAATAATAGCAGATTTCAAGA 1260  
DB 1201 CAGAGAACTCTAGAGATCTGAGATGTTCTTGATTAACAATAATAGCAGATTTCAAGA 1260  
QY 1261 AAGTTAAATGAGTGGTTTTCCAGAAAGTGAATCTGTAGTTCTGATGATCAATGATG 1320  
DB 1261 AAGTTAAATGAGTGGTTTTCCAGAAAGTGAATCTGTAGTTCTGATGATCAATGATG 1320  
QY 1321 GGGAGTCTGAATCAAAATGCCAAAGTGAATGTAATGGAAGTCTTAAATGAGGTAGATG 1380  
DB 1321 GGGAGTCTGAATCAAAATGCCAAAGTGAATGTAATGGAAGTCTTAAATGAGGTAGATG 1380  
QY 1381 AATATTCCTGTTCTTCAAGAGAAATAGACTTACTGCGCAGTATCCTCATGAGGCTTTAA 1440  
DB 1381 AATATTCCTGTTCTTCAAGAGAAATAGACTTACTGCGCAGTATCCTCATGAGGCTTTAA 1440  
QY 1441 TATGTAAGAGTGAAGAGTCTCACTCAATCAGTAGAGTAAATGGAAGCAAAATAT 1500  
DB 1441 TATGTAAGAGTGAAGAGTCTCACTCAATCAGTAGAGTAAATGGAAGCAAAATAT 1500  
QY 1501 TTGGGAAAACCTATCGGAAGAGCAAGCCCTCCCAATTAAGCATGTAACCTGAAAATC 1560  
DB 1501 TTGGGAAAACCTATCGGAAGAGCAAGCCCTCCCAATTAAGCATGTAACCTGAAAATC 1560  
QY 1561 TAATTTATAGAGCATTTTGTACTGAGCAGATATATCAAGAGGCTCCCTCACAATA 1620  
DB 1561 TAATTTATAGAGCATTTTGTACTGAGCAGATATATCAAGAGGCTCCCTCACAATA 1620  
QY 1621 AATTAAGAGTGAAGAGACCTACATCAGGCTTTCATCTGAGATTTTATCAAGAAAG 1680  
DB 1621 AATTAAGAGTGAAGAGACCTACATCAGGCTTTCATCTGAGATTTTATCAAGAAAG 1680  
QY 1681 CAGTTTGGCAGTTCAAAAGACTCCTGAAATGATTAATCAGGAACTAAACCAAGGAGC 1740  
DB 1681 CAGTTTGGCAGTTCAAAAGACTCCTGAAATGATTAATCAGGAACTAAACCAAGGAGC 1740  
QY 1741 AGAATGCTCAAGTGAATATTAATAATAGTGCATGAGAAATTAACCAAAAGGTGAT 1800  
DB 1741 AGAATGCTCAAGTGAATATTAATAATAGTGCATGAGAAATTAACCAAAAGGTGAT 1800  
QY 1801 CTATTCAGAAATGAGAAAAATCTTAACCAATAGATCACTGAAAAAGAAATCTGCTTCA 1860  
DB 1801 CTATTCAGAAATGAGAAAAATCTTAACCAATAGATCACTGAAAAAGAAATCTGCTTCA 1860  
QY 1861 AAAGGAAAGCTGAACCTATAGCAGCAGATTAAGCAATATGGAATCTCGAATTAATATCC 1920  
DB 1861 AAAGGAAAGCTGAACCTATAGCAGCAGATTAAGCAATATGGAATCTCGAATTAATATCC 1920

QY 1921 ACAATTCAAAAGCACCCTAAAAGAAATAGGCTGAGAGGAAGTCTTACCAAGCATATTC 1980  
DB 1921 ACAATTCAAAAGCACCCTAAAAGAAATAGGCTGAGAGGAAGTCTTACCAAGCATATTC 1980  
QY 1981 ATGGGCTTGAACCTAGTATGATGAGAAATCTTAAGCCCACTTAATTTGATGAAATTCGAA 2040  
DB 1981 ATGGGCTTGAACCTAGTATGATGAGAAATCTTAAGCCCACTTAATTTGATGAAATTCGAA 2040  
QY 2041 TTGATAGTGTCTTACGAGTGAAGAGATTAAGAAAAAAGTCAACCAATATGCGAGTCA 2100  
DB 2041 TTGATAGTGTCTTACGAGTGAAGAGATTAAGAAAAAAGTCAACCAATATGCGAGTCA 2100  
QY 2101 GGCACAGCAGAAACCTCAACTCATGGAAGTAAAGAACTGCAACTGAGCCAGAGAAGA 2160  
DB 2101 GGCACAGCAGAAACCTCAACTCATGGAAGTAAAGAACTGCAACTGAGCCAGAGAAGA 2160  
QY 2161 GTAAACAGCCCAATGAACAGCAAGTAAAGACATGACAGTATCTTTCCAGAGTGA 2220  
DB 2161 GTAAACAGCCCAATGAACAGCAAGTAAAGACATGACAGTATCTTTCCAGAGTGA 2220  
QY 2221 AGTTAACAAATGACCTGGTCTTTTCTTAAGTGTCAAAATPACAGTGAATTAAGAT 2280  
DB 2221 AGTTAACAAATGACCTGGTCTTTTCTTAAGTGTCAAAATPACAGTGAATTAAGAT 2280  
QY 2281 TTGTCAATCTAGGCTTCCAAAGAGAAAAAGAGAAACTAGAAACAGTTAAAGTGT 2340  
DB 2281 TTGTCAATCTAGGCTTCCAAAGAGAAAAAGAGAAACTAGAAACAGTTAAAGTGT 2340  
QY 2341 CTAAATATGCTGANAACCCCAAGATCTCATGTTAAGTGAAGAAAGGTTTGCAAACTG 2400  
DB 2341 CTAAATATGCTGANAACCCCAAGATCTCATGTTAAGTGAAGAAAGGTTTGCAAACTG 2400  
QY 2401 AAAGATCTGTAGAGTAGAGTATTTCACTGGTACCTGGATCGATTTATGGCAGTCAAG 2460  
DB 2401 AAAGATCTGTAGAGTAGAGTATTTCACTGGTACCTGGATCGATTTATGGCAGTCAAG 2460  
QY 2461 AAAGATCTGTAGAGTAGAGTATTTCACTGGTACCTGGATCGATTTATGGCAGTCAAG 2520  
DB 2461 AAAGATCTGTAGAGTAGAGTATTTCACTGGTACCTGGATCGATTTATGGCAGTCAAG 2520  
QY 2521 GTGTGAGTCAAGTGCAGCATTTGAAAAACCCCAAGGACATTAATCAAGGTTTCCAAAG 2580  
DB 2521 GTGTGAGTCAAGTGCAGCATTTGAAAAACCCCAAGGACATTAATCAAGGTTTCCAAAG 2580  
QY 2581 AATATAGAAATGACACAGAAAGCTTTAAGTATCATGTTGGGACATGAAATTAACACAGTC 2640  
DB 2581 AATATAGAAATGACACAGAAAGCTTTAAGTATCATGTTGGGACATGAAATTAACACAGTC 2640  
QY 2641 GGGAAACAGCATAGAAATGGAAGAAAGTGAACCTTGAAGTCAATTTGCAAGATATCAT 2700  
DB 2641 GGGAAACAGCATAGAAATGGAAGAAAGTGAACCTTGAAGTCAATTTGCAAGATATCAT 2700  
QY 2701 TCAAGGTTTCAAGCGCAGTCAATTTGCTGCTGTTTCAAAATCCAGGAAATGCGAAGAG 2760  
DB 2701 TCAAGGTTTCAAGCGCAGTCAATTTGCTGCTGTTTCAAAATCCAGGAAATGCGAAGAG 2760  
QY 2761 AATGNGCAACATCTCTGCGCCACCTGAGGTCTTTAAGAAACAAAGTCCAAAGTCACT 2820  
DB 2761 AATGNGCAACATCTCTGCGCCACCTGAGGTCTTTAAGAAACAAAGTCCAAAGTCACT 2820  
QY 2821 TTGAATGTGAACAAAAGAGAAAAATCAAGAAAAAGATGAATATATCAAGCTGTAC 2880  
DB 2821 TTGAATGTGAACAAAAGAGAAAAATCAAGAAAAAGATGAATATATCAAGCTGTAC 2880  
QY 2881 AGACAGTTAATATCACTGACAGGCTTCTGCTGTTGTCGAAAGATTAACCAAGTGTATA 2940  
DB 2881 AGACAGTTAATATCACTGACAGGCTTCTGCTGTTGTCGAAAGATTAACCAAGTGTATA 2940  
QY 2941 ATGCGCAATGTAGATCAAGAGAGGCTTGAAGTTTGTCTATCATCTCAAGTCAAGAGCA 3000  
DB 2941 ATGCGCAATGTAGATCAAGAGAGGCTTGAAGTTTGTCTATCATCTCAAGTCAAGAGCA 3000  
QY 3001 AGGAACTGACATCTACTTCAAAATTAACATGGAATTTTACAAAACCATATCTGATAC 3060

Db 3001 AGAACTGACCTACCTTACCCAAATTAACATGACTTTTACAAAACCATATCGTATAC 3060  
Qy 3061 CACCACTTTTCCCACTCAAGTCTTTGTTAAACTTAATGAAGAAAATCTGCTAGAG 3120  
Db 3061 CACCACTTTTCCCACTCAAGTCTTTGTTAAACTTAATGAAGAAAATCTGCTAGAG 3120  
Qy 3121 AAAACTTGAAGAACTTCAATGTCACTGAAGAGAAATGGAAATGAGAACTTCCAA 3180  
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Qy 3181 GTACAGTGAAGCAATTAAGCCGTAATTAACATTAAGAAAAATGTTTAAAGAGCCAGCT 3240  
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Qy 3241 CAAGCAATTTATTAAGTAAGTTCAGATCTAATGAAGTGGGCTCCAGTATTAATGA 3300  
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Qy 3301 TAGGTTCCAGTGAAGAACTTCAAGCAAGAACTAGTAGAAAAGAGGGCCAAATTTGA 3360  
Db 3301 TAGGTTCCAGTGAAGAACTTCAAGCAAGAACTAGTAGAAAAGAGGGCCAAATTTGA 3360  
Qy 3361 ATGCTATGCTTAGATTAGGGGTTTTCGAACTGAGGCTATTAACAAAGCTTCTCGAA 3420  
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Qy 3421 GTAAATGTAGACATCTCTGAATTAATAAAGCAAGAAATGAAGAGTTCAGCTGTA 3480  
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Qy 3481 ATACAGATTTCTCTCCATATCTGATTTCAATTAAGCAAGCCCTAATGGGAAGTAC 3540  
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Qy 3541 ATGCATCTCAGGTTTGTCTGAGACACTGATGACCTGTTAGATGATGTAATTAAG 3600  
Db 3541 ATGCATCTCAGGTTTGTCTGAGACACTGATGACCTGTTAGATGATGTAATTAAG 3600  
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Db 3601 AAGATCTAGTTTGTGTAATAATGAATTAAGAAAGTCTGCTTTTACCAAAAGG 3660  
Qy 3661 TCCAGAGAGAGGCTTAGCAGAGTCTAGCCCTTCAACCATACATTTGGCTCAG 3720  
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Qy 3721 GTTACCGAAGAGGGCCAAAGAAATTAAGTCTCAGAGAGAACTTATCTAGTAGAG 3780  
Db 3721 GTTACCGAAGAGGGCCAAAGAAATTAAGTCTCAGAGAGAACTTATCTAGTAGAG 3780  
Qy 3781 AAGAGTCCCTGCTTCCAACTGTTATTTGGTAAGTAAACAATATCTCTCAGT 3840  
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Qy 3841 CTACTAGGATAGACCGTGTGCTACCGAGTGTCTGTAGAACAACAGAGAGAAATTA 3900  
Db 3841 CTACTAGGATAGACCGTGTGCTACCGAGTGTCTGTAGAACAACAGAGAGAAATTA 3900  
Qy 3841 CTACTAGGATAGACCGTGTGCTACCGAGTGTCTGTAGAACAACAGAGAGAAATTA 3900  
Db 3841 CTACTAGGATAGACCGTGTGCTACCGAGTGTCTGTAGAACAACAGAGAGAAATTA 3900  
Qy 3901 TATCATTTGAAGAAATAGCTTAATGAATGATGAGTAAATTTGGCAAGGATCTC 3960  
Db 3901 TATCATTTGAAGAAATAGCTTAATGAATGATGAGTAAATTTGGCAAGGATCTC 3960  
Qy 3961 AAGAAATACCTTATGAGGAAACAAATTTGCTAGCTTTTCTTCAAGTGA 4020  
Db 3961 AAGAAATACCTTATGAGGAAACAAATTTGCTAGCTTTTCTTCAAGTGA 4020  
Qy 4021 GTAAATTTGAAGAACTTGAAGTGAAGAAACACCCAGAGTCTTTCTGATTTGTTCT 4080  
Db 4021 GTAAATTTGAAGAACTTGAAGTGAAGAAACACCCAGAGTCTTTCTGATTTGTTCT 4080  
Qy 4081 CCAAACTAATGAGCATCAGTCTGAAGCCAGGAGTGTCTGAGTGAAGGAATTTG 4140

Db 4081 CCAAACTAATGAGCATCAGTCTGAAGCCAGGAGTGTCTGAGTGAAGGAATTTG 4140  
Qy 4141 TTTGATGATGAAGAAAGAGAAAGGCTTGAAGAAATTAATGAAGAGCAAGGA 4200  
Db 4141 TTTGATGATGAAGAAAGAGAAAGGCTTGAAGAAATTAATGAAGAGCAAGGA 4200  
Qy 4201 TGAATTTCAAACTTAGTGAAGAGCATCTGGGTGAGAGTGAAGAAAGGCTCTGAG 4260  
Db 4201 TGAATTTCAAACTTAGTGAAGAGCATCTGGGTGAGAGTGAAGAAAGGCTCTGAG 4260  
Qy 4261 ACTGCTCAGGCTATCTCTCAGAGTGAATTTAACAATCAGAGAGGATACCATC 4320  
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Qy 4321 AACATTAACCTGATTAAGCTCCAGAGGAAATGGCTGAAGTGAAGCTGTTAGAACGC 4380  
Db 4321 AACATTAACCTGATTAAGCTCCAGAGGAAATGGCTGAAGTGAAGCTGTTAGAACGC 4380  
Qy 4381 ATGGAGCCAGCTTCTAAGCTAACCCTTCATATAGTGAATCTCTGCTTGAAG 4440  
Db 4381 ATGGAGCCAGCTTCTAAGCTAACCCTTCATATAGTGAATCTCTGCTTGAAG 4440  
Qy 4441 ACTCGAAATTCAGAGCAAGACATGAGAAAGCAAGTAACTTCAAGAAAGTA 4500  
Db 4441 ACTCGAAATTCAGAGCAAGACATGAGAAAGCAAGTAACTTCAAGAAAGTA 4500  
Qy 4501 GTAAATACCTTAAGCCAGAAATCCAGAGGCTTCTGCTGAGCAAGTTGAGTGTCTG 4560  
Db 4501 GTAAATACCTTAAGCCAGAAATCCAGAGGCTTCTGCTGAGCAAGTTGAGTGTCTG 4560  
Qy 4561 CAGATAGTTCTACAGTAAATAAAGAACAGAGTGAAGAAAGTATCCCTTGAAT 4620  
Db 4561 CAGATAGTTCTACAGTAAATAAAGAACAGAGTGAAGAAAGTATCCCTTGAAT 4620  
Qy 4621 GCCATCATTAAGATAGTGTGATGATGATGATGATGATGATGATGATGATGATG 4680  
Db 4621 GCCATCATTAAGATAGTGTGATGATGATGATGATGATGATGATGATGATGATG 4680  
Qy 4681 ACTACCATTCAGAGAGGCTTAAGGTTGATGATGATGATGATGATGATGATGATG 4740  
Db 4681 ACTACCATTCAGAGAGGCTTAAGGTTGATGATGATGATGATGATGATGATGATG 4740  
Qy 4741 AGTGGGCAACAGATTTGAGGAAATCATCTTAATTTGCAAGGAAATCTAGAGGA 4800  
Db 4741 AGTGGGCAACAGATTTGAGGAAATCATCTTAATTTGCAAGGAAATCTAGAGGA 4800  
Qy 4801 CCCCTTACCTGGAATCTGGAATCAGCTCTTCTGATGACCTGGAATCTGATCTTG 4860  
Db 4801 CCCCTTACCTGGAATCTGGAATCAGCTCTTCTGATGACCTGGAATCTGATCTTG 4860  
Qy 4861 AAGAGAGCCCAAGTCAAGTCTGTTGGCAATACATCTTCAACCTCTGATGA 4920  
Db 4861 AAGAGAGCCCAAGTCAAGTCTGTTGGCAATACATCTTCAACCTCTGATGA 4920  
Qy 4921 AAGTCCCAATTTGAAGTTCAGAACTGACCAGAGGCTCAGCTCTCTACTACTG 4980  
Db 4921 AAGTCCCAATTTGAAGTTCAGAACTGACCAGAGGCTCAGCTCTCTACTACTG 4980  
Qy 4981 ATACTGCTGATTAATGCAATGAAGAAAGTGTGAGAGGAGAGCAAGATTTGACG 5040  
Db 4981 ATACTGCTGATTAATGCAATGAAGAAAGTGTGAGAGGAGAGCAAGATTTGACG 5040  
Qy 5041 CTTCAACAGAAAGGCTCAACAAAGAAATGCTCAGTGTGTCTGCTGACCCAGAG 5100  
Db 5041 CTTCAACAGAAAGGCTCAACAAAGAAATGCTCAGTGTGTCTGCTGACCCAGAG 5100  
Qy 5101 AATTATGCTGCTGATCAAGTTCAGAGAAACACATCATCTTAATCTAATTA 5160  
Db 5101 AATTATGCTGCTGATCAAGTTCAGAGAAACACATCATCTTAATCTAATTA 5160  
Qy 5161 CTGAAGAGATCTCATCTGTTGTAAGAAACAGATGCTGAGTGTGTGTAAGGAGC 5220  
Db 5161 CTGAAGAGATCTCATCTGTTGTAAGAAACAGATGCTGAGTGTGTGTAAGGAGC 5220

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OY 5221 TGAATATATTTCTAGGAATGGGAGGAGAAATGGGTAGTATTTCTGGTGACCC 5280
DB 5221 TGAATATATTTCTAGGAATGGGAGGAGAAATGGGTAGTATTTCTGGTGACCC 5280
OY 5281 AGTCTATTAAAGAAAGAAAATGCTGAATGAGCATGATTTTGAAGTCAGAGAGATGTGG 5340
DB 5281 AGTCTATTAAAGAAAGAAAATGCTGAATGAGCATGATTTTGAAGTCAGAGAGATGTGG 5340
OY 5341 TCAATGGAAGAAACCAACCAAGGTCCAAAGCCGAGCAAGAAATCCCAAGACAGAAAAGATCT 5400
DB 5341 TCAATGGAAGAAACCAACCAAGGTCCAAAGCCGAGCAAGAAATCCCAAGACAGAAAAGATCT 5400
OY 5401 TCAGGGGGCTAGAAATCTGTTGCTATGAGGCCCTTACCAACATGCCCAGATCAACTGG 5460
DB 5401 TCAGGGGGCTAGAAATCTGTTGCTATGAGGCCCTTACCAACATGCCCAGATCAACTGG 5460
OY 5461 AATGATGATGACAGCTGTGTGTGTCTGTGTGTGAAGAGCTTTCATCATTTACCCCTTG 5520
DB 5461 AATGATGATGACAGCTGTGTGTGTCTGTGTGTGAAGAGCTTTCATCATTTACCCCTTG 5520
OY 5521 GCAGAGGTGTCACCCCAATTTGTTGTTGACGCCAGATGCTTGAACAGAGCAATGGCT 5580
DB 5521 GCAGAGGTGTCACCCCAATTTGTTGTTGACGCCAGATGCTTGAACAGAGCAATGGCT 5580
OY 5581 TCCATGCAATTTGGGAGAGATGTGTGAGGACCTGTGTGTGACCCGAGATGGGTGTGGACA 5640
DB 5581 TCCATGCAATTTGGGAGAGATGTGTGAGGACCTGTGTGTGACCCGAGATGGGTGTGGACA 5640
OY 5641 GTGTAGCACTGTACCAAGTGCAGAGAGCTGAGACACTTACCTGATACCCAGATCCCCACA 5700
DB 5641 GTGTAGCACTGTACCAAGTGCAGAGAGCTGAGACACTTACCTGATACCCAGATCCCCACA 5700
OY 5701 GCCACTACTGA 5711
DB 5701 GCCACTACTGA 5711

RESULT 5
AAV46470
ID AAV46470 standard; cDNA, 5711 BP.
XX
AC AAV46470;
XX
DT 18-NOV-1998 (first entry)
XX
DE Human BRCA1 omi3 polymorphism #6 cDNA.
XX
KM BRCA1; omi3; human; breast and ovarian cancer predisposing gene;
KM polymorphism; susceptibility; anti-oncogene; tumour suppressor;
KM chromosome 17q; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 120..5711
FT FT /*tag= a
FT FT /product= "BRCA1 omi3 protein"
FT FT 4427
FT FT /*tag= b
FT FT /note= "This polymorphic variation can be a T or C
nucleotide"
```

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XX Allen AC, Alvares CP, Critz BS, Murphy PD, Olson SJ;
PI Scheller DB, Zeng B;
XX WPI: 1998-296774/26.
DR
XX BRCA1 omi3 gene coding sequences - useful for distinguishing between
PT polymorphisms and mutation(s) in the screening for disposition to
PT breast or ovarian cancer
XX
PS Claim 2e, Page -: 54pp; English.
XX
CC This sequence encodes a human BRCA1 (breast and ovarian cancer
CC predisposing gene) omi3 gene in which a polymorphic variation occurs at
CC nucleotide 4427. This sequence and other polymorphic variations of this
CC sequence are useful for the identification of an individual who may or
CC may not have an increased susceptibility to breast or ovarian cancer.
CC The sequences used identify gene changes which are due to polymorphisms,
CC rather than cancer causing mutations. BRCA1 is an anti-oncogene (tumour
CC suppressor) which is involved in genetic inheritance of cancers,
CC especially breast and ovarian cancer. It is found at human chromosome
CC 17q which is known to be linked to cancer susceptibility, especially
CC breast cancer. Cells containing a mutation in this gene lose the
CC wild-type function of BRCA1 and are more susceptible to cancers.
CC NOTE: This sequence does not appear in the specification but has been
CC created from the wild type BRCA1 omi3 gene represented in AAV46450.
XX
SQ Sequence 5711 BP, 1953 A; 1098 C; 1277 G; 1382 T; 1 other;

Query Match 100.0%; Score 5710.6; DB:19; Length 5711;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5710; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 AGCTGCTGAGACTTCCTGAGACCCCGACCAAGGTGGGTTTCTAGATACTGGGCC 60
DB 1 AGCTGCTGAGACTTCCTGAGACCCCGACCAAGGTGGGTTTCTAGATACTGGGCC 60
OY 61 CCTGCGCTCAGAGAGGCTTCAACCTCTGCTGTGGGTAAAGTCAATGGAACAGAAAGAA 120
DB 61 CCTGCGCTCAGAGAGGCTTCAACCTCTGCTGTGGGTAAAGTCAATGGAACAGAAAGAA 120
OY 121 TGAATTTATCTGCTCTTCCGCTTGAAGAGTACAAAATGTCATTATGTCACAGAAA 180
DB 121 TGAATTTATCTGCTCTTCCGCTTGAAGAGTACAAAATGTCATTATGTCACAGAAA 180
OY 121 TGAATTTATCTGCTCTTCCGCTTGAAGAGTACAAAATGTCATTATGTCACAGAAA 180
DB 121 TGAATTTATCTGCTCTTCCGCTTGAAGAGTACAAAATGTCATTATGTCACAGAAA 180
OY 181 TCTTAGAGTGCCCATCTGTCTGAGTATCAAGAACTGCTCCACAAAGTGAGCC 240
DB 181 TCTTAGAGTGCCCATCTGTCTGAGTATCAAGAACTGCTCCACAAAGTGAGCC 240
OY 181 TCTTAGAGTGCCCATCTGTCTGAGTATCAAGAACTGCTCCACAAAGTGAGCC 240
DB 181 TCTTAGAGTGCCCATCTGTCTGAGTATCAAGAACTGCTCCACAAAGTGAGCC 240
OY 241 ACATATTTTGAATTTTGGATGCTGAACTTCTCAACGAGAAAGGCTTTCACAGT 300
DB 241 ACATATTTTGAATTTTGGATGCTGAACTTCTCAACGAGAAAGGCTTTCACAGT 300
OY 241 ACATATTTTGAATTTTGGATGCTGAACTTCTCAACGAGAAAGGCTTTCACAGT 300
DB 241 ACATATTTTGAATTTTGGATGCTGAACTTCTCAACGAGAAAGGCTTTCACAGT 300
OY 301 GTCCCTTATGATAGATGATATTAACAAAGAGAGCTTCAAGAAAGTACGATTTAGTC 360
DB 301 GTCCCTTATGATAGATGATATTAACAAAGAGAGCTTCAAGAAAGTACGATTTAGTC 360
OY 301 GTCCCTTATGATAGATGATATTAACAAAGAGAGCTTCAAGAAAGTACGATTTAGTC 360
DB 301 GTCCCTTATGATAGATGATATTAACAAAGAGAGCTTCAAGAAAGTACGATTTAGTC 360
OY 361 AACTGTGGAAGAGCTATGAAATCAATTTGTGCTTTTCACTTGAACAGGTTTGGAGT 420
DB 361 AACTGTGGAAGAGCTATGAAATCAATTTGTGCTTTTCACTTGAACAGGTTTGGAGT 420
OY 421 ATGCAAAACAGCTATATTTTGCAGAAAAGGAAATATCTCTCGAATCATTTAAAGATG 480
DB 421 ATGCAAAACAGCTATATTTTGCAGAAAAGGAAATATCTCTCGAATCATTTAAAGATG 480
OY 481 AAGTTTATATCATCAAGATATGAGGCTACAGAAACCGTGCAGAAAGACTTTCACAGAGT 540
DB 481 AAGTTTATATCATCAAGATATGAGGCTACAGAAACCGTGCAGAAAGACTTTCACAGAGT 540
OY 541 AACCAGAAATCCTCTCTGAGGAAACGAGTCCAGTCCAGTCACTCTTAACTTGGAA 600
DB 541 AACCAGAAATCCTCTCTGAGGAAACGAGTCCAGTCCAGTCACTCTTAACTTGGAA 600
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QY 601 CTGTGAAACTGTGAGACAAAGCAGATACACCTCTCAAAAACGCTGTCTACATTG 660  
Db 601 CTGTGAAACTGTGAGACAAAGCAGATACACCTCTCAAAAACGCTGTCTACATTG 660  
QY 661 AATTGGAGTCTGATTTCTTCTGAAAGATACCTTAATAAGCACTTATTTGACGTGGAG 720  
Db 661 AATTGGAGTCTGATTTCTTCTGAAAGATACCTTAATAAGCACTTATTTGACGTGGAG 720  
QY 721 ATCAAAATTTGTACAAATCAACCCCTCAAGAACCAAGGATGAATCAAGTTGATTCTG 780  
Db 721 ATCAAAATTTGTACAAATCAACCCCTCAAGAACCAAGGATGAATCAAGTTGATTCTG 780  
QY 781 CAAAAAAGGCTGCTTGTGAATTTTCTGAGCGAGTGAACAAATGATGAACATCAAC 840  
Db 781 CAAAAAAGGCTGCTTGTGAATTTTCTGAGCGAGTGAACAAATGATGAACATCAAC 840  
QY 841 CCAATATATATGATTTTGAACACCACTGAGAAAGCTGACGTGAGAGCATCCGAAAGT 900  
Db 841 CCAATATATATGATTTTGAACACCACTGAGAAAGCTGACGTGAGAGCATCCGAAAGT 900  
QY 901 ATCAGGATAGTTCTGTTTCAAACTTGATGTGAGCATGTGACAAATGATCTGACCA 960  
Db 901 ATCAGGATAGTTCTGTTTCAAACTTGATGTGAGCATGTGACAAATGATCTGACCA 960  
QY 961 GCTCATTAAGACATGAGAACAGCAGTTTATTACTCACTAAAGACAGATGATGAA 1020  
Db 961 GCTCATTAAGACATGAGAACAGCAGTTTATTACTCACTAAAGACAGATGATGAA 1020  
QY 1021 AGGCTGAATTTCTGATTAATAAAGCAACGCTGCTTACAGAGAGCCATACAGAT 1080  
Db 1021 AGGCTGAATTTCTGATTAATAAAGCAACGCTGCTTACAGAGAGCCATACAGAT 1080  
QY 1081 GGGCTGGAAGTGAAGAAACATGATATGATGAGCGACCTCCAGACAGAAAAAGGTAG 1140  
Db 1081 GGGCTGGAAGTGAAGAAACATGATATGATGAGCGACCTCCAGACAGAAAAAGGTAG 1140  
QY 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAGATGAAATGAAATGAGAACTGCCATGCT 1200  
Db 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAGATGAAATGAAATGAGAACTGCCATGCT 1200  
QY 1201 CAGAGAACTCTAGAGATCTGAAAGATGTTCTTGGATTAACCTAAATAGCAGATTCA 1260  
Db 1201 CAGAGAACTCTAGAGATCTGAAAGATGTTCTTGGATTAACCTAAATAGCAGATTCA 1260  
QY 1261 AAGTTATGAGTGTCTTTCAGAAAGTATGATGATTTGAGCTGATGATCTGACATGATG 1320  
Db 1261 AAGTTATGAGTGTCTTTCAGAAAGTATGATGATTTGAGCTGATGATCTGACATGATG 1320  
QY 1321 GGGAGTCTGAATCAAAATGCCAAAGTATGATGATTTGAGCGTTCTAAATGAGTATG 1380  
Db 1321 GGGAGTCTGAATCAAAATGCCAAAGTATGATGATTTGAGCGTTCTAAATGAGTATG 1380  
QY 1381 AATATTTCTGTTCTTCAAGAGAAATGACTTACTGCGCAGTATCTTCAATGAGGCTTTAA 1440  
Db 1381 AATATTTCTGTTCTTCAAGAGAAATGACTTACTGCGCAGTATCTTCAATGAGGCTTTAA 1440  
QY 1441 TATGTAAAGTGAAGATTTCACTGCAATCACTAGAGATATTTGAGCAAAATAT 1500  
Db 1441 TATGTAAAGTGAAGATTTCACTGCAATCACTAGAGATATTTGAGCAAAATAT 1500  
QY 1501 TTGGGAAAACTATCGGAAGAGCAAGCTCCCACTTAAGCCATGTAATGAAAAATC 1560  
Db 1501 TTGGGAAAACTATCGGAAGAGCAAGCTCCCACTTAAGCCATGTAATGAAAAATC 1560  
QY 1561 TAAATTTAGAGATTTTGTACTGAGCCACAGATATACAGAGGCTCCCTCACAATA 1620  
Db 1561 TAAATTTAGAGATTTTGTACTGAGCCACAGATATACAGAGGCTCCCTCACAATA 1620  
QY 1621 AATTAAGCGTAAAGAGACCTACATCAGGCTTATCTGAGATTTTATCAAGAAAG 1680  
Db 1621 AATTAAGCGTAAAGAGACCTACATCAGGCTTATCTGAGATTTTATCAAGAAAG 1680  
QY 1681 CAGATTGGCACTTCAAAAGACTCTGAAATGATTAATCAGGGAACCTAACCAACGAGC 1740

Db 1681 CAGATTGGCACTTCAAAAGACTCTGAAATATTAATCAGGGAACCTAACCAACGAGC 1740  
QY 1741 AGAATGCTCAATGATGAATATTAATTAATGAGTCAATGAATTAACAAAGTGAT 1800  
Db 1741 AGAATGCTCAATGATGAATATTAATTAATGAGTCAATGAATTAACAAAGTGAT 1800  
QY 1801 CTATTCAGATGAGAAAAATCTTAACCCAAATGAATCACTGCAAAAGATCTGCTTCA 1860  
Db 1801 CTATTCAGATGAGAAAAATCTTAACCCAAATGAATCACTGCAAAAGATCTGCTTCA 1860  
QY 1861 AAAAGAACTGAACCTATTAAGCAGATTAAGCAATGGAATGGAATTAATTAATTC 1920  
Db 1861 AAAAGAACTGAACCTATTAAGCAGATTAAGCAATGGAATGGAATTAATTAATTC 1920  
QY 1921 ACAATTCAAAACCTTAATAAAGATTAAGCTGAGAGAAAGTCTTACAGAGCATTC 1980  
Db 1921 ACAATTCAAAACCTTAATAAAGATTAAGCTGAGAGAAAGTCTTACAGAGCATTC 1980  
QY 1981 ATGCGCTGAATGATGATGATGATTAAGCCACCTAATTTGATCTGAATTCGAA 2040  
Db 1981 ATGCGCTGAATGATGATGATGATTAAGCCACCTAATTTGATCTGAATTCGAA 2040  
QY 2041 TTGATATGTTTCTAGCAGTGAAGATTAAGAAAAAAGTACCAACCAATGCCAGTCA 2100  
Db 2041 TTGATATGTTTCTAGCAGTGAAGATTAAGAAAAAAGTACCAACCAATGCCAGTCA 2100  
QY 2101 GGCACAGCAAAACCTTAACATCTAGGAAGTAAAGAACTTCACTGAGCCAGAA 2160  
Db 2101 GGCACAGCAAAACCTTAACATCTAGGAAGTAAAGAACTTCACTGAGCCAGAA 2160  
QY 2161 GTAACAGCAATGAACAGACAGTAAAGACATGACAGTATCTTTCCAGAGCTGA 2220  
Db 2161 GTAACAGCAATGAACAGACAGTAAAGACATGACAGTATCTTTCCAGAGCTGA 2220  
QY 2221 AGTTAACAAATGACCTGTTCTTTTACTAAGTGTTCAAATACAGTGAATTAAGAA 2280  
Db 2221 AGTTAACAAATGACCTGTTCTTTTACTAAGTGTTCAAATACAGTGAATTAAGAA 2280  
QY 2281 TTGTCAATCTGACCTTCCAAAGAGAAAGAAAGAAAGAACTTAAGAAAGTAT 2340  
Db 2281 TTGTCAATCTGACCTTCCAAAGAGAAAGAAAGAAAGAACTTAAGAAAGTAT 2340  
QY 2341 CTAATATGCTGAACCCCAAGATCTCATGTTAAGTGAAGAAAGGTTTGCACAC 2400  
Db 2341 CTAATATGCTGAACCCCAAGATCTCATGTTAAGTGAAGAAAGGTTTGCACAC 2400  
QY 2401 AAAAGTCTGTAGAGATGACAGATTTTCACTGATCCTGATCTGATTAAGCACTCAG 2460  
Db 2401 AAAAGTCTGTAGAGATGACAGATTTTCACTGATCCTGATCTGATTAAGCACTCAG 2460  
QY 2461 AAAAGTATCTGTTACTGGAAGTTAGCACTCTAGGAGCAAAACAGAACCAATTAAT 2520  
Db 2461 AAAAGTATCTGTTACTGGAAGTTAGCACTCTAGGAGCAAAACAGAACCAATTAAT 2520  
QY 2521 GTGTAGTCAAGTGTGACAGATTTGAAAACCCCAAGGACTAATTCATGTTTCCAAAG 2580  
Db 2521 GTGTAGTCAAGTGTGACAGATTTGAAAACCCCAAGGACTAATTCATGTTTCCAAAG 2580  
QY 2581 ATAAATGAAATGACACAGAAAGCTTTAAGTATCAATTGGACATGAAGTTAACACAGTC 2640  
Db 2581 ATAAATGAAATGACACAGAAAGCTTTAAGTATCAATTGGACATGAAGTTAACACAGTC 2640  
QY 2641 GGGAAACAAAGCTTAAGAAATGGAAGAAAGTGAATGCTCAATTTTGCAGAAATCAT 2700  
Db 2641 GGGAAACAAAGCTTAAGAAATGGAAGAAAGTGAATGCTCAATTTTGCAGAAATCAT 2700  
QY 2701 TCAAGTTTCAAAAGGCGCAGTATTTGCTGTTTCAATTCAGAGAAATGAGAAAGG 2760  
Db 2701 TCAAGTTTCAAAAGGCGCAGTATTTGCTGTTTCAATTCAGAGAAATGAGAAAGG 2760  
QY 2761 AATGTCAACATTTCTGCCCCACTGCTGCTTAAAGAAACAAAGTCCAAAGTCACTT 2820

|    |      |   |      |
|----|------|---|------|
| Db | 2761 | AATGTCGAACATTTCTCTGCCCACTCTGGGTCCTTTAAAGAAACAAGTCCAAAGTCACCTT   | 2820 |
| QY | 2821 | TTGAATGTGAACAAAGAGAAAGAAATCAAGAAAGAAATGAGTCTTAATATCATCAGCCTGTAC | 2880 |
| Db | 2821 | TTGAATGTGAACAAAGAGAAAGAAATCAAGAAAGAAATGAGTCTTAATATCATCAGCCTGTAC | 2880 |
| QY | 2881 | AGACGTTAATATCACTGCAGGCTTCTGTGGTTGGTCAGAAAGATTAAGCACTTGATA       | 2940 |
| Db | 2881 | AGACGTTAATATCACTGCAGGCTTCTGTGGTTGGTCAGAAAGATTAAGCACTTGATA       | 2940 |
| QY | 2941 | ATGCCAAATGTATGATCAAGAGAGGCTCTAGGTTTTGTCTATCATCTCAGTTCAGAGCA     | 3000 |
| Db | 2941 | ATGCCAAATGTATGATCAAGAGAGGCTCTAGGTTTTGTCTATCATCTCAGTTCAGAGCA     | 3000 |
| QY | 3001 | ACGAAACTGGACTCATTACTCCAAATPAACATGACTTTTACAAACCCATATGTATAC       | 3060 |
| Db | 3001 | ACGAAACTGGACTCATTACTCCAAATPAACATGACTTTTACAAACCCATATGTATAC       | 3060 |
| QY | 3061 | CACCACTTTTCCCATCAAGTCAATTTGTAAAACTAAATGTAAAAAATCTGTAAGG         | 3120 |
| Db | 3061 | CACCACTTTTCCCATCAAGTCAATTTGTAAAACTAAATGTAAAAAATCTGTAAGG         | 3120 |
| QY | 3121 | AAAACTTTGAGAGAACCTCAATCTCACCTGAAGAGAAATGGGAAATGAGAACATTCGAA     | 3180 |
| Db | 3121 | AAAACTTTGAGAGAACCTCAATCTCACCTGAAGAGAAATGGGAAATGAGAACATTCGAA     | 3180 |
| QY | 3181 | GTACAGTGAACCAATTAGCCGTAATPACTTGAAGAAAAATGTTTTTAAAGAGCCAGCT      | 3240 |
| Db | 3181 | GTACAGTGAACCAATTAGCCGTAATPACTTGAAGAAAAATGTTTTTAAAGAGCCAGCT      | 3240 |
| QY | 3241 | CAAGCAATTAATGAAGTAGGTCCAGTCTAATGAAGGGGCTCCAGATTAATGA            | 3300 |
| Db | 3241 | CAAGCAATTAATGAAGTAGGTCCAGTCTAATGAAGGGGCTCCAGATTAATGA            | 3300 |
| QY | 3301 | TAGGTTCCAGTATGAAAAATTCAAGACAGAACTAGTAGAAACAGAGGGCCAAATTTGA      | 3360 |
| Db | 3301 | TAGGTTCCAGTATGAAAAATTCAAGACAGAACTAGTAGAAACAGAGGGCCAAATTTGA      | 3360 |
| QY | 3361 | ATGCTATGCTTGAATTTAGGGGTTTTGCACCTGAGTCTTAAACAAAGTCTTCTGGA        | 3420 |
| Db | 3361 | ATGCTATGCTTGAATTTAGGGGTTTTGCACCTGAGTCTTAAACAAAGTCTTCTGGA        | 3420 |
| QY | 3421 | GTAATTTGATGATCCCTGAAATTAAGAAAGCAAAATTAAGAAAGTAGTTCAGCTGTA       | 3480 |
| Db | 3421 | GTAATTTGATGATCCCTGAAATTAAGAAAGCAAAATTAAGAAAGTAGTTCAGCTGTA       | 3480 |
| QY | 3481 | ATACAGATTTCTCTCCATACTGATTTCAATTAATTAGAACAGCCTTAGGGAATGATGC      | 3540 |
| Db | 3481 | ATACAGATTTCTCTCCATACTGATTTCAATTAATTAGAACAGCCTTAGGGAATGATGC      | 3540 |
| QY | 3541 | ATGCAATTCAGGTTTGTCTGAGACACCTGATGACCTGTTAGATGATGATGAATTAAGG      | 3600 |
| Db | 3541 | ATGCAATTCAGGTTTGTCTGAGACACCTGATGACCTGTTAGATGATGATGAATTAAGG      | 3600 |
| QY | 3601 | AAGATCTAGTTTTGTGTAAGAAATGACATTAAGGAAAGTTGCTGTTTTTAAAGCAAGCG     | 3660 |
| Db | 3601 | AAGATCTAGTTTTGTGTAAGAAATGACATTAAGGAAAGTTGCTGTTTTTAAAGCAAGCG     | 3660 |
| QY | 3661 | TCCAGAGAGAGAGCTTAGCAGAGTCTAGCCCTTTACCCATACACATTTGGCTCAGG        | 3720 |
| Db | 3661 | TCCAGAGAGAGAGCTTAGCAGAGTCTAGCCCTTTACCCATACACATTTGGCTCAGG        | 3720 |
| QY | 3721 | GTTACCGAAGAGGGGCCAAGAAATTAGAGCTTCAGAGAACTTATCTAGTAGAGATG        | 3780 |
| Db | 3721 | GTTACCGAAGAGGGGCCAAGAAATTAGAGCTTCAGAGAACTTATCTAGTAGAGATG        | 3780 |
| QY | 3781 | AAGACCTTCCCTGCTTCCAAACCTGTATTTGTGTAAGTAAGTAATATACCTTCTCAGT      | 3840 |
| Db | 3781 | AAGACCTTCCCTGCTTCCAAACCTGTATTTGTGTAAGTAAGTAATATACCTTCTCAGT      | 3840 |
| QY | 3841 | CTACTAGGCATAGCACCGTTGCTACCGAGTGTCTGTAAAGACACAGAGAGAAATTTAT      | 3900 |
| Db | 3841 | CTACTAGGCATAGCACCGTTGCTACCGAGTGTCTGTAAAGACACAGAGAGAAATTTAT      | 3900 |

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|----|------|--|------|
| QY | 3901 | TATCATTTGAAGATATGCTTTAAATGACTGAGTAACACAGTAAATATGTGGCAAAAGCATCTC  | 3968 |
| Db | 3901 | TATCATTTGAAGATATGCTTTAAATGACTGAGTAACACAGTAAATATGTGGCAAAAGCATCTC  | 3968 |
| QY | 3961 | AGGAACATCACCTTAGTAGAGGAAACAAATGTCTGCTAGCTGTGTTCTTCACAGTCA        | 4020 |
| Db | 3961 | AGGAACATCACCTTAGTAGAGGAAACAAATGTCTGCTAGCTGTGTTCTTCACAGTCA        | 4020 |
| QY | 4021 | GTGAATTGGAAGACTTGACTGCAATACAAACACCAGAGTCCTTCTTGATTGGTCTTT        | 4086 |
| Db | 4021 | GTGAATTGGAAGACTTGACTGCAATACAAACACCAGAGTCCTTCTTGATTGGTCTTT        | 4086 |
| QY | 4081 | CCAAACAATAGGCGATCAGTCTGAAACCCAGGGGCTTGGTGTGAGTACAAGAAATTGG       | 4140 |
| Db | 4081 | CCAAACAATAGGCGATCAGTCTGAAACCCAGGGGCTTGGTGTGAGTACAAGAAATTGG       | 4140 |
| QY | 4141 | TTTCAGATGATGAAAGAAAAGAGAAACGGGCTTGGAAAGAAATATTCMAAGAGCAACCA      | 4200 |
| Db | 4141 | TTTCAGATGATGAAAGAAAAGAGAAACGGGCTTGGAAAGAAATATTCMAAGAGCAACCA      | 4200 |
| QY | 4201 | TGGAATTCAACTTAGGTAGAGCAGCATTTGGGTGTGAGATGGAAACMAAGCCTCTTGAG      | 4266 |
| Db | 4201 | TGGAATTCAACTTAGGTAGAGCAGCATTTGGGTGTGAGATGGAAACMAAGCCTCTTGAG      | 4266 |
| QY | 4261 | ACTGCTCAGGGCTATCTCTCAGAGTGCATTTTAAACACTCAGCAGAGGATACATGC         | 4320 |
| Db | 4261 | ACTGCTCAGGGCTATCTCTCAGAGTGCATTTTAAACACTCAGCAGAGGATACATGC         | 4320 |
| QY | 4321 | AACATTAACCTGATTAAGAGCTCCAGCAGAAATGGCTGAACCTAGAGCTGTGTAACACG      | 4386 |
| Db | 4321 | AACATTAACCTGATTAAGAGCTCCAGCAGAAATGGCTGAACCTAGAGCTGTGTAACACG      | 4386 |
| QY | 4381 | ATGGAGCAGCGCTTCTTAACAGCTAACCTTCATATAAGAGCTCCCTGCGCTTGAG          | 4448 |
| Db | 4381 | ATGGAGCAGCGCTTCTTAAACAGCTAACCTTCATATAAGAGCTCTCTGCTTGAG           | 4448 |
| QY | 4441 | ACCTGCGAAATCCAGAACAAAGCAGATCAGAAAAAGCAGTATTAACTTCACAGAAAGTA      | 4500 |
| Db | 4441 | ACCTGCGAAATCCAGAACAAAGCAGATCAGAAAAAGCAGTATTAACTTCACAGAAAGTA      | 4500 |
| QY | 4501 | GTGAATTAACCTTAATGAAGCCAGAAATCCAGAAAGCCTTTCGCTGACAGTAAGTTAGAGTCTG | 4566 |
| Db | 4501 | GTGAATTAACCTTAATGAAGCCAGAAATCCAGAAAGCCTTTCGCTGACAGTAAGTTAGAGTCTG | 4566 |
| QY | 4561 | CAGATAGTCTACACAGTAAATAAAGAACACAGAGAGTGAAGGTCATCCCCCTCTAAAT       | 4620 |
| Db | 4561 | CAGATAGTCTACACAGTAAATAAAGAACACAGAGAGTGAAGGTCATCCCCCTCTAAAT       | 4620 |
| QY | 4621 | GCCCATCTTATGATGATAGTGGTGCATGCAACAGTTGCTTGGGAGTCTTCAGAAATGAA      | 4686 |
| Db | 4621 | GCCCATCTTATGATGATAGTGGTGCATGCAACAGTTGCTTGGGAGTCTTCAGAAATGAA      | 4686 |
| QY | 4681 | ACTACCCATCTCAAGAGGAGCTCAATTAAGTTGTGATGTGAGAGAGCAACAGCTGGAG       | 4740 |
| Db | 4681 | ACTACCCATCTCAAGAGGAGCTCAATTAAGTTGTGATGTGAGAGAGCAACAGCTGGAG       | 4740 |
| QY | 4741 | AGTCTGGGCCACACGATTTGACGGAACATCTTACCTTCCAAAGCAAGATCTTAGAGGAA      | 4800 |
| Db | 4741 | AGTCTGGGCCACACGATTTGACGGAACATCTTACCTTCCAAAGCAAGATCTTAGAGGAA      | 4800 |
| QY | 4801 | CCCCCTTACCTGGAATCTGGAATCAAGCCTCTTCTCTGATGAGACCTGAACTTATCTCTTG    | 4866 |
| Db | 4801 | CCCCCTTACCTGGAATCTGGAATCAAGCCTCTTCTCTGATGAGACCTGAACTTATCTCTTG    | 4866 |
| QY | 4861 | AAGACAGAGCCCCAGAGTCAGCTGTGTGTGGCAACATACCATCTTCAACCTCTGATTTGA     | 4920 |
| Db | 4861 | AAGACAGAGCCCCAGAGTCAGCTGTGTGTGGCAACATACCATCTTCAACCTCTGATTTGA     | 4920 |
| QY | 4921 | AAGTTTCCCAATTGAAGTTGCAATATGTGCCACAGGCTCAGCTGTGCTCATACTAGT        | 4986 |
| Db | 4921 | AAGTTTCCCAATTGAAGTTGCAATATGTGCCACAGGCTCAGCTGTGCTCATACTAGT        | 4986 |

| Chr | Position | RefSeq | Gene | Accession | Length | GC | GC3 | GC3+5 | GC3-5 | GC3-1 | GC3-2 | GC3-3 | GC3-4 | GC3-5 | GC3-6 | GC3-7 | GC3-8 | GC3-9 | GC3-10 | GC3-11 | GC3-12 | GC3-13 | GC3-14 | GC3-15 | GC3-16 | GC3-17 | GC3-18 | GC3-19 | GC3-20 | GC3-21 | GC3-22 | GC3-23 | GC3-24 | GC3-25 | GC3-26 | GC3-27 | GC3-28 | GC3-29 | GC3-30 | GC3-31 | GC3-32 | GC3-33 | GC3-34 | GC3-35 | GC3-36 | GC3-37 | GC3-38 | GC3-39 | GC3-40 | GC3-41 | GC3-42 | GC3-43 | GC3-44 | GC3-45 | GC3-46 | GC3-47 | GC3-48 | GC3-49 | GC3-50 | GC3-51 | GC3-52 | GC3-53 | GC3-54 | GC3-55 | GC3-56 | GC3-57 | GC3-58 | GC3-59 | GC3-60 | GC3-61 | GC3-62 | GC3-63 | GC3-64 | GC3-65 | GC3-66 | GC3-67 | GC3-68 | GC3-69 | GC3-70 | GC3-71 | GC3-72 | GC3-73 | GC3-74 | GC3-75 | GC3-76 | GC3-77 | GC3-78 | GC3-79 | GC3-80 | GC3-81 | GC3-82 | GC3-83 | GC3-84 | GC3-85 | GC3-86 | GC3-87 | GC3-88 | GC3-89 | GC3-90 | GC3-91 | GC3-92 | GC3-93 | GC3-94 | GC3-95 | GC3-96 | GC3-97 | GC3-98 | GC3-99 | GC3-100 | GC3-101 | GC3-102 | GC3-103 | GC3-104 | GC3-105 | GC3-106 | GC3-107 | GC3-108 | GC3-109 | GC3-110 | GC3-111 | GC3-112 | GC3-113 | GC3-114 | GC3-115 | GC3-116 | GC3-117 | GC3-118 | GC3-119 | GC3-120 | GC3-121 | GC3-122 | GC3-123 | GC3-124 | GC3-125 | GC3-126 | GC3-127 | GC3-128 | GC3-129 | GC3-130 | GC3-131 | GC3-132 | GC3-133 | GC3-134 | GC3-135 | GC3-136 | GC3-137 | GC3-138 | GC3-139 | GC3-140 | GC3-141 | GC3-142 | GC3-143 | GC3-144 | GC3-145 | GC3-146 | GC3-147 | GC3-148 | GC3-149 | GC3-150 | GC3-151 | GC3-152 | GC3-153 | GC3-154 | GC3-155 | GC3-156 | GC3-157 | GC3-158 | GC3-159 | GC3-160 | GC3-161 | GC3-162 | GC3-163 | GC3-164 | GC3-165 | GC3-166 | GC3-167 | GC3-168 | GC3-169 | GC3-170 | GC3-171 | GC3-172 | GC3-173 | GC3-174 | GC3-175 | GC3-176 | GC3-177 | GC3-178 | GC3-179 | GC3-180 | GC3-181 | GC3-182 | GC3-183 | GC3-184 | GC3-185 | GC3-186 | GC3-187 | GC3-188 | GC3-189 | GC3-190 | GC3-191 | GC3-192 | GC3-193 | GC3-194 | GC3-195 | GC3-196 | GC3-197 | GC3-198 | GC3-199 | GC3-200 | GC3-201 | GC3-202 | GC3-203 | GC3-204 | GC3-205 | GC3-206 | GC3-207 | GC3-208 | GC3-209 | GC3-210 | GC3-211 | GC3-212 | GC3-213 | GC3-214 | GC3-215 | GC3-216 | GC3-217 | GC3-218 | GC3-219 | GC3-220 | GC3-221 | GC3-222 | GC3-223 | GC3-224 | GC3-225 | GC3-226 | GC3-227 | GC3-228 | GC3-229 | GC3-230 | GC3-231 | GC3-232 | GC3-233 | GC3-234 | GC3-235 | GC3-236 | GC3-237 | GC3-238 | GC3-239 | GC3-240 | GC3-241 | GC3-242 | GC3-243 | GC3-244 | GC3-245 | GC3-246 | GC3-247 | GC3-248 | GC3-249 | GC3-250 | GC3-251 | GC3-252 | GC3-253 | GC3-254 | GC3-255 | GC3-256 | GC3-257 | GC3-258 | GC3-259 | GC3-260 | GC3-261 | GC3-262 | GC3-263 | GC3-264 | GC3-265 | GC3-266 | GC3-267 | GC3-268 | GC3-269 | GC3-270 | GC3-271 | GC3-272 | GC3-273 | GC3-274 | GC3-275 | GC3-276 | GC3-277 | GC3-278 | GC3-279 | GC3-280 | GC3-281 | GC3-282 | GC3-283 | GC3-284 | GC3-285 | GC3-286 | GC3-287 | GC3-288 | GC3-289 | GC3-290 | GC3-291 | GC3-292 | GC3-293 | GC3-294 | GC3-295 | GC3-296 | GC3-297 | GC3-298 | GC3-299 | GC3-300 | GC3-301 | GC3-302 | GC3-303 | GC3-304 | GC3-305 | GC3-306 | GC3-307 | GC3-308 | GC3-309 | GC3-310 | GC3-311 | GC3-312 | GC3-313 | GC3-314 | GC3-315 | GC3-316 | GC3-317 | GC3-318 | GC3-319 | GC3-320 | GC3-321 | GC3-322 | GC3-323 | GC3-324 | GC3-325 | GC3-326 | GC3-327 | GC3-328 | GC3-329 | GC3-330 | GC3-331 | GC3-332 | GC3-333 | GC3-334 | GC3-335 | GC3-336 | GC3-337 | GC3-338 | GC3-339 | GC3-340 | GC3-341 | GC3-342 | GC3-343 | GC3-344 | GC3-345 | GC3-346 | GC3-347 | GC3-348 | GC3-349 | GC3-350 | GC3-351 | GC3-352 | GC3-353 | GC3-354 | GC3-355 | GC3-356 | GC3-357 | GC3-358 | GC3-359 | GC3-360 | GC3-361 | GC3-362 | GC3-363 | GC3-364 | GC3-365 | GC3-366 | GC3-367 | GC3-368 | GC3-369 | GC3-370 | GC3-371 | GC3-372 | GC3-373 | GC3-374 | GC3-375</ |
|-----|----------|--------|------|-----------|--------|----|-----|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|-----------|
|-----|----------|--------|------|-----------|--------|----|-----|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|--------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|---------|-----------|

|    |  |               |
|----|--|---------------|
| FT | variation  | 2201          |
| FT |  | /*tag= b      |
| FT | /note= "This polymorphic variation can be a C or T nucleotide"           |               |
| XX |  |               |
| XX |  |               |
| XX |  |               |
| XX |  |               |
| XX | US5750400-A.   |               |
| PD | 12-MAY-1998.   |               |
| XX |  |               |
| XX |  |               |
| XX | 12-FEB-1997;   | 97US-0798691. |
| PR | 12-FEB-1996;   | 96US-0598591. |
| PR | 12-FEB-1997;   | 97US-0798691. |
| PA | (ONCO-) ONCORMED INC.  |               |
| PI | Allien AC, Alvares CP, Critz BS, Murphy PD, Olson SJ,                    |               |
| PI | Schelter DB, Zeng B;   |               |
| XX | WPI; 1998-296774/26.   |               |
| DR |  |               |
| XX |  |               |
| PT | BRCA1 omi gene coding sequences - useful for distinguishing between      |               |
| PT | polymorphisms and mutation(s) in the screening for disposition to        |               |
| PT | breast or ovarian cancer   |               |
| XX |  |               |
| PS | Claim 2e; Page -: 54pp; English.   |               |
| XX |  |               |
| CC | This sequence encodes a human BRCA1 (breast and ovarian cancer           |               |
| CC | predisposing gene) omi gene in which a polymorphic variation occurs at   |               |
| CC | nucleotide 2201. This sequence and other polymorphic variations of this  |               |
| CC | sequence are useful for the identification of an individual who may or   |               |
| CC | may not have an increased susceptibility to breast or ovarian cancer.    |               |
| CC | The sequences used identify gene changes which are due to polymorphisms, |               |
| CC | rather than cancer causing mutations. BRCA1 is an anti-oncogene (tumour  |               |
| CC | suppressor) which is involved in genetic inheritance of cancers,         |               |
| CC | especially breast and ovarian cancer. It is found at human chromosome    |               |
| CC | 17q which is known to be linked to cancer susceptibility, especially     |               |
| CC | breast cancer. Cells containing a mutation in this gene lose the         |               |
| CC | wild-type function of BRCA1 and are more susceptible to cancers.         |               |
| CC | NOTE: This sequence does not appear in the specification but has been    |               |
| CC | created from the wild type BRCA1 omi gene represented in AAV46448.       |               |
| XX |  |               |
| SO | Sequence 5711 BP, 1953 A; 1099 C; 1277 G; 1381 T; 1 other:               |               |
|    |  |               |
|    | Query Match: 100.0%; Score 5710.6; DB 19; Length 5711;                   |               |
|    | Best Local Similarity 100.0%; Pred. No. 0;                               |               |
|    | Matches 5710; Conservative 1; Mismatches 0; Indels 0; Gaps 0             |               |
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| DB | 1 AGCTGCGTGAACCTTCCTGGACCCCGCACAGGCTGTGGGGTTTCTCAGATTAACCTGGGCC          | 60            |
| OY | CCTGGCGTCAGAGGCGCTTCAACCCTGCTCTGGGGTAAAGTTCATTGGAACGAAAGA                | 120           |
| DB | 61 CCTGGCGTCAGAGGCGCTTCAACCCTGCTCTGGGGTAAAGTTCATTGGAACGAAAGA             | 120           |
| OY | 121 TGGATTTATCGCTCTTGCGCGTTGAAGAAGTACAATAATGCTAATGCATGACAGAAA            | 180           |
| DB | 121 TGGATTTATCGCTCTTGCGCGTTGAAGAAGTACAATAATGCTAATGCATGACAGAAA            | 180           |
| OY | 181 TCTTAGAGTGTCCCATCTGCTCGAGTGTGATCAAGAACTGTCTCCACAAAGTGACCC            | 240           |
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| OY | 241 ACAATATTTGGAAATTTTGGCANGCTGGAACCTTCAACGAGAAAGAGGCGCTTCAACT           | 300           |
| DB | 241 ACAATATTTGGAAATTTTGGCANGCTGGAACCTTCAACGAGAAAGAGGCGCTTCAACT           | 300           |
| OY | 301 GTCCCTTATATGTAAGATGATATAACCAAAGAGGCGCTCAAGAAAGTACGAGATTAGTC          | 360           |
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Db 361 AACTGTGGAAGAGCTATTGAAAATCATTTGTGCTTTTCAAGCTTGACACAGGTTGAGAT 420  
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 5521 GCACAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5580  
 5581 TCATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5640  
 5581 TCATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5640  
 5641 GTGTAGCACTCTACAGAGTCCAGAGAGTCCAGAGAGTCCAGAGAGTCCAGAGAGTCC 5700  
 5641 GTGTAGCACTCTACAGAGTCCAGAGAGTCCAGAGAGTCCAGAGAGTCCAGAGAGTCC 5700  
 5701 GCCACTACTGA 5711  
 5701 GCCACTACTGA 5711

RESULT 7  
 AAV46452  
 ID AAV46452 standard; cDNA; 5711 BP.  
 XX  
 AC AAV46452;

18-NOV-1998 (first entry)  
 Human BRCA1 om1 polymorphism #2 cDNA.  
 BRCA1: om1; human; breast and ovarian cancer predisposing gene;  
 polymorphism; susceptibility; anti-oncogene; tumour suppressor;  
 chromosome 17q; ss.  
 Homo sapiens.  
 Key Location/Qualifiers  
 CDS 120..5711  
 FT /tag= a  
 FT /product= "BRCA1 om1 protein"  
 FT variation 2430  
 FT /tag= b  
 FT /note= "This polymorphic variation can be a T or C  
 nucleotide"  
 US5750400-A.  
 12-MAY-1998.  
 12-FEB-1997; 97US-0798691.  
 12-FEB-1996; 96US-0598591.  
 12-FEB-1997; 97US-0798691.  
 (ONCO-) ONCORMED INC.  
 Allen AC, Alvares CP, Critz BS, Murphy PD, Olson SJ;  
 Schelter DB, Zeng B;  
 WPI; 1998-296774/26.  
 BRCA1 om1 gene coding sequences - useful for distinguishing between  
 PT polymorphisms and mutation(s) in the screening for disposition to  
 breast or ovarian cancer  
 Claim 2e; Page -; 54pp; English.  
 This sequence encodes a human BRCA1 (breast and ovarian cancer  
 CC predisposing gene) om1 gene in which a polymorphic variation occurs at  
 CC nucleotide 2430. This sequence and other polymorphic variations of this  
 CC sequence are useful for the identification of an individual who may or  
 CC may not have an increased susceptibility to breast or ovarian cancer.  
 CC The sequences used identify gene changes which are due to polymorphisms,  
 CC rather than cancer causing mutations. BRCA1 is an anti-oncogene (tumour  
 CC suppressor) which is involved in genetic inheritance of cancers,  
 CC especially breast and ovarian cancer. It is found at human chromosome  
 CC 17q which is known to be linked to cancer susceptibility, especially  
 CC breast cancer. Cells containing a mutation in this gene lose the  
 CC wild-type function of BRCA1 and are more susceptible to cancers.  
 CC NOTE: This sequence does not appear in the specification but has been  
 CC created from the wild type BRCA1 om1 gene represented in AAV46448.  
 SO Sequence 5711 BP; 1953 A; 1098 C; 1277 G; 1382 T; 1 other;  
 Query Match 100.0%; Score 5710.6; DB 19; Length 5711;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 5710; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 1 AGCTGGCTGAGACTTCTGACCCCGACCAAGGCTGTGGGTTCTAGATACTGGGCC 60  
 1 AGCTGGCTGAGACTTCTGACCCCGACCAAGGCTGTGGGTTCTAGATACTGGGCC 60  
 61 CTTGGCTCAGAGAGGCTTCAACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120  
 61 CTTGGCTCAGAGAGGCTTCAACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120  
 121 TGGATTATCTGCTTCTGCGTTGAAGAGTACAAATGTCATTATGCTATGCAAGAAA 180  
 121 TGGATTATCTGCTTCTGCGTTGAAGAGTACAAATGTCATTATGCTATGCAAGAAA 180



Db 121 TGAATTAATCTGCTCTTGGCGTTGAGAGATCAAAAATGTCATTAATGCTATGACAGAAA 180  
 QY 181 TCTTAGAGTGTCCATCTGCTGTGGAGTTGATCAAGAGAACCTGTCTCCAGAAAGTGTACC 240  
 Db 181 TCTTAGAGTGTCCATCTGCTGTGGAGTTGATCAAGAGAACCTGTCTCCAGAAAGTGTACC 240  
 QY 241 ACATATTTTGGCAATTTTGGCAATGCTGAAATCTTCAACAGAGAGAGGGGCTTTCACAGT 300  
 Db 241 ACATATTTTGGCAATTTTGGCAATGCTGAAATCTTCAACAGAGAGAGGGGCTTTCACAGT 300  
 QY 301 GTCTTTATATGTAAGATATTAACCAAAAGAGAGCTTCAAGAGAGATGCAAGATTTAGTC 360  
 Db 301 GTCTTTATATGTAAGATATTAACCAAAAGAGAGCTTCAAGAGAGATGCAAGATTTAGTC 360  
 QY 361 AACTTGTGAAGAGCTATTTGAAATCAATTTGTGCTTTTCAAGCTTGAACAGAGTTTGGAGT 420  
 Db 361 AACTTGTGAAGAGCTATTTGAAATCAATTTGTGCTTTTCAAGCTTGAACAGAGTTTGGAGT 420  
 QY 421 ATGCAAAACAGCTATTAATTTTGGCAAAAGAGAAATTAATCTCTCTGAACATCTAAAGATG 480  
 Db 421 ATGCAAAACAGCTATTAATTTTGGCAAAAGAGAAATTAATCTCTCTGAACATCTAAAGATG 480  
 QY 481 AAGTTTATATCTATCCAAAGATGCGCTACAGAAACCTGTCCAAAGAGCTTCTACAGATG 540  
 Db 481 AAGTTTATATCTATCCAAAGATGCGCTACAGAAACCTGTCCAAAGAGCTTCTACAGATG 540  
 QY 541 AACCCGAAATCCCTCTCTGAGAGAAACAGTCTCAGTGTCCAACTCTTACCTTGGAA 600  
 Db 541 AACCCGAAATCCCTCTCTGAGAGAAACAGTCTCAGTGTCCAACTCTTACCTTGGAA 600  
 QY 601 CTGTGAGAACTCTGAGAGCAAAAGAGCGGATACAACTCTCAAAAGAGCTGTGTACATTTG 660  
 Db 601 CTGTGAGAACTCTGAGAGCAAAAGAGCGGATACAACTCTCAAAAGAGCTGTGTACATTTG 660  
 QY 661 AATTGGATCTGATCTTCTGGAAGATACCGTTAATAAGCACTTATTTGAGTGTGGAG 720  
 Db 661 AATTGGATCTGATCTTCTGGAAGATACCGTTAATAAGCACTTATTTGAGTGTGGAG 720  
 QY 721 ATCAGAAATGTTAACAATACCCCTCAAGAGAACAGGATGAATCAGTTTGGATTTCTG 780  
 Db 721 ATCAGAAATGTTAACAATACCCCTCAAGAGAACAGGATGAATCAGTTTGGATTTCTG 780  
 QY 781 CAAAAAAGGCTGCTGTGGAATTTTCTGAGACGATGTAAACAATCTGAACATCATCAAC 840  
 Db 781 CAAAAAAGGCTGCTGTGGAATTTTCTGAGACGATGTAAACAATCTGAACATCATCAAC 840  
 QY 841 CCGATATATATGATTTTGAACCACTGAGAGAGGCTGACCTGAGAGGATCCAGAAAAGT 900  
 Db 841 CCGATATATATGATTTTGAACCACTGAGAGAGGCTGACCTGAGAGGATCCAGAAAAGT 900  
 QY 901 ATCAGGATGATCTGTTTCAAACTGTGATGTGAGAGCATGTGCAACAATCTCATGCCA 960  
 Db 901 ATCAGGATGATCTGTTTCAAACTGTGATGTGAGAGCATGTGCAACAATCTCATGCCA 960  
 QY 961 GCTCATATACAGATGAGAACAGCAGTTTATTAATCTCACTAAAGACAGATGAATGTAGAA 1020  
 Db 961 GCTCATATACAGATGAGAACAGCAGTTTATTAATCTCACTAAAGACAGATGAATGTAGAA 1020  
 QY 1021 AGGCTGAATTTCTGTAATTAAGCAAAACGCTGTGAGAGAGGCAACATTAACAGAT 1080  
 Db 1021 AGGCTGAATTTCTGTAATTAAGCAAAACGCTGTGAGAGAGGCAACATTAACAGAT 1080  
 QY 1081 GGGCTGGAAGTGAAGAAACAGTATGATGAGGAGGAGCTCCACACACAGAAAAGGTTG 1140  
 Db 1081 GGGCTGGAAGTGAAGAAACAGTATGATGAGGAGGAGCTCCACACACAGAAAAGGTTG 1140  
 QY 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAGATGGAATTAAGCAAAATCCATGCT 1200  
 Db 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAGATGGAATTAAGCAAAATCCATGCT 1200  
 QY 1201 CAGAGAAATCTTAAGATGATGATGCTTGTGATTAACATTAATGAGAGATTTACAG 1260  
 Db 1201 CAGAGAAATCTTAAGATGATGATGCTTGTGATTAACATTAATGAGAGATTTACAG 1260

QY 1261 AAGTTAATGATGATGTTTCCAGAGATGATGAATGTTAGGTTCTGATGATCAATGATG 1320  
 Db 1261 AAGTTAATGATGATGTTTCCAGAGATGATGAATGTTAGGTTCTGATGATCAATGATG 1320  
 QY 1321 GGGAGTCTGAATCAAAATGCCAAAGTATGATGATTTGAACGTTCTTAATGAGTATGATG 1380  
 Db 1321 GGGAGTCTGAATCAAAATGCCAAAGTATGATGATTTGAACGTTCTTAATGAGTATGATG 1380  
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 Db 1381 AATATTTCTGTTCTTGAAGAAAATAGATCTTATGCTGACAGTATCTCATGAGGCTTTAA 1440  
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 Db 1441 TATGTAAAGTGAAGAGTTCATCTCCAAATCAGTATGAGATTAATTTGAAGCAAAATAT 1500  
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 Db 1501 TTGGGAAAACCTATCGGAAGAGGCAAGCCTCCCAACTTAAGCCATGTAACGAAATATC 1560  
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 Db 1561 TAATTTAGAGAGATTTGTTTACTGAGCCACAGATTAATACAGAGGCTCCCTCAAAAT 1620  
 QY 1621 AATTAAGGCTTAAGAGAGAGCCTACATCAGGCTTCATCTGAGATTTTATCAAGAAAG 1680  
 Db 1621 AATTAAGGCTTAAGAGAGAGCCTACATCAGGCTTCATCTGAGATTTTATCAAGAAAG 1680  
 QY 1681 CAGATTTGGCAGTTCCAAAAGAGCTCTGAAATGATTAATCAGGAGATTAACCAAAAGAG 1740  
 Db 1681 CAGATTTGGCAGTTCCAAAAGAGCTCTGAAATGATTAATCAGGAGATTAACCAAAAGAG 1740  
 QY 1741 AGAATGCTCAAGTGAATATTTACTTAATAGTGTATGAGATTAACCAAAAGAGATTT 1800  
 Db 1741 AGAATGCTCAAGTGAATATTTACTTAATAGTGTATGAGATTAACCAAAAGAGATTT 1800  
 QY 1801 CTATTGAGATGAGAAAATCCTAACCAATGAAATCCTCGAAAAGAGATCGCTTTCA 1860  
 Db 1801 CTATTGAGATGAGAAAATCCTAACCAATGAAATCCTCGAAAAGAGATCGCTTTCA 1860  
 QY 1861 AAAAGAAAGCTGAACCTATTAAGCAGATTAAGCAATATGAAATCGAATTAATATTC 1920  
 Db 1861 AAAAGAAAGCTGAACCTATTAAGCAGATTAAGCAATATGAAATCGAATTAATATTC 1920  
 QY 1921 ACAATTTCAAAAGCACTTAATAAGATAGGCTGAGAGAGATCTTCTACAGGCAATATTC 1980  
 Db 1921 ACAATTTCAAAAGCACTTAATAAGATAGGCTGAGAGAGATCTTCTACAGGCAATATTC 1980  
 QY 1981 ATGCGCTGACATGATGATCAGTAAAGATCTTAAGCCACCTAATTTGATGATTTGCA 2040  
 Db 1981 ATGCGCTGACATGATGATCAGTAAAGATCTTAAGCCACCTAATTTGATGATTTGCA 2040  
 QY 2041 TTGATAGTTGTTCTAGCAGTGAAGATTAAGAAAAGAGTAAACCAATGTCAGTCA 2100  
 Db 2041 TTGATAGTTGTTCTAGCAGTGAAGATTAAGAAAAGAGTAAACCAATGTCAGTCA 2100  
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 QY 2161 GTAAACAGCAAAATGAGAGAGAGCAAGTAAAGACATGACAGTATCTTCCAGAGCTGA 2220  
 Db 2161 GTAAACAGCAAAATGAGAGAGAGCAAGTAAAGACATGACAGTATCTTCCAGAGCTGA 2220  
 QY 2221 AGTTAACAAATGACACTGTTCTTTTACTAAGTGTCAATACAGTGAATTTAAAGAT 2280  
 Db 2221 AGTTAACAAATGACACTGTTCTTTTACTAAGTGTCAATACAGTGAATTTAAAGAT 2280  
 QY 2281 TTGTCAATCTTACCTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2340  
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Query Match 100.0%; Score 5710.6; DB 19; Length 5711;  
Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;  
Matches 5710; Conservative 1;

QY 1 AGCTGCTGAGACCTTCTGSAACCCGACACAGCTGTGGGGTTCACAGATACTGGGCC 60  
DB 1 AGCTGCTGAGACCTTCTGSAACCCGACACAGCTGTGGGGTTCACAGATACTGGGCC 60

QY 61 CCTGCGCTCAGAGAGCCTTCACTCTGCTGTGGGTAAAGTTGATTGAAACGAAAGAA 120  
DB 61 CCTGCGCTCAGAGAGCCTTCACTCTGCTGTGGGTAAAGTTGATTGAAACGAAAGAA 120

QY 121 TGGATTTATCTGCTCTGCGGCTTGAAGAGTAACTTATGCTATGACGAAA 180  
DB 121 TGGATTTATCTGCTCTGCGGCTTGAAGAGTAACTTATGCTATGACGAAA 180

QY 181 TCTTAGAGTGTCCATCTGTCTGAGATTGATCAAGAACTGTCTCCAGAAAGTGACC 240  
DB 181 TCTTAGAGTGTCCATCTGTCTGAGATTGATCAAGAACTGTCTCCAGAAAGTGACC 240

QY 241 ACATATTTTGCAATTTTTCATGCTGAACTTCTCAACGAGAAAGAGGCTTCAAGT 300  
DB 241 ACATATTTTGCAATTTTTCATGCTGAACTTCTCAACGAGAAAGAGGCTTCAAGT 300

QY 301 GTCCCTTATGTAAGATGATATACCAAAAGAGCCTACAGAAAGTACAGATTAGTC 360  
DB 301 GTCCCTTATGTAAGATGATATACCAAAAGAGCCTACAGAAAGTACAGATTAGTC 360

QY 361 AACTTGTGAAGAGCTATTGAAATCATTTGTCTTTGAGCTTGAACAGAGTTTGAAT 420  
DB 361 AACTTGTGAAGAGCTATTGAAATCATTTGTCTTTGAGCTTGAACAGAGTTTGAAT 420

QY 421 ATGCAAAAGCTATATTTTTCGAAAAAGAAATTAACCTCTCTGAACTTAAAAAGATG 480  
DB 421 ATGCAAAAGCTATATTTTTCGAAAAAGAAATTAACCTCTCTGAACTTAAAAAGATG 480

QY 481 AAGTTTCTATCATCCAAAGATAGGGCTCAGAAACCGTSCCAAAAGACTTCTACAGAGT 540  
DB 481 AAGTTTCTATCATCCAAAGATAGGGCTCAGAAACCGTSCCAAAAGACTTCTACAGAGT 540

QY 541 AACCAGAAATCTCTTCTTGACAGAAACCAAGTCTCAGTGTCCAACCTCTTAACTTTGAA 600  
DB 541 AACCAGAAATCTCTTCTTGACAGAAACCAAGTCTCAGTGTCCAACCTCTTAACTTTGAA 600

QY 601 CTGTGAGAACTCTGAGACAAAGCAGCGATACAACTCAAAAGAGCTGTCTACATTG 660  
DB 601 CTGTGAGAACTCTGAGACAAAGCAGCGATACAACTCAAAAGAGCTGTCTACATTG 660

QY 661 AATTGGATCTGATCTTCTGAAGATACCGTTAATTAAGCACTTAATTGACAGTGGAG 720  
DB 661 AATTGGATCTGATCTTCTGAAGATACCGTTAATTAAGCACTTAATTGACAGTGGAG 720

QY 721 ATCAAGAAATTTTCAAAATCACCCCTCAAGGAAACCGAGATGAAATCACTTTGSAATTCTG 780  
DB 721 ATCAAGAAATTTTCAAAATCACCCCTCAAGGAAACCGAGATGAAATCACTTTGSAATTCTG 780

QY 781 CAAAAAAGGCTGCTGTGATTTTCTGAGACGAGATTAACAAATATCTGAACATCATCAAC 840  
DB 781 CAAAAAAGGCTGCTGTGATTTTCTGAGACGAGATTAACAAATATCTGAACATCATCAAC 840

QY 841 CCAGTAATTAATGATTTGAAACCACTGAGAACGCTGACAGAGCACTCCAGAAAGT 900  
DB 841 CCAGTAATTAATGATTTGAAACCACTGAGAACGCTGACAGAGCACTCCAGAAAGT 900

QY 901 ATCAGGATGATCTGTTTCAAACTTGATGAGAGCAATGTGCAAAATACATCATGCCA 960  
DB 901 ATCAGGATGATCTGTTTCAAACTTGATGAGAGCAATGTGCAAAATACATCATGCCA 960

QY 961 GCTCATTTACAGATAGAAACAGCAAGTTTATTACTCACTAAAGACAAATGATGAGAA 1020  
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DB 1081 GGGCTGAAATGAGAAACATGTATATGATAGCGGACTCCAGACACAGAAAAAGGTAG 1140

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QY 1201 CAGAGAAATCTAGAGATACCTAGATGTTCTTGATTAACCTAAATAGCAGATTCAGA 1260  
DB 1201 CAGAGAAATCTAGAGATACCTAGATGTTCTTGATTAACCTAAATAGCAGATTCAGA 1260

QY 1261 AAGTTAATGAGTGGTTTCCAGAAAGTATGACTGTTAGTTCTGATGACTCAGATGATG 1320  
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QY 1321 GGGAGTCTGAATCAATGSCAAAGTAGCTGATTTGAGACGTTCTAAATGAGGTAGTG 1380  
DB 1321 GGGAGTCTGAATCAATGSCAAAGTAGCTGATTTGAGACGTTCTAAATGAGGTAGTG 1380

QY 1381 AATATTCGTGTTCTTCAAGAGAAATAGACTTACCTGCGCAGATGATCTCATGAGCCTTAA 1440  
DB 1381 AATATTCGTGTTCTTCAAGAGAAATAGACTTACCTGCGCAGATGATCTCATGAGCCTTAA 1440

QY 1441 TATGTAAAGTGAAAGAGTTCACTCCAAATATGATAGAGATTAATTTGAAACAAATAT 1500  
DB 1441 TATGTAAAGTGAAAGAGTTCACTCCAAATATGATAGAGATTAATTTGAAACAAATAT 1500

QY 1501 TTGGGAAACCTATGGAAGAGGCAAGCCCTCCCACTTAAGCATGATTAAGTAAATC 1560  
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DB 1561 TAATTATAGAGACTTTGTTACTAGACCAAGATATATCAAGAGCGTCCCTCAAAATA 1620

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DB 1621 AATTAAAGCTTAAAGAGACCTTACATCAGGCTTCACTCTGAGAGATTTTATCAAGAA 1680

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DB 1681 CAGATTTGGCAGTTCAAAAGACTCCTGAAATGATTAATCAGGGAATTAACCAAGCGAGC 1740

QY 1741 AGAATGATCAAGTATGATTAATTAATTAAGTGTCTATGAGATTAACCAAGAGGTATT 1800  
DB 1741 AGAATGATCAAGTATGATTAATTAATTAAGTGTCTATGAGATTAACCAAGAGGTATT 1800

QY 1801 CTATTCAAGATGAGAAAAATCTCTAATCCCAATATGAAATCACTTCGAAAAAGATTCGCTTCA 1860  
DB 1801 CTATTCAAGATGAGAAAAATCTCTAATCCCAATATGAAATCACTTCGAAAAAGATTCGCTTCA 1860

QY 1861 AAACGAAAGCTGAACCTTAAGCAGAGTATTAACCAATATGAGAACTGCAATTAATATTC 1920  
DB 1861 AAACGAAAGCTGAACCTTAAGCAGAGTATTAACCAATATGAGAACTGCAATTAATATTC 1920

QY 1921 ACAATTTCAAAAGCACTTAAAGAAATAGGCTGAGAGAAAGCTTCTACAGGATATTC 1980  
DB 1921 ACAATTTCAAAAGCACTTAAAGAAATAGGCTGAGAGAAAGCTTCTACAGGATATTC 1980

QY 1981 ATGCGCTTGAACCTAGTATCTAGTGAATCTTAAGCCCACTTAATTTGATGAAATTTGCAAA 2040  
DB 1981 ATGCGCTTGAACCTAGTATCTAGTGAATCTTAAGCCCACTTAATTTGATGAAATTTGCAAA 2040

QY 2041 TTGATAGTGTCTTACAGAGTGAAGATTAAGAAAAAGTACCAATATGCAATGCAATGCA 2100  
DB 2041 TTGATAGTGTCTTACAGAGTGAAGATTAAGAAAAAGTACCAATATGCAATGCAATGCA 2100

QY 2101 GGCACAGCAGAAACCTCACTCATGAGAGTAAAGAACTGCAACTGAGCAAGAGAA 2160

2101 GGCACGACGAGAAACCTACAACTCATGAAAGGTAAAGAACCTGCACTGGAGCCAGAAAGA 2160  
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2161 GTACAGAGCCAAATGAAAGAGAGAAAGAAAGACATGACAGTGTACTTTCCCGAGACTGA 2220  
2221 AGTTAAACAAATGACACCTGGTCTTTTACTAGTAGTTCAAATACAGTGAACCTAAAGAAAT 2280  
2221 AGTTAAACAAATGACACCTGGTCTTTTACTAGTAGTTCAAATACAGTGAACCTAAAGAAAT 2280  
2281 TTGTCAATCTTACCTCTTCCAGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 2340  
2281 TTGTCAATCTTACCTCTTCCAGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 2340  
2341 CTAAATATGCTGAAGACCCCAAGATCTCATGTTAGTGAAGAAAGGTTTGGCAACCTG 2400  
2341 CTAAATATGCTGAAGACCCCAAGATCTCATGTTAGTGAAGAAAGGTTTGGCAACCTG 2400  
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2401 AAGATCTGTAGAGAGTAGAGATTTCACTGGTACTGGTACTGATTAATGAGCACTCAG 2460  
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2521 GTGTAGTCAAGTGTGAGCACTTGAAGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAG 2580  
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2641 GGGAAACAAAGCATAGAAATGAAAGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAG 2700  
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2701 TCAAGGTTTCAAGGCGCCAGTCACTTGTCTGTCTGTTTCAATCCAGAAATTCAGAGAGAG 2760  
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2761 AATGTGCAACATTTCTGTGCGCACTCTGGGCTCTTAAAGAAACAAATCCAAAGTCACTT 2820  
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2821 TTGAATGTGAACAAAGAAAGAAAGAAATCAAGAAAGAAAGTGTCTAATATCAAGCTGTAC 2880  
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2941 ATGCCAAATGTAGTATCAAGAGAGGCTCTAGGTTTGTCTATCATCTCAGTTCAGAGGCA 3000  
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3001 AGGAAACGAGACATTTACTCTCAAAATPAAACATGAGCTTTTACAAAACCATATCGTATAC 3060  
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3061 CACACATTTTCCCATCAAGTCAATTTGTAAACCTAAATGTAAAGAAATTCGCTGAGAG 3120  
3121 AAAACTTTGAGGAACATTCATGTCACTGAAAGAAAGAAATGGGAAATGAAACATTTCCAA 3180  
3121 AAAACTTTGAGGAACATTCATGTCACTGAAAGAAAGAAATGGGAAATGAAACATTTCCAA 3180  
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3241 CAAGCAATTTAATGAAAGTAGAGTTCAGTACTAATGAAGTGGGCTCAGTATTAATGA 3300  
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3421 GTAAATGTAGATCTGTAATTAAGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGG 3480  
3421 GTAAATGTAGATCTGTAATTAAGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGG 3480  
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3481 ATACAGATTTCTCTCATATCTGATTTAGATTTAGATTTAGATTTAGATTTAGATTTAG 3540  
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RESULT 9
AAV46454
ID AAV46454 standard; cDNA, 5711 BP.
XX
XX AAV46454;
AC
XX
XX 18-NOV-1998 (first entry)
DT
XX
DE Human BRCA1 omil polymorphism #4 cDNA.
XX
XX BRCA1; omil; human; breast and ovarian cancer predisposing gene;
KW polymorphism; susceptibility; anti-oncogene; tumor suppressor;
XX chromosome 17q; ss.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH 120..5711
FT CDS /*tag= a
FT /product= "BRCA1 omil protein"
FT variation 3232
FT /*tag= b
FT /note= "This polymorphic variation can be an A or G
nucleotide"
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XX
XX 12-MAY-1998.
PD
XX
XX 12-FEB-1997; 97US-0798691.
PF
XX
XX 12-FEB-1996; 96US-0598591.
PR
XX 12-FEB-1997; 97US-0798691.
PA (ONCO-) ONCORMED INC.
XX
XX Allen AC, Alvares CP, Critz BS, Murphy PD, Olson SJ;
PI Scheller DB, Zeng B;
PI
XX
XX WPI; 1998-296774/26.
DR
XX
XX BRCA1 omil gene coding sequences - useful for distinguishing between
PT polymorphisms and mutation(s) in the screening for disposition to
PT breast or ovarian cancer
XX
XX Claim 2e; Page -: 54pp; English.
PS
XX This sequence encodes a human BRCA1 (breast and ovarian cancer
CC

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CC predisposing gene) omil gene in which a polymorphic variation occurs at  
CC nucleotide 3232. This sequence and other polymorphic variations of this  
CC sequence are useful for the identification of an individual who may or  
CC may not have an increased susceptibility to breast or ovarian cancers.  
CC The sequences used identify gene changes which are due to polymorphisms,  
CC rather than cancer causing mutations. BRCA1 is an anti-oncogene (tumour  
CC suppressor) which is involved in genetic inheritance of cancers,  
CC especially breast and ovarian cancer. It is found at human chromosome  
CC 17q which is known to be linked to cancer susceptibility, especially  
CC breast cancer. Cells containing a mutation in this gene lose the  
CC wild-type function of BRCA1 and are more susceptible to cancers.  
CC NOTE: This sequence does not appear in the specification but has been  
CC created from the wild type BRCA1 omil gene represented in AAV46448.  
XX  
SQ Sequence 5711 BP; 1953 A; 1099 C; 1276 G; 1382 T; 1 other;

Query Match 100.0%; Score 5710.6; DB 19; Length 5711;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 5710; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTCGCTGAGACTTCCTGAGACCCCGACAGGCTGAGGTTTCTCAGATACTGGGCC 60  
DB 1 AGCTCGCTGAGACTTCCTGAGACCCCGACAGGCTGAGGTTTCTCAGATACTGGGCC 60  
QY 61 CCTGCGCTGAGAGGCTTACCCCTCTGCTCTGGGTAAGTTCAATGGAACAGAAAGAA 120  
DB 61 CCTGCGCTGAGAGGCTTACCCCTCTGCTCTGGGTAAGTTCAATGGAACAGAAAGAA 120  
QY 121 TGAATTTATGCTGCTTTCGGGTTGAAGAGTACAAAATGCTAATATGCTATGCAAGAAA 180  
DB 121 TGAATTTATGCTGCTTTCGGGTTGAAGAGTACAAAATGCTAATATGCTATGCAAGAAA 180  
QY 181 TCTTAAGAGTCCCATCTGCTGAGATGATCAAGAAACCTGCTCCACAAAGTGTGACC 240  
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RESULT 10  
 AAV4645  
 ID AAV4645 standard; cDNA; 5711 BP.  
 XX  
 AC AAV4645;  
 XX  
 DT 18-NOV-1998 (first entry)  
 XX  
 DE Human BRCA1 om1 polymorphism #5 cDNA.  
 XX  
 KW BRCA1; om1; human; breast and ovarian cancer predisposing gene;  
 KW polymorphism; susceptibility; anti-oncogene; tumour suppressor;  
 KW chromosome 17q; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH key Location/Qualifiers  
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 FT /\*tag= a  
 FT /product= "BRCA1 om1 protein"  
 FT variation  
 FT FT 3667  
 FT /tag= b  
 FT /note= "This polymorphic variation can be an A or G  
 nucleotide"

US5750400-A.  
 PD 12-MAY-1998.  
 XX  
 PD 12-FEB-1997; 97US-0798691.  
 XX  
 PR 12-FEB-1996; 96US-0598591.  
 XX  
 PR 12-FEB-1997; 97US-0798691.

XX (ONCO-) ONCOMED INC.  
XX Allen AC, Alvares CP, Critz BS, Murphy PD, Olson SJ;  
PI Schelter DB, Zeng B;  
XX WPI, 1998-296774/26.  
XX  
PT BRCA1 omi gene coding sequences - useful for distinguishing between  
PT polymorphisms and mutation(s) in the screening for disposition to  
PT breast or ovarian cancer  
XX  
PS Claim 2e; Page -; 54bp; English.  
XX  
CC This sequence encodes a human BRCA1 (breast and ovarian cancer  
CC predisposing gene) omi gene in which a polymorphic variation occurs at  
CC nucleotide 3667. This sequence and other polymorphic variations of this  
CC sequence are useful for the identification of an individual who may or  
CC may not have an increased susceptibility to breast or ovarian cancer.  
CC The sequences used identify gene changes which are due to polymorphisms,  
CC rather than cancer causing mutations. BRCA1 is an anti-oncogene (tumour  
CC suppressor) which is involved in genetic inheritance of cancers,  
CC especially breast and ovarian cancer. It is found at human chromosome  
CC 17q which is known to be linked to cancer susceptibility, especially  
CC breast cancer. Cells containing a mutation in this gene lose the  
CC wild-type function of BRCA1 and are more susceptible to cancers.  
CC NOTE: This sequence does not appear in the specification but has been  
CC created from the wild type BRCA1 omi gene represented in AAIV46448.  
XX  
SQ Sequence 5711 BP, 1953 A; 1099 C; 1276 G; 1382 T; 1 other;  
Query Match 100.0%; Score 5710.6; DB 19; Length 5711;  
Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;  
Matches 5710; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
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DB 1 AGCTCGTAGAGACTTCTGAGACCCCGACACAGGCTGTGGGTTTCTCAGATACTGGGCC 60  
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DB 61 CCTGGCTCAGAGAGGCTTCACTCTGTCTGTGGTAAAGTTCACTTGAACGAAAGAA 120  
QY 121 TGGATTATCTGCTCTGCGGTTGAAGAGTACAAAGTCACTTATGCTATGCGAATA 180  
DB 121 TGGATTATCTGCTCTGCGGTTGAAGAGTACAAAGTCACTTATGCTATGCGAATA 180  
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Db 3721 GTTACCGAAGAGGAGGCAAGAAATTAAGTCTCAAGAGAACTTATCTAGTGAATG 3780  
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FT      /*tag= a
FT      /product= "BRCA1 om1 protein"
FT      4427
FT      variation //tag= b
FT      /note= "This polymorphic variation can be a T or C
FT      nucleotide"
PN      US5750400-A.
XX
PD      12-MAY-1998.
XX
PF      12-FEB-1997; 97US-0798691.
XX
PR      12-FEB-1996; 96US-0598591.
PR      12-FEB-1997; 97US-0798691.
XX
PA      (ONCO-) ONCOMED INC.
PI      Allen AC, Alvares CP, Critz BS, Murphy PD, Olson SU,
PI      Schelter DB, Zeng B;
XX
DR      WPI; 1998-296774/26.
XX
PT      BRCA1 om1 gene coding sequences - useful for distinguishing between
PT      polymorphisms and mutation(s) in the screening for disposition to
PT      breast or ovarian cancer
XX
PS      Claim 2e; Page -; 54pp; English.
XX
CC      This sequence encodes a human BRCA1 (breast and ovarian cancer
CC      predisposing gene) om1 gene in which a polymorphic variation occurs at
CC      nucleotide 4427. This sequence and other polymorphic variations of this
CC      sequence are useful for the identification of an individual who may or
CC      may not have an increased susceptibility to breast or ovarian cancer.
CC      The sequences used identify gene changes which are due to polymorphisms,
CC      rather than cancer causing mutations. BRCA1 is an anti-oncogene (tumour
CC      suppressor) which is involved in genetic inheritance of cancers,
CC      especially breast and ovarian cancer. It is found at human chromosome
CC      17q which is known to be linked to cancer susceptibility, especially
CC      breast cancer. Cells containing a mutation in this gene lose the
CC      wild-type function of BRCA1 and are more susceptible to cancers.
CC      NOTE: This sequence does not appear in the specification but has been
CC      created from the wild type BRCA1 om1 gene represented in AAV46448.
XX
SQ      Sequence 5711 BP; 1953 A; 1098 C; 1277 G; 1382 T; 1 other;
Query Match 100.0%; Score 5710.6; DB 19; Length 5711;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5710; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY      301 GTCTCTTATATGAAGATGATATTAACCAAAAGAGCTTACAGAAAGATGAGATTTAGTC 360
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RESULT 12  
AAV46457  
ID AAV46457 standard; cDNA; 5711 BP.



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Db 2041 TTGATAGTGTCTTACAGTAGAAGATTAAGAAAAAGTAAGCAACCAATTCAGTCA 2100
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Db 2281 TTGTCATCTTACCTTCCAGAGAGAGAAAAAGAGAGAACTAGAAACAGTTAAAGTGT 2340
|||||
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Db 3361 ATGCTATGCTTAGATTAGAGGTTTTCGAACTGAGGCTATTAACAAAGTCTTCTGGA 3420
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Db 5581 TCCATGCAATTGGCGAGATGTGAGGACCTGTGGTACCCGAGAGTGGGTGGACA 5640  
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QY 5701 GCCACTACTGA 5711  
Db 5701 GCCACTACTGA 5711

RESULT 13  
AAV46450  
ID AAV46450 standard; cdna; 5711 BP.  
XX AAV46450;  
AC AAV46450;  
XX  
XX 18-NOV-1998 (first entry)  
DE Human BRCA1 omi3 cDNA.  
XX  
XX BRCA1; omi3; human; breast and ovarian cancer predisposing gene;  
KW Polymorphism; susceptibility; anti-oncogene; tumour suppressor;  
KW Chromosome 17q; ss.  
XX  
XX Homo sapiens.  
FH Key Location/Qualifiers  
FT CDS 120..5711  
FT FT /\*tag= a  
FT FT /product= "BRCA1 omi3 protein"  
XX  
XX PN US5750400-A.  
XX 12-MAY-1998.  
XX  
XX 12-FEB-1997; 97US-0798691.  
XX  
XX 12-FEB-1996; 96US-0598591.  
PR 12-FEB-1997; 97US-0798691.  
XX  
XX (ONCO-) ONCOMED INC.  
XX  
XX Allen AC, Alvares CP, Critz BS, Murphy PD, Olson SJ,  
PI Schelter DB, Zeng B;  
XX  
XX WPI; 1998-296774/26.  
DR P-PSDB; AAW76100.  
XX  
XX BRCA1 omi3 gene coding sequences - useful for distinguishing between  
PT polymorphisms and mutation(s) in the screening for disposition to  
PT breast or ovarian cancer  
XX  
XX Claim 2e; Column 55-62; 54pp; English.  
XX  
XX This sequence encodes the human BRCA1 (breast and ovarian cancer  
CC predisposing gene) omi3 gene. This sequence and polymorphic variations of  
CC this sequence are useful for the identification of an individual who may  
CC or may not have an increased susceptibility to breast or ovarian cancer.  
CC The sequences used identify gene changes which are due to polymorphisms,  
CC suppressor) which is involved in genetic inheritance of cancers,  
CC especially breast and ovarian cancer. It is found at human chromosome 17q  
CC which is known to be linked to cancer susceptibility, especially breast  
CC cancer. Cells containing a mutation in this gene lose the wild-type  
CC function of BRCA1 and are more susceptible to cancers.  
XX  
XX Sequence 5711 BP; 1953 A; 1098 C; 1277 G; 1383 T; 0 other;

Query Match 100.0%; Score 5709.4; DB 19; Length 5711;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 5710; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGCTGCTGAGACTTCTCTGGAACCCGACAGAGCTGTGGGTTTCTCAGATAACTGGCC 60  
1 AGCTGCTGAGACTTCTCTGGAACCCGACAGAGCTGTGGGTTTCTCAGATAACTGGCC 60  
Db 1 AGCTGCTGAGACTTCTCTGGAACCCGACAGAGCTGTGGGTTTCTCAGATAACTGGCC 60  
QY 61 CCTGCGCTCAGAGAGGCTTCACTCTGCTGTGGTAAAGTTTCAATGGAACAGAAAGAA 120  
61 CCTGCGCTCAGAGAGGCTTCACTCTGCTGTGGTAAAGTTTCAATGGAACAGAAAGAA 120  
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1021 AGGCTGAATTTCTGTATATAAAGCAACAGCTGTGCTTAGCAAGAGCCCAATACAGAT 1080  
Db 1021 AGGCTGAATTTCTGTATATAAAGCAACAGCTGTGCTTAGCAAGAGCCCAATACAGAT 1080

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DB 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAAAGAAATGAAGAAAGTAGGCTGCT 1200
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DB 1321 GGGAGCTGAATCAAAATGCCAAAGTAGCTGATGATGATGATGATGATGATG 1380
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Qy 4681 ACTACCCATCTCAAGAGAGCTCATTAAGTGTGTAATGTGAGAGAACCAAGCTGGAAG 4740  
Db 4681 ACTACCCATCTCAAGAGAGCTCATTAAGTGTGTAATGTGAGAGAACCAAGCTGGAAG 4740  
Qy 4741 AGTCTGGGACACAGATTTGACGAGAAACATTTCTTCCAGAGGCAAGATCTAGAGGAA 4800  
Db 4741 AGTCTGGGACACAGATTTGACGAGAAACATTTCTTCCAGAGGCAAGATCTAGAGGAA 4800  
Qy 4801 CCCCTTACCTGGAATCTGGAATCTGGAATCTGGAATCTGGAATCTGGAATCTGGAATCT 4860  
Db 4801 CCCCTTACCTGGAATCTGGAATCTGGAATCTGGAATCTGGAATCTGGAATCTGGAATCT 4860  
Qy 4861 AAGAGAGAGCCCGAGAGTCACTGCTGTGAGCAATACATCTTCAACCTCTGCATGTA 4920  
Db 4861 AAGAGAGAGCCCGAGAGTCACTGCTGTGAGCAATACATCTTCAACCTCTGCATGTA 4920  
Qy 4921 AAGTCCCAATTTGAAGTTGACAGATCTGCCAGGCTCCAGTGTGCTCATACTCTG 4980  
Db 4921 AAGTCCCAATTTGAAGTTGACAGATCTGCCAGGCTCCAGTGTGCTCATACTCTG 4980  
Qy 4981 ATACTGCTGGTATATGCAATGGAAGAGTGTGACAGGAGAGACCCAGAAATGACAG 5040  
Db 4981 ATACTGCTGGTATATGCAATGGAAGAGTGTGACAGGAGAGACCCAGAAATGACAG 5040  
Qy 5041 CTTCAACGAAAGGCTCAACAAAGAAATGTCCATGTGTGTCTGAGCTGACCCCAAG 5100  
Db 5041 CTTCAACGAAAGGCTCAACAAAGAAATGTCCATGTGTGTCTGAGCTGACCCCAAG 5100  
Qy 5101 AATTTATGCTGCTGTAACAAGTTGCCAGAAAAACACATCACTTAATTAATTAATTA 5160  
Db 5101 AATTTATGCTGCTGTAACAAGTTGCCAGAAAAACACATCACTTAATTAATTAATTA 5160  
Qy 5161 CTGAAGAGACTACTGATGTTGTTATGAAAAAGATGCTGAGTTGTGTGAACGAGAC 5220  
Db 5161 CTGAAGAGACTACTGATGTTGTTATGAAAAAGATGCTGAGTTGTGTGAACGAGAC 5220  
Qy 5221 TGAATTAATTTCTAGAAATTTGCGGAGAGAAATGGAGTATGCTATTTCTGAGTACC 5280  
Db 5221 TGAATTAATTTCTAGAAATTTGCGGAGAGAAATGGAGTATGCTATTTCTGAGTACC 5280



|    |      |   |      |
|----|------|---|------|
| OY | 5281 | AGTCATTAAGAAAGAAAGAAATGCTGATGAGCATGATTTTGAATGACAGAGAAATGCG      | 5340 |
| Db | 5281 | AGCTATTAAAGAAAGAAAGAAATGCTGATGAGCATGATTTTGAAGTCAAGAGAAATGTGG    | 5340 |
| OY | 5341 | TCATATGAAAGAAACCAACAGGTCCAAAGCAGACAAGAAATCCACAGACAAAGAATCT      | 5400 |
| Db | 5341 | TCAATGAGAAAGAAACCAACAGGTCCAAAGCAGACAAGAAATCCACAGACAAAGAATCT     | 5400 |
| OY | 5401 | TCAGGGGGCTGAAATTCGTGTCATATGGGCCCCCTTACCAACATGCCCCACAGATCACTGG   | 5460 |
| Db | 5401 | TCAGGGGGCTGAAATTCGTGTCATATGGGCCCCCTTACCAACATGCCCCACAGATCACTGG   | 5460 |
| OY | 5461 | AATGATATGATACAGCTGTGTGATGCTTCTGTGTGTAAGAGACTTTCAATCATTCACCCCTG  | 5520 |
| Db | 5461 | AATGATATGATACAGCTGTGTGATGCTTCTGTGTGTAAGAGACTTTCAATCATTCACCCCTG  | 5520 |
| OY | 5521 | GCACAGGTGTCACCCCAATTGTGTGTTGTGACCGACAGATGCTTGACAGAGACAATGGCT    | 5580 |
| Db | 5521 | GCACAGGTGTCACCCCAATTGTGTGTTGTGACCGACAGATGCTTGACAGAGACAATGGCT    | 5580 |
| OY | 5581 | TCCATATGCAATTGGGGCAGATGTGTGAGGACCTGTGTGTGACCCGAGATGGGTTGTGGACA  | 5640 |
| Db | 5581 | TCCATATGCAATTGGGGCAGATGTGTGAGGACCTGTGTGTGACCCGAGATGGGTTGTGGACA  | 5640 |
| OY | 5641 | GTGTAGCACTTACACAGTCCAGAGAGCTGTGACACCTAATCTGTATACCCACAGATCCCCACA | 5700 |
| Db | 5641 | GTGTAGCACTTACACAGTCCAGAGAGCTGTGACACCTAATCTGTATACCCACAGATCCCCACA | 5700 |
| OY | 5701 | GCACACTACTGA  | 5711 |
| Db | 5701 | GCACACTACTGA  | 5711 |

|    |   |
|----|---|
| XX | AAV46465  |
| ID | AAV46465 standard; cDNA; 5711 BP.   |
| AC | AAV46465;   |
| DT | 18-NOV-1998 (first entry)   |
| DE | Human BRCA1 omi3 polymorphism #1 CDNA.  |
| KW | BRCA1; omi3; .human; breast and ovarian cancer predisposing gene;<br>polymorphism; susceptibility; anti-oncogene; tumour suppressor;<br>chromosome 17q; ss.                               |
| OS | Homo sapiens.   |
| FH | Key Location/Qualifiers<br>CDS 120..5711<br>FT /*tag= a /product= "BRCA1 omi3 protein"<br>FT variation 2201<br>FT /*tag= b /note= "This polymorphic variation can be a C or T nucleotide" |
| PN | US5750400-A.  |
| PD | 12-MAY-1998.  |
| Pf | 12-FEB-1997; 97US-0798691.  |
| PR | 12-FEB-1996; 96US-0586591.<br>12-FEB-1997; 97US-0798691.  |
| PA | (ONCO-) ONCORMED INC.   |
| PI | Allan AC, Alvares CP, Critz BS, Murphy PD, Olson SJ,<br>Scheller DB, Zeng B;<br>WP1: 1998-296774/26.  |

| Query Match   | Best Local Similarity | Score | DB     | Length |
|---|-----------------------|-------|--------|--------|
| Matches 5709; Conservative 1; Mismatches 1; Indels 0; Gaps 0;     | 100.0%;               | 5709; | DB 19; | 5711;  |
| 1 AGCTGCGTGAAGACTCTCTGGAACCCCGACGAGCGTGTGGGGTTCTCAGATACTGGCC      | 100.0%;               | 5709; | DB 19; | 5711;  |
| 1 AGCTGCGTGAAGACTCTCTGGAACCCCGACGAGCGTGTGGGGTTCTCAGATACTGGCC      | 100.0%;               | 5709; | DB 19; | 5711;  |
| 61 CTTGCGCTCAGAGAGCCCTTCAACCTCTGCTTGGGTAAAGTTTGAACAGAAAGAA        | 100.0%;               | 5709; | DB 19; | 5711;  |
| 61 CTTGCGCTCAGAGAGCCCTTCAACCTCTGCTTGGGTAAAGTTTGAACAGAAAGAA        | 100.0%;               | 5709; | DB 19; | 5711;  |
| 121 TGGATTATCTGCTCTTTCGCGTTGAAGAGTACAAATGTCATTATATGTCAGAA         | 100.0%;               | 5709; | DB 19; | 5711;  |
| 121 TGGATTATCTGCTCTTTCGCGTTGAAGAGTACAAATGTCATTATATGTCAGAA         | 100.0%;               | 5709; | DB 19; | 5711;  |
| 181 TCTTAGAGTGTCCCATCTGCTGTGGAAGTATCAAGAACTGTCTCAAGAAAGTAC        | 100.0%;               | 5709; | DB 19; | 5711;  |
| 181 TCTTAGAGTGTCCCATCTGCTGTGGAAGTATCAAGAACTGTCTCAAGAAAGTAC        | 100.0%;               | 5709; | DB 19; | 5711;  |
| 241 ACAATATTTTCAAAATTTTGCATGCTGAACTCTTCAACGAGAAAGGCGCTCACAGT      | 100.0%;               | 5709; | DB 19; | 5711;  |
| 241 ACAATATTTTCAAAATTTTGCATGCTGAACTCTTCAACGAGAAAGGCGCTCACAGT      | 100.0%;               | 5709; | DB 19; | 5711;  |
| 301 GTCTTTATATGATGATGATATTAACAAAGAGAGCTTACAAAGAAAGTACGAGATTAGT    | 100.0%;               | 5709; | DB 19; | 5711;  |
| 301 GTCTTTATATGATGATGATATTAACAAAGAGAGCTTACAAAGAAAGTACGAGATTAGT    | 100.0%;               | 5709; | DB 19; | 5711;  |
| 361 AACCTGTTGAAGAGCTATTAATAATCAATTTGCTTTCAAGCTTGAACAGAGTTGAGT     | 100.0%;               | 5709; | DB 19; | 5711;  |
| 361 AACCTGTTGAAGAGCTATTAATAATCAATTTGCTTTCAAGCTTGAACAGAGTTGAGT     | 100.0%;               | 5709; | DB 19; | 5711;  |
| 421 ATGCAAAACAGCTATTAATTTTGCAGAAAGAAATTAATCTCTCCTGAACATTAAGATG    | 100.0%;               | 5709; | DB 19; | 5711;  |
| 421 ATGCAAAACAGCTATTAATTTTGCAGAAAGAAATTAATCTCTCCTGAACATTAAGATG    | 100.0%;               | 5709; | DB 19; | 5711;  |
| 481 AAGTTTCTATCATCCAAAGATAGGGCTACAGAAACCGTGCAGAAAGAAAGTCTTACAGAGT | 100.0%;               | 5709; | DB 19; | 5711;  |
| 481 AAGTTTCTATCATCCAAAGATAGGGCTACAGAAACCGTGCAGAAAGAAAGTCTTACAGAGT | 100.0%;               | 5709; | DB 19; | 5711;  |
| 541 AACCCGAAATCTCTTCTTGCAGAAACAGAGTCTCAGTGTCAACTCTTACCTTGGAA      | 100.0%;               | 5709; | DB 19; | 5711;  |
| 541 AACCCGAAATCTCTTCTTGCAGAAACAGAGTCTCAGTGTCAACTCTTACCTTGGAA      | 100.0%;               | 5709; | DB 19; | 5711;  |
| 601 CTGTGAGAACTCTGAGAGCAAGAGGAGTATCAACTCAAAAGACGCTGTGTCTACATTG    | 100.0%;               | 5709; | DB 19; | 5711;  |
| 601 CTGTGAGAACTCTGAGAGCAAGAGGAGTATCAACTCAAAAGACGCTGTGTCTACATTG    | 100.0%;               | 5709; | DB 19; | 5711;  |
| 661 AATTTGGATCTGATTTCTTGAAGATACCGTTAATAAGCACTTATTTGCAAGTGTGGAG    | 100.0%;               | 5709; | DB 19; | 5711;  |
| 661 AATTTGGATCTGATTTCTTGAAGATACCGTTAATAAGCACTTATTTGCAAGTGTGGAG    | 100.0%;               | 5709; | DB 19; | 5711;  |

Db 661 AATTGGGATCTGATTTCTTCTGAAGATACCGTTTATTAAGCACTTATTCAGATGTGGAG 720  
Qy 721 ATCAAGAAATGTTTACAAATCAACCCCTCAAGAAACAGGATGAATCAGTTGGATTCTG 780  
Db 721 ATCAAGAAATGTTTACAAATCAACCCCTCAAGAAACAGGATGAATCAGTTGGATTCTG 780  
Qy 781 CAAAAAGGCTGCTTGTGAATTTTCTGAGACGAGATGAACAAATCTGAACATCATCAAC 840  
Db 781 CAAAAAGGCTGCTTGTGAATTTTCTGAGACGAGATGAACAAATCTGAACATCATCAAC 840  
Qy 841 CCAGTAATATGATTTTGAACAACCTGAGAACGCTGACGCTGAGAGGCAATCCAGAAAGT 900  
Db 841 CCAGTAATATGATTTTGAACAACCTGAGAACGCTGACGCTGAGAGGCAATCCAGAAAGT 900  
Qy 901 ATCAGGGTATGTTCTGTTTCAAACTTGATGTGAGCCATGTGGCAAAATCTCATGCCA 960  
Db 901 ATCAGGGTATGTTCTGTTTCAAACTTGATGTGAGCCATGTGGCAAAATCTCATGCCA 960  
Qy 961 GCTGATTACAGATGAGAACAGCAGTTTATTACTGCTAAGACAGAAATGATGAGAA 1020  
Db 961 GCTGATTACAGATGAGAACAGCAGTTTATTACTGCTAAGACAGAAATGATGAGAA 1020  
Qy 1021 AGGCTGAATTTCTGTAATTAACCAACAGCTGCTGCTTACGAAAGAGCCAACTAACAGAT 1080  
Db 1021 AGGCTGAATTTCTGTAATTAACCAACAGCTGCTGCTTACGAAAGAGCCAACTAACAGAT 1080  
Qy 1081 GGGCTGCAAGTACGAAACATGTAATGATAGCGGCACTCCGACACAGAAAAAAGGTG 1140  
Db 1081 GGGCTGCAAGTACGAAACATGTAATGATAGCGGCACTCCGACACAGAAAAAAGGTG 1140  
Qy 1141 ATCTGAATGCTGATCCCTGCTGAGAGAAAGAAATGGAATAGCAGAACTGCCATGCT 1200  
Db 1141 ATCTGAATGCTGATCCCTGCTGAGAGAAAGAAATGGAATAGCAGAACTGCCATGCT 1200  
Qy 1201 CAGAGAACTCTAGAGATCTGAAAGATGTTCTTGATTAACATAATAGCAGATTTACA 1260  
Db 1201 CAGAGAACTCTAGAGATCTGAAAGATGTTCTTGATTAACATAATAGCAGATTTACA 1260  
Qy 1261 AAGTTAATGATGCTTTCCAGAAAGTGAACCTGTAGGTTCTGATGACTCATGAGGCTTTAA 1320  
Db 1261 AAGTTAATGATGCTTTCCAGAAAGTGAACCTGTAGGTTCTGATGACTCATGAGGCTTTAA 1320  
Qy 1321 GGGAGTCTGAATCAAAATGCAAGTAGCTGATGATGAGACGTTCTAAATGAGGTATG 1380  
Db 1321 GGGAGTCTGAATCAAAATGCAAGTAGCTGATGATGAGACGTTCTAAATGAGGTATG 1380  
Qy 1381 AATAATCTGTTCTTCAAGAAAAATGACTTACTGCGCAGTATCCTCATGAGGCTTTAA 1440  
Db 1381 AATAATCTGTTCTTCAAGAAAAATGACTTACTGCGCAGTATCCTCATGAGGCTTTAA 1440  
Qy 1441 TATGTAAAGTGAAGAGTCTCCAAATCAGTAGAGTAATTTGAAGAATAAATAT 1500  
Db 1441 TATGTAAAGTGAAGAGTCTCCAAATCAGTAGAGTAATTTGAAGAATAAATAT 1500  
Qy 1501 TTGGGAAAAACCTATCGGAAGAGGCAAGGCTCCCACTTAAGCCATGTAACGAAATC 1560  
Db 1501 TTGGGAAAAACCTATCGGAAGAGGCAAGGCTCCCACTTAAGCCATGTAACGAAATC 1560  
Qy 1561 TAAATTAAGAGACTTTGTTACTGAGCCACAGATAATACAGAGCGTCCCTCACAAAT 1620  
Db 1561 TAAATTAAGAGACTTTGTTACTGAGCCACAGATAATACAGAGCGTCCCTCACAAAT 1620  
Qy 1621 AATTAAAGCTTAAAGAGAGACTACATCAGGCTTCTCATCTGAGATTTTATCAGAAAG 1680  
Db 1621 AATTAAAGCTTAAAGAGAGACTACATCAGGCTTCTCATCTGAGATTTTATCAGAAAG 1680  
Qy 1681 CAGATTTGGCAGTTCAAAAAGATCTCTGAAATGATTAATCAGGAACTAACCAAGGAGC 1740  
Db 1681 CAGATTTGGCAGTTCAAAAAGATCTCTGAAATGATTAATCAGGAACTAACCAAGGAGC 1740  
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Db 1741 AGAATGTCAAGTATGATTAATTAATAGTGTGATGAGATAAACAAGGTGAT 1800  
Db 1741 AGAATGTCAAGTATGATTAATTAATAGTGTGATGAGATAAACAAGGTGAT 1800  
Qy 1801 CTATTCAGAAATGAGAAAAATCTTAACCAATAGATCACTCGAATAAAGAAATCTCTTCA 1860  
Db 1801 CTATTCAGAAATGAGAAAAATCTTAACCAATAGATCACTCGAATAAAGAAATCTCTTCA 1860  
Qy 1861 AAACGAAAGCTGAACCTTAATAGCAGAGATTAACCAATATGAACTCGAATTAATATCC 1920  
Db 1861 AAACGAAAGCTGAACCTTAATAGCAGAGATTAACCAATATGAACTCGAATTAATATCC 1920  
Qy 1921 ACAATTTCAAAAGCACTTAAAGAAATAGGCTGAGAGAGAACTCTTCAACGAGCATATTC 1980  
Db 1921 ACAATTTCAAAAGCACTTAAAGAAATAGGCTGAGAGAGAACTCTTCAACGAGCATATTC 1980  
Qy 1981 ATGGCTTGAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2040  
Db 1981 ATGGCTTGAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2040  
Qy 2041 TTGATAGTGTCTCTAGCAGTGAAGATTAAGAAAAAAGTACAAACCAATATGCAATGCA 2100  
Db 2041 TTGATAGTGTCTCTAGCAGTGAAGATTAAGAAAAAAGTACAAACCAATATGCAATGCA 2100  
Qy 2101 GGCACAGCAAAACCTTACACTCATGAGAGTAAAGAACTTGCAACTGAGCCAAAGAGA 2160  
Db 2101 GGCACAGCAAAACCTTACACTCATGAGAGTAAAGAACTTGCAACTGAGCCAAAGAGA 2160  
Qy 2161 GTTAAACGCAAAATGAACAGCAAGTAAAGAAAGATGACAGTATCTTCCAGAGCTGA 2220  
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Qy 2281 TTGTCAATCTTACCTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2340  
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Qy 2341 CTAAATATGCTGAAG 2400  
Db 2341 CTAAATATGCTGAAG 2400  
Qy 2401 AAAGATCTGTAG 2460  
Db 2401 AAAGATCTGTAG 2460  
Qy 2461 AAAGATCTGTAG 2520  
Db 2461 AAAGATCTGTAG 2520  
Qy 2521 GTGTAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 2580  
Db 2521 GTGTAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 2580  
Qy 2581 ATAAATGAATGACACAG 2640  
Db 2581 ATAAATGAATGACACAG 2640  
Qy 2641 GGGAAACAGAGATGAGAAATGAGAAAGTGAACCTGATGCTCAATATTTGAGAAATCAT 2700  
Db 2641 GGGAAACAGAGATGAGAAATGAGAAAGTGAACCTGATGCTCAATATTTGAGAAATCAT 2700  
Qy 2701 TCAAGGTTTCAAGAGGAG 2760  
Db 2701 TCAAGGTTTCAAGAGGAG 2760  
Qy 2761 AATGTGCAAACTTCTGAG 2820  
Db 2761 AATGTGCAAACTTCTGAG 2820  
Qy 2821 TTGAATGTGAACAAAG 2880  
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 QY 2941 ATGCCAATGTATATCAAGAGAGCTTCTGTGTGTGTGTGAGAAAGATTAAGCCAGTTGAT 3000  
 DB 2941 ATGCCAATGTATATCAAGAGAGCTTCTGTGTGTGTGTGAGAAAGATTAAGCCAGTTGAT 3000  
 QY 3001 AGCAATGTATATCAAGAGAGCTTCTGTGTGTGTGTGAGAAAGATTAAGCCAGTTGAT 3060  
 DB 3001 AGCAATGTATATCAAGAGAGCTTCTGTGTGTGTGTGAGAAAGATTAAGCCAGTTGAT 3060  
 QY 3061 CACCACTTTTCCCATCAAGTCAATTTGTTAAATGTAAGAAATCTGCTAGAG 3120  
 DB 3061 CACCACTTTTCCCATCAAGTCAATTTGTTAAATGTAAGAAATCTGCTAGAG 3120  
 QY 3121 AAAACTTTGAGAGAACTTCAATGTCACTGAAAGAGAAATGGAAATGAGAACTTCCA 3180  
 DB 3121 AAAACTTTGAGAGAACTTCAATGTCACTGAAAGAGAAATGGAAATGAGAACTTCCA 3180  
 QY 3181 GTACAGTGAAGCAATTAAGCCGTAATTAATTAAGAAATGTTTAAAGAGCCAGCT 3240  
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 QY 3241 CAAAGCAATTTAAATGAAGTGTCCAGTACTAATGAAGTGGCTCCAGTAAATGAA 3300  
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 QY 3661 TCCAGAGAGAGAGCTTACAGAGAGTCTAGCCCTTCAACCATACATTTGGCTCAG 3720  
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 QY 3721 GTTACCGAAGAGGCGCAAGAAATTAAGTCTCAGAGAGAACTTATCTAGTGAAG 3780  
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 DB 3781 AAGAGCTTCCCTGCTTCAACACTTGTATTTGGTAAAGTAAATATACCTTCACT 3840  
 QY 3841 CTACTAGGAGATAGCACTGTTGCTACCGAGTGTCTGTAAAGAACAGAGAGAAATTTAT 3900  
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 DB 3901 TATCATTTGAAGAAATGCTTAATGATGAGTAAACAGGATTAATTTGGCAAGGCACTTC 3960

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 DB 3961 AGCAATCATCCTTATAGTGAAGAAACAAATGTTCTAGTCTGTTCTTCCAGTGA 4020  
 QY 4021 GTGAATTTGAAGACTTGAAGTGAAGAAATTAAGCAAGCCAGATCTTCTGATTTGTTCTT 4080  
 DB 4021 GTGAATTTGAAGACTTGAAGTGAAGAAATTAAGCAAGCCAGATCTTCTGATTTGTTCTT 4080  
 QY 4081 CCAAAATTAAGAGGCTTCAAGTGAAGAGGAGGAGTGTGATGATGATGATGATGATG 4140  
 DB 4081 CCAAAATTAAGAGGCTTCAAGTGAAGAGGAGGAGTGTGATGATGATGATGATGATG 4140  
 QY 4141 TTTCAATGATGAAGAAAGAGAAAGGAGGAGTGTGATGATGATGATGATGATGATG 4200  
 DB 4141 TTTCAATGATGAAGAAAGAGAAAGGAGGAGTGTGATGATGATGATGATGATGATG 4200  
 QY 4201 TGGATTTAAATTTAGTGAAGAGCACTTGGTGTGAGTGAAGTGAAGTGAAGTGAAG 4260  
 DB 4201 TGGATTTAAATTTAGTGAAGAGCACTTGGTGTGAGTGAAGTGAAGTGAAGTGAAG 4260  
 QY 4261 ACTGCTCAGAGGCTTATCTCTCAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 4320  
 DB 4261 ACTGCTCAGAGGCTTATCTCTCAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 4320  
 QY 4321 AACATTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 4380  
 DB 4321 AACATTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 4380  
 QY 4381 ATGGAAGCCAGGCTTCTTAACAGTCACTTCCATCATTAAGTGAAGTGAAGTGAAG 4440  
 DB 4381 ATGGAAGCCAGGCTTCTTAACAGTCACTTCCATCATTAAGTGAAGTGAAGTGAAG 4440  
 QY 4441 ACCGAGGAAATCCAGAAACAAAGCAATGAGAAAGCAATTTAACTTACAGAAAGT 4500  
 DB 4441 ACCGAGGAAATCCAGAAACAAAGCAATGAGAAAGCAATTTAACTTACAGAAAGT 4500  
 QY 4501 GTGAATTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 4560  
 DB 4501 GTGAATTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 4560  
 QY 4561 CAGATGATTTCTACAGTAAATTAAGAAACAGAGTGAAGTGAAGTGAAGTGAAGTGAAG 4620  
 DB 4561 CAGATGATTTCTACAGTAAATTAAGAAACAGAGTGAAGTGAAGTGAAGTGAAGTGAAG 4620  
 QY 4621 GGCATCATTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 4680  
 DB 4621 GGCATCATTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 4680  
 QY 4681 ACTACCATCTCAAGAGAGCTCATTAAGGTTGTTGATGAGAGGCAAGAGTGAAG 4740  
 DB 4681 ACTACCATCTCAAGAGAGCTCATTAAGGTTGTTGATGAGAGGCAAGAGTGAAG 4740  
 QY 4741 AGTGTGGGCAAGATTTGAGAGAAATCTTACTTGTGCAAGGCAAGATCTAGAGGAA 4800  
 DB 4741 AGTGTGGGCAAGATTTGAGAGAAATCTTACTTGTGCAAGGCAAGATCTAGAGGAA 4800  
 QY 4801 CCCCTTACTGGAATCTGGAATCAGCTTCTGATGAGAGGCTGATGATGATGATGATG 4860  
 DB 4801 CCCCTTACTGGAATCTGGAATCAGCTTCTGATGAGAGGCTGATGATGATGATGATG 4860  
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 DB 4861 AAGAGAGAGCCAGAGTCAAGTCTGTTGAGCAATACATCTTCAACCTCTGATGA 4920  
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 DB 4921 AAGTTCCTCAATTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 4980  
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 DB 4981 ATACTGCTGGGATTAATCAATGAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 5040  
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Db 5041 CTTACAGAGAGAGGTCAACAAAGATGTCATGTTGCTGCGCCAGACCCAGAG 5100  
QY 5101 AATTTATGCTGCTGACAGTTTGCAGAAAACACCACTCACTTAATCTAATTA 5160  
Db 5101 AATTTATGCTGCTGACAGTTTGCAGAAAACACCACTCACTTAATCTAATTA 5160  
QY 5161 CTGAGAGACTACTGATGTTGTTATGAAAACAGATGCTGAGTTGTTGTTGTAACGGAC 5220  
Db 5161 CTGAGAGACTACTGATGTTGTTATGAAAACAGATGCTGAGTTGTTGTTGTAACGGAC 5220  
QY 5221 TGAATATATTTCTAGAAATGCGGAGAGAAAATGGGTAGTATTTCTGGTGACCC 5280  
Db 5221 TGAATATATTTCTAGAAATGCGGAGAGAAAATGGGTAGTATTTCTGGTGACCC 5280  
QY 5281 AGTCTATTAAGAAAGAAAATGCTGAATGACATGATTTTGAAGTCAGAGAGATGTG 5340  
Db 5281 AGTCTATTAAGAAAGAAAATGCTGAATGACATGATTTTGAAGTCAGAGAGATGTG 5340  
QY 5341 TCAATGAGAGAAACCAAGGTCCAAAGCGAGCAAGAAATCCAGAGCAGAAAGATCT 5400  
Db 5341 TCAATGAGAGAAACCAAGGTCCAAAGCGAGCAAGAAATCCAGAGCAGAAAGATCT 5400  
QY 5401 TCAGGGGGCTAGAAATCTGTGCTATGCGCCCTTCACCAACATGCCACAGATCAACTGG 5460  
Db 5401 TCAGGGGGCTAGAAATCTGTGCTATGCGCCCTTCACCAACATGCCACAGATCAACTGG 5460  
QY 5461 AATGATGCTACAGCTGTGTGCTTCTGTGTGTAAGAGCTTTCATCTATTCACCCCTTG 5520  
Db 5461 AATGATGCTACAGCTGTGTGCTTCTGTGTGTAAGAGCTTTCATCTATTCACCCCTTG 5520  
QY 5521 GCACAGGTGTCACCCCAATTTGTTGTGACAGCCAGATGCTGACAGAGACAATGGCT 5580  
Db 5521 GCACAGGTGTCACCCCAATTTGTTGTGACAGCCAGATGCTGACAGAGACAATGGCT 5580  
QY 5581 TCCATGCAATTTGGGAGATGTGTGAGGCACTGTGTGTGACCCGAGAGTGGTGTGACA 5640  
Db 5581 TCCATGCAATTTGGGAGATGTGTGAGGCACTGTGTGTGACCCGAGAGTGGTGTGACA 5640  
QY 5641 GTGTAGCACTCTACAGAGTCCAGAGCTGAGACACCTACCTGATACCCAGATCCCCCA 5700  
Db 5641 GTGTAGCACTCTACAGAGTCCAGAGCTGAGACACCTACCTGATACCCAGATCCCCCA 5700  
QY 5701 GCCACTACTGA 5711  
Db 5701 GCCACTACTGA 5711

Search completed: June 13, 2003, 00:36:15  
Job time : 1122 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 12, 2003, 23:59:20 ; Search time 720.5 Seconds  
(without alignments)  
11477.967 Million cell updates/sec

Title: US-09-734-672-3

Perfect score: 5711  
Sequence: 1 AGCTCGCTGAGACTTCTCTG9.....TCCCCGACGCACTACTGA 5711

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 1029858 seqs, 724030393 residues

Total number of hits satisfying chosen parameters: 2059716

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

Published Applications NA:  
1: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq:\*  
2: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq:\*  
3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*  
4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq:\*  
5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*  
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13: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*  
14: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score  | Query Match | Length | ID | Description         |
|------------|--------|-------------|--------|----|---------------------|
| 1          | 5711   | 100.0       | 5711   | 9  | US-09-734-672-3     |
| 2          | 5711   | 100.0       | 5711   | 9  | US-09-982-828-5     |
| 3          | 5703   | 99.9        | 5711   | 9  | US-09-734-672-5     |
| 4          | 5703   | 99.9        | 5711   | 9  | US-09-982-828-3     |
| 5          | 5703   | 99.9        | 5711   | 9  | US-10-022-819-1     |
| 6          | 5701.4 | 99.8        | 5711   | 9  | US-09-734-672-1     |
| 7          | 5701.4 | 99.8        | 5711   | 9  | US-09-982-828-1     |
| 8          | 364.6  | 6.4         | 499    | 9  | US-09-911-904-127   |
| 9          | 175.4  | 3.1         | 424    | 10 | US-09-864-761-4552  |
| 10         | 147    | 2.6         | 147    | 10 | US-09-864-761-21299 |
| 11         | 121    | 2.1         | 121    | 9  | US-09-818-875-653   |
| 12         | 121    | 2.1         | 121    | 9  | US-09-818-875-654   |
| 13         | 121    | 2.1         | 121    | 9  | US-09-818-875-657   |
| 14         | 121    | 2.1         | 121    | 9  | US-09-818-875-658   |
| 15         | 121    | 2.1         | 121    | 9  | US-09-818-875-661   |
| 16         | 121    | 2.1         | 121    | 9  | US-09-818-875-662   |
| 17         | 121    | 2.1         | 121    | 9  | US-09-818-875-665   |
| 18         | 121    | 2.1         | 121    | 9  | US-09-818-875-666   |
| 19         | 121    | 2.1         | 121    | 9  | US-09-818-875-669   |

|      |     |     |     |   |                   |                   |
|------|-----|-----|-----|---|-------------------|-------------------|
| C 20 | 121 | 2.1 | 121 | 9 | US-09-818-875-670 | Sequence 670, App |
| C 21 | 121 | 2.1 | 121 | 9 | US-09-818-875-673 | Sequence 673, App |
| C 22 | 121 | 2.1 | 121 | 9 | US-09-818-875-674 | Sequence 674, App |
| C 23 | 121 | 2.1 | 121 | 9 | US-09-818-875-677 | Sequence 677, App |
| C 24 | 121 | 2.1 | 121 | 9 | US-09-818-875-678 | Sequence 678, App |
| C 25 | 121 | 2.1 | 121 | 9 | US-09-818-875-681 | Sequence 681, App |
| C 26 | 121 | 2.1 | 121 | 9 | US-09-818-875-682 | Sequence 682, App |
| C 27 | 121 | 2.1 | 121 | 9 | US-09-818-875-685 | Sequence 685, App |
| C 28 | 121 | 2.1 | 121 | 9 | US-09-818-875-686 | Sequence 686, App |
| C 29 | 121 | 2.1 | 121 | 9 | US-09-818-875-689 | Sequence 689, App |
| C 30 | 121 | 2.1 | 121 | 9 | US-09-818-875-690 | Sequence 690, App |
| C 31 | 121 | 2.1 | 121 | 9 | US-09-818-875-693 | Sequence 693, App |
| C 32 | 121 | 2.1 | 121 | 9 | US-09-818-875-694 | Sequence 694, App |
| C 33 | 121 | 2.1 | 121 | 9 | US-09-818-875-697 | Sequence 697, App |
| C 34 | 121 | 2.1 | 121 | 9 | US-09-818-875-698 | Sequence 698, App |
| C 35 | 121 | 2.1 | 121 | 9 | US-09-818-875-701 | Sequence 701, App |
| C 36 | 121 | 2.1 | 121 | 9 | US-09-818-875-702 | Sequence 702, App |
| C 37 | 121 | 2.1 | 121 | 9 | US-09-818-875-705 | Sequence 705, App |
| C 38 | 121 | 2.1 | 121 | 9 | US-09-818-875-706 | Sequence 706, App |
| C 39 | 121 | 2.1 | 121 | 9 | US-09-818-875-709 | Sequence 709, App |
| C 40 | 121 | 2.1 | 121 | 9 | US-09-818-875-710 | Sequence 710, App |
| C 41 | 121 | 2.1 | 121 | 9 | US-09-818-875-713 | Sequence 713, App |
| C 42 | 121 | 2.1 | 121 | 9 | US-09-818-875-714 | Sequence 714, App |
| C 43 | 121 | 2.1 | 121 | 9 | US-09-818-875-717 | Sequence 717, App |
| C 44 | 121 | 2.1 | 121 | 9 | US-09-818-875-718 | Sequence 718, App |
| C 45 | 121 | 2.1 | 121 | 9 | US-09-818-875-721 | Sequence 721, App |

#### ALIGNMENTS

RESULT 1  
US-09-734-672-3  
Sequence 3, Application US/09734672  
Publication No. US20020183268A1  
GENERAL INFORMATION:  
APPLICANT: Murphy, Patricia D.  
Allen, Antonette C.  
Alvares, Christopher P.  
Critz, Brenda S.  
Olson, Sheri J.  
Schelter, Denise B.  
Zeng, Bin  
TITLE OF INVENTION: Coding Sequences of the Human  
BRCA1 Gene  
NUMBER OF SEQUENCES: 72  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Morgan Lewis & Bockius LLP  
STREET: 1111 Pennsylvania Ave., N.W.  
CITY: Washington  
STATE: District of Columbia  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/734,672  
FILING DATE: 03-Dec-2000  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/966,436  
FILING DATE: 07-NO. US20020183268A1-97  
APPLICATION NUMBER: US 08/598,591  
FILING DATE: 12-Feb-96  
ATTORNEY/AGENT INFORMATION:  
NAME: Michael S. Tuscan  
REGISTRATION NUMBER: 43,210  
REFERENCE/DOCKET NUMBER: 44921-5055-02-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-739-3000  
TELEFAX: 202-739-3001

INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5711 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: No. US20020183268A1 Relevant  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
STRAIN: BRCA1  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: 17  
MAP POSITION: 17q21  
SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
us-09-734-672-3

Query Match 100.0%; Score 5711; DB 9; Length 5711;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 5711; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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1 AGCTGGCTGAGACTCTCTGGAGACCCGACAGGCTGTGGGTTCTCAGATACGTGGCC 60  
61 CCTGGCTCAGAGAGGCTTCACTCTGCTGGTAAAGTTCAATGGAACAGAAAGAA 120  
61 CCTGGCTCAGAGAGGCTTCACTCTGCTGGTAAAGTTCAATGGAACAGAAAGAA 120  
121 TGGATTTATCTGCTCTTCCGCTTGAAGAAAGTCAAAATGTCAATTAATGCTATGCAAAA 180  
121 TGGATTTATCTGCTCTTCCGCTTGAAGAAAGTCAAAATGTCAATTAATGCTATGCAAAA 180  
181 TCTTGAAGTCCCATCTGTCTGGAGTGTATCAAGAAACCTGTCTCAACAAAGTGGACC 240  
181 TCTTGAAGTCCCATCTGTCTGGAGTGTATCAAGAAACCTGTCTCAACAAAGTGGACC 240  
241 ACATATTTTGCAAATTTTGCATGCTGAAACCTTCTCAACAGAGAAAGGCTTTCACAGT 300  
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301 GTCTCTTATGTAAAGATGATATTAACCAAAAGAGCTTCAAGAAAGTGAAGTTTAACT 360  
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361 AACCTGTGAAGAGCTATTTGAAGAAATGATTTGCTTTGAGCTTGAACAGGTTTGAAGT 420  
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661 AATTGGGATCTGATTTCTTGAAGATACCGTTAATAAGCACTTATGCAAGTGGAG 720  
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721 ATCAAGATTTGTAAACATCACCCCTCAAGAAACCGAGATGAAATCAGTTGGATTCG 780  
721 ATCAAGATTTGTAAACATCACCCCTCAAGAAACCGAGATGAAATCAGTTGGATTCG 780  
781 CAAAAAGGCTGCTTGTGAATTTTCTGAGACGAGATGTAACAAATACGAAACATCATCAAC 840

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841 CCAGTAATATATTTTGAACACCACTGAGAAAGCTGAGCTGAGAGGATCACAAAAGT 900  
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901 ATCAGGATGTTCTGTTTCAAACTGATGAGCCATGTGGCAAAATATCTATGCA 960  
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961 GCTCATTAACAGATGAGAAACAGCACTTATTAATCACTAAGAGAGATGATGAGAA 1020  
961 GCTCATTAACAGATGAGAAACAGCACTTATTAATCACTAAGAGAGATGATGAGAA 1020  
1021 AGGCTGAATTTCTGTATTAAGCAACAGCTGGCTTGAAGAGAGCCCAATATACAT 1080  
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1081 GGGCTGGAAGTAAAGAAACATGTATGATAGGCGACTCCAGCAGACAGAAAAAAGTAG 1140  
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1261 AAGTTAATGAGTGTCTTCCAGAGTGAATGATGTTAGTTCTGATGACTCACATGATG 1320  
1261 AAGTTAATGAGTGTCTTCCAGAGTGAATGATGTTAGTTCTGATGACTCACATGATG 1320  
1321 GGGAGTCTGAATCAATCCAAAGTAGCTGATGATTTGAGAGCTTCAATGAGTAGTG 1380  
1321 GGGAGTCTGAATCAATCCAAAGTAGCTGATGATTTGAGAGCTTCAATGAGTAGTG 1380  
1381 AATATTCGCTCTTCAAGAGAAATGAGCTTACGAGTGTGATGAGCTTCAATGAGTAGTG 1440  
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1621 AATTAAAGGCTAAAGAGACCTTACATCAGGCTTCACTGAGAGATTTTATCAAGAAAG 1680  
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1801 CTATTCAAGATGAGAAATATCTTAACCAATAGATCACTGAGAAAGAAATCTGCTTCA 1860  
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1861 AAACGAAAGCTGAACCTTAATGAGCAGAGATTAAGCAATATGAACTCGAATTAATATCC 1920  
1861 AAACGAAAGCTGAACCTTAATGAGCAGAGATTAAGCAATATGAACTCGAATTAATATCC 1920



|    |      |   |      |
|----|------|---|------|
| Db | 1861 | AAACGAAAGCTGACCTTAAGCAGACGATATAGCAATATGTGAATCTGAAATTTAAATATCC     | 1920 |
| Qy | 1921 | ACAATTTCAAAAGCACCTTAATAAAAGATAGCGTGAGGAGAGCTTTCTACAGCAATATTC      | 1980 |
| Db | 1921 | ACAAATTTCAAAAGCACCTTAATAAAAGATAGCGTGAGGAGAGCTTTCTACAGCAATATTC     | 1980 |
| Qy | 1981 | ATGGCCTTGAACCTACTAGTCACTAGTAATAATCTTAAGCCACCTTAATTGTACTGAATTGGCAA | 2040 |
| Db | 1981 | ATGGCCTTGAACCTACTAGTCACTAGTAATAATCTTAAGCCACCTTAATTGTACTGAATTGGCAA | 2040 |
| Qy | 2041 | TTGATAGTTGGTCTCTGACAGTGAAGATTAAGAAAAAAAAGTACCAACAAATGCGACGCA      | 2100 |
| Db | 2041 | TTGATAGTTGGTCTCTGACAGTGAAGATTAAGAAAAAAAAGTACCAACAAATGCGACGCA      | 2100 |
| Qy | 2101 | GGCACAGACAGAAACCTACAACTCATGGAAGGTAAAGAAACCTGCACTGAGCCAAAGAGA      | 2160 |
| Db | 2101 | GGCACAGACAGAAACCTACAACTCATGGAAGGTAAAGAAACCTGCACTGAGCCAAAGAGA      | 2160 |
| Qy | 2161 | GTAACAAAGCCAAATGTAACAGACAGTAATAAAGACATGACAGGATTCCTTCCAGAGCTGA     | 2220 |
| Db | 2161 | GTAACAAAGCCAAATGTAACAGACAGTAATAAAGACATGACAGGATTCCTTCCAGAGCTGA     | 2220 |
| Qy | 2221 | AGTTAAACAAAGCACCTGCTGTTCTTTACTAAGTGTCAAAATACAGATGAACCTTAAGAT      | 2280 |
| Db | 2221 | AGTTAAACAAAGCACCTGCTGTTCTTTACTAAGTGTCAAAATACAGATGAACCTTAAGAT      | 2280 |
| Qy | 2281 | TTGTCAATCTAGACCTTCCAAAGAGAAAAAGAAAGAAACGTAGAAACAGTTAAAGAT         | 2340 |
| Db | 2281 | TTGTCAATCTAGACCTTCCAAAGAGAAAAAGAAAGAAACGTAGAAACAGTTAAAGAT         | 2340 |
| Qy | 2341 | CTAATTAATGCTGAAGACCCCAAAGATCTCATGTTAAGTGAAGAAAGGTTTTGGCAACTG      | 2400 |
| Db | 2341 | CTAATTAATGCTGAAGACCCCAAAGATCTCATGTTAAGTGAAGAAAGGTTTTGGCAACTG      | 2400 |
| Qy | 2401 | AAAGATCTGTAGAGGTAGAGTGAAGTATTTCAATGTGTACTGTATACGATTAATGGCACTCAGG  | 2460 |
| Db | 2401 | AAAGATCTGTAGAGGTAGAGTGAAGTATTTCAATGTGTACTGTATACGATTAATGGCACTCAGG  | 2460 |
| Qy | 2461 | AAAGTATCTCGTTACTGTGAAGTTAGCACTTAGAGGAAGGCAAAAAACAGAACCAATTAAT     | 2520 |
| Db | 2461 | AAAGTATCTCGTTACTGTGAAGTTAGCACTTAGAGGAAGGCAAAAAACAGAACCAATTAAT     | 2520 |
| Qy | 2521 | GTGTGAGTCAAGTGTGACAGATTTTGAAACCCCAAGGAGCAATTAATCATGTTGTTCCAAAG    | 2580 |
| Db | 2521 | GTGTGAGTCAAGTGTGACAGATTTTGAAACCCCAAGGAGCAATTAATCATGTTGTTCCAAAG    | 2580 |
| Qy | 2581 | ATTAATAGAAATGACACAGAAAGGCTTTAGTATCCATTGGGACATGAAGTTAACCAAGCTC     | 2640 |
| Db | 2581 | ATTAATAGAAATGACACAGAAAGGCTTTAGTATCCATTGGGACATGAAGTTAACCAAGCTC     | 2640 |
| Qy | 2641 | GGGAAACACAGCATAGAAATGGAAGAAATGTGAATCTGATGCTCAGATTTTGGAGAAATCAT    | 2700 |
| Db | 2641 | GGGAAACACAGCATAGAAATGGAAGAAATGTGAATCTGATGCTCAGATTTTGGAGAAATCAT    | 2700 |
| Qy | 2701 | TCAAAGTTTCAAAGGCGCAGTCAATTGCTCTGTTTCAAATCCAGAAATCCAGAAAGG         | 2760 |
| Db | 2701 | TCAAAGTTTCAAAGGCGCAGTCAATTGCTCTGTTTCAAATCCAGAAATCCAGAAAGG         | 2760 |
| Qy | 2761 | AATGTGCAACATCTCTGCGCCACTCTGGGTCTTTAAAGAAACAAAGTCCAAAGTCACTT       | 2820 |
| Db | 2761 | AATGTGCAACATCTCTGCGCCACTCTGGGTCTTTAAAGAAACAAAGTCCAAAGTCACTT       | 2820 |
| Qy | 2821 | TTGAATGTGAACAAAGAGAAAGAAATCAAGGAAAGAAATGAAGTCTTAATTCAGGCTGTAC     | 2880 |
| Db | 2821 | TTGAATGTGAACAAAGAGAAAGAAATCAAGGAAAGAAATGAAGTCTTAATTCAGGCTGTAC     | 2880 |
| Qy | 2881 | AGACAGTTAATATCACTGACAGCTTCTCTGTGTGTGATCAGAAAGATTAAGCCAGTTGATA     | 2940 |
| Db | 2881 | AGACAGTTAATATCACTGACAGCTTCTCTGTGTGTGATCAGAAAGATTAAGCCAGTTGATA     | 2940 |
| Qy | 2941 | ATGCCAAATGTATGATCAAAAGAGGCTCTAGGTTTGTCTATCATCTCACTTCAGAGCA        | 3000 |
| Db | 2941 | ATGCCAAATGTATGATCAAAAGAGGCTCTAGGTTTGTCTATCATCTCACTTCAGAGCA        | 3000 |

|    |      |             |                        |                            |                          |      |
|----|------|-------------|------------------------|----------------------------|--------------------------|------|
| QY | 3001 | ACGAACCTGGA | CTATTACTCCAAATAAC      | TGACCTTTTACAAACCCATATG     | GTATAC                   | 3065 |
| Db | 3001 | ACGAACCTGGA | CTCATTACTCCAAATAAC     | TGACCTTTTACAAACCCATATG     | GTATAC                   | 3066 |
| QY | 3061 | CACCACTTTT  | CCCATCAAGTCATTGGTTAA   | AAATGTAAAGAAATCTG          | CTAGAGG                  | 3120 |
| Db | 3061 | CACCACTTTT  | CCCATCAAGTCATTGGTTAA   | AAATGTAAAGAAATCTG          | CTAGAGG                  | 3120 |
| QY | 3121 | AAAACCTT    | GAGAACATTC             | CAATGTCACTGAAAGAAATG       | GGAAATGAGAACATTTCCAA     | 3180 |
| Db | 3121 | AAAACCTT    | GAGAACATTC             | CAATGTCACTGAAAGAAATG       | GGAAATGAGAACATTTCCAA     | 3180 |
| QY | 3181 | GTACGTGAG   | CAACATTAGCCGTATATAC    | TTAGAGAAATGTTTTTAAGAGCCACT |                          | 3240 |
| Db | 3181 | GTACGTGAG   | CAACATTAGCCGTATATAC    | TTAGAGAAATGTTTTTAAGAGCCACT |                          | 3240 |
| QY | 3241 | CAGCAATATT  | TAATGAACTAGGTTCCAGTACT | AATGAAATGGGCTCCAGTATTA     | TGAAA                    | 3300 |
| Db | 3241 | CAGCAATATT  | TAATGAACTAGGTTCCAGTACT | AATGAAATGGGCTCCAGTATTA     | TGAAA                    | 3300 |
| QY | 3301 | TAGGTTCC    | AGTATGAAAAACATTC       | ACAGAGAACTTGTATGAAAACAGAGG | CCAAATTTGA               | 3360 |
| Db | 3301 | TAGGTTCC    | AGTATGAAAAACATTC       | ACAGAGAACTTGTATGAAAACAGAGG | CCAAATTTGA               | 3360 |
| QY | 3361 | ATGCTATCT   | TAGATTAGGGGTTTTTGCA    | CCCTGAGGCTTATTAACAAAGTCTT  | CCCTGGA                  | 3420 |
| Db | 3361 | ATGCTATCT   | TAGATTAGGGGTTTTTGCA    | CCCTGAGGCTTATTAACAAAGTCTT  | CCCTGGA                  | 3420 |
| QY | 3421 | GTAAATTG    | TAGCATCTGAAATTA        | AAAAAGCAAAATATGAAGAACTT    | CAGCTGTA                 | 3480 |
| Db | 3421 | GTAAATTG    | TAGCATCTGAAATTA        | AAAAAGCAAAATATGAAGAACTT    | CAGCTGTA                 | 3480 |
| QY | 3481 | ATACAGATTT  | CTCTCCATATCTGATTTG     | AGATACTTAGAACAGCTAT        | TGAGGAAGTATG             | 3540 |
| Db | 3481 | ATACAGATTT  | CTCTCCATATCTGATTTG     | AGATACTTAGAACAGCTAT        | TGAGGAAGTATG             | 3540 |
| QY | 3541 | ATGCATCT    | CAGGTTGTTCTGAGAC       | ACCTGATGACCTGTATGAT        | GTGATAAATAAGG            | 3600 |
| Db | 3541 | ATGCATCT    | CAGGTTGTTCTGAGAC       | ACCTGATGACCTGTATGAT        | GTGATAAATAAGG            | 3600 |
| QY | 3601 | AAGATACT    | AGATTTTGTCTGAAATAT     | GATACATTAAGGAAAGTTCTG      | CTGTTTTAGCAAAACG         | 3660 |
| Db | 3601 | AAGATACT    | AGATTTTGTCTGAAATAT     | GATACATTAAGGAAAGTTCTG      | CTGTTTTAGCAAAACG         | 3660 |
| QY | 3661 | TCCAGAAAG   | AGAGCTTAGCAGAGAGT      | CCTACCCCTTCA               | CCCATACACATTTGGCTCAGG    | 3720 |
| Db | 3661 | TCCAGAAAG   | AGAGCTTAGCAGAGAGT      | CCTACCCCTTCA               | CCCATACACATTTGGCTCAGG    | 3720 |
| QY | 3721 | GTTACCGA    | AGGGGCCAAGAAATTA       | GAAGTCTTCAGAAAGAGACT       | TATCTATGAGAGT            | 3780 |
| Db | 3721 | GTTACCGA    | AGGGGGCCAAAGAAATTA     | GAAGTCTTCAGAAAGAGACT       | TATCTATGAGAGT            | 3780 |
| QY | 3781 | AAGAGCTT    | CCCTGCTCCACACTTG       | TATTTGGTAAATGAACAAT        | TATACCTCTCAGT            | 3840 |
| Db | 3781 | AAGAGCTT    | CCCTGCTCCACACTTG       | TATTTGGTAAATGAACAAT        | TATACCTCTCAGT            | 3840 |
| QY | 3841 | CTACTAGG    | CAATAGCACCGTGTCTAC     | CGAGTGTCTGTCTA             | AGAACACAGAGAGAAATTA      | 3900 |
| Db | 3841 | CTACTAGG    | CAATAGCACCGTGTCTAC     | CGAGTGTCTGTCTA             | AGAACACAGAGAGAAATTA      | 3900 |
| QY | 3901 | TATCATTT    | GAAGAAATAGCTTAAT       | TGACGTGCAGTAAC             | CAAGTAAATTTGGCAAAAGCATTC | 3960 |
| Db | 3901 | TATCATTT    | GAAGAAATAGCTTAAT       | TGACGTGCAGTAAC             | CAAGTAAATTTGGCAAAAGCATTC | 3960 |
| QY | 3961 | AGGAACAT    | CACTTAGTAGAGAAACAA     | AAATTTTGTCTAGCTTTTCTT      | CAACAGTGCA               | 4020 |
| Db | 3961 | AGGAACAT    | CACTTAGTAGAGAAACAA     | AAATTTTGTCTAGCTTTTCTT      | CAACAGTGCA               | 4020 |
| QY | 4021 | GTGAATTG    | GAAGACTTGACGTCA        | AAATACAAACCCAGAGAT         | CTTTCTTGATTTGGTTCTT      | 4080 |
| Db | 4021 | GTGAATTG    | GAAGACTTGACGTCA        | AAATACAAACCCAGAGAT         | CTTTCTTGATTTGGTTCTT      | 4080 |

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4141 TTTGAGATGATGAAGAAAGAGAAAGGCTTGGAGAAATTAATCAAGAAAGCAAGCA 4200  
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4201 TGGATTCAACTTAGTGAAGAGCATCTGGGCTGAGAGTGAACAACGCTCTGAG 4260  
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5221 TGAATATTTTCTAGGATTTGCGAGAGAAATGGTATGATGATTTTCTGGGTGACC 5280  
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5701 GGCCTACTGA 5711  
5701 GGCCTACTGA 5711

RESULT 2  
US-09-982-828-5  
Sequence 5, Application US/09982828  
Publication No. US20030022184A1  
GENERAL INFORMATION:  
APPLICANT: Murphy, Patricia D.  
Allen, Antoinette C.  
Alvares, Christopher P.  
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Thurber, Denise  
Zeng, Bin  
TITLE OF INVENTION: Coding Sequences of the Human  
NUMBER OF SEQUENCES: 72  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Morgan Lewis & Bockius LLP  
STREET: 1111 Pennsylvania Avenue N. W.  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/982,828  
FILING DATE: 22-Oct-2001  
CLASSIFICATION: <Unknown>  
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APPLICATION NUMBER: US 09/074,453

FILED DATE: 1998-05-06  
APPLICATION NUMBER: US 08/798,691  
FILING DATE: 1997-02-12  
APPLICATION NUMBER: US 08/598,591  
FILING DATE: 1996-02-12  
ATTORNEY/AGENT INFORMATION:  
NAME: Michael S. Tuscan  
REGISTRATION NUMBER: 43,210  
REFERENCE/DOCKET NUMBER: 44921-5053-01-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-739-3000  
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INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5711 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
STRAIN: BRCA1 (om13)  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: 17  
MAP POSITION: 17q21  
SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
US-09-982-828-5

Query Match 100.0%; Score 5711; DB 9; Length 5711;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 5711; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTCGCTGAGACTTCCGTGAGCCCGACAGGCTGTGGGTTTCTCAGATACTGAGCC 60  
DB 1 AGCTCGCTGAGACTTCCGTGAGCCCGACAGGCTGTGGGTTTCTCAGATACTGAGCC 60  
QY 61 CTTGCGCTGAGAGGCGCTTCACTCTGCTGTGGGTTAAAGTTCAATGGAAACAGAAAGAA 120  
DB 61 CTTGCGCTGAGAGGCGCTTCACTCTGCTGTGGGTTAAAGTTCAATGGAAACAGAAAGAA 120  
QY 121 TGGATTATCTGCTCTTCGGGTTGAAAGATACAAAATGCTATTATGCTATGCAAGAAA 180  
DB 121 TGGATTATCTGCTCTTCGGGTTGAAAGATACAAAATGCTATTATGCTATGCAAGAAA 180  
QY 181 TCTTAAGTGTCCCATCTGCTGAGAGTGTATCAAGAACTGTCTCCACAAAGTGTGACC 240  
DB 181 TCTTAAGTGTCCCATCTGCTGAGAGTGTATCAAGAACTGTCTCCACAAAGTGTGACC 240  
QY 241 ACAATATTTTGCAGAAATTTTGCATGCTGAACTTCTCAACAGAAAGAGGCTTTCACAGT 300  
DB 241 ACAATATTTTGCAGAAATTTTGCATGCTGAACTTCTCAACAGAAAGAGGCTTTCACAGT 300  
QY 301 GTCTTTATGTAGATGATATACCAAAAGAGGCTTCAAGAAAGTACAGATTTTATGTC 360  
DB 301 GTCTTTATGTAGATGATATACCAAAAGAGGCTTCAAGAAAGTACAGATTTTATGTC 360  
QY 361 AACTTGTGAAGAGCTATTGAAATCATTTGTGCTTTTTCAGCTTGAACAGGTTTGGAGT 420  
DB 361 AACTTGTGAAGAGCTATTGAAATCATTTGTGCTTTTTCAGCTTGAACAGGTTTGGAGT 420  
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DB 421 ATGCAAAACAGCTAATTTTGCAGAAAGAGAAATATCTCTCTGAACATCTTAAAGATG 480  
QY 481 AATTTTCTATCATCCCAAGATGAGGCTACAGAAACCGTCCAAAGATCTTACAGAGT 540  
DB 481 AATTTTCTATCATCCCAAGATGAGGCTACAGAAACCGTCCAAAGATCTTACAGAGT 540  
QY 541 AACCCGAAATCTTCTCTTGCAGAAACAGCTCTCAGATGCAACTCTTAACTTGAAG 600  
DB 541 AACCCGAAATCTTCTCTTGCAGAAACAGCTCTCAGATGCAACTCTTAACTTGAAG 600  
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DB 601 CTGTGAAACTGTGAGAGCAAAAGCAGGATACAACTCTCAAAAGAGCTGTCTTACATTG 660  
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DB 661 AATTTGATCTGATTTCTTTCGAAAGATACGTTAATAGCAACTTATTTGAGTGTGGAG 720  
QY 721 ATCAAGATTTGTAACAATCACCCCTCAAGAAACAGGAGTAAATCAGTTTGGATCTG 780  
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QY 781 CAAAAAAGCTGCTGTGATTTTCTGACAGGATTAACAAATATCTGAACATCATCAAC 840  
DB 781 CAAAAAAGCTGCTGTGATTTTCTGACAGGATTAACAAATATCTGAACATCATCAAC 840  
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DB 841 CCAGTAAATATATTTTGAACACACAGAGAGGCTGACCTGAGAGGCAATCCGAAAGT 900  
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QY 961 GCTCATTAAGCATGAGAAACAGAGTTTATCTACTAATAAGACAGATGATGAGAA 1020  
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DB 1081 GGGCTGGAAGTAAAGAAACATGTAATGATAGGCGGACTCCAGCACAGAAAAAAGGTAG 1140  
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QY 1381 AATATTTGCTTCTTCAAGAAATATGATTAATGATGATGATGATGATGATGATG 1440  
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DB 1561 TAAATATAGACATTTGTTATGAGCCACATATATACAAAGGCTCCCTCAAGAAAT 1620  
QY 1621 AATTAAGGCTAAAGAGACCTATACAGGCTTCACTGAGATTTTATCAAGAAAG 1680  
DB 1621 AATTAAGGCTAAAGAGACCTATACAGGCTTCACTGAGATTTTATCAAGAAAG 1680  
QY 1681 CAGATTTGAGCTTCAAAAGACTCTGTAATGATTAATGAGGAACTAACCAAGGAGC 1740

Db 1681 CAGATTTGGCAGTTCAAAAAGACTCTCTGAATATGAATAATCAGGGAATAACCAACGAGC 1740  
Qy 1741 AGAATGCTCAAGTGAATGAAATATTAATAAGTGCATAGAAATTAACAAAAGGAGAT 1800  
Db 1741 AGAATGCTCAAGTGAATGAAATATTAATAAGTGCATAGAAATTAACAAAAGGAGAT 1800  
Qy 1801 CTATTCAGAAATGAGAAAAATCTTAACCCAAATAGAAATCACTCGAAAAAGATCGCTTCA 1860  
Db 1801 CTATTCAGAAATGAGAAAAATCTTAACCCAAATAGAAATCACTCGAAAAAGATCGCTTCA 1860  
Qy 1861 AAACGAAAGCTGAACCTTAATAGCAGCAGATTAAGCAATATGAACTCGAATTAATATCC 1920  
Db 1861 AAACGAAAGCTGAACCTTAATAGCAGCAGATTAAGCAATATGAACTCGAATTAATATCC 1920  
Qy 1921 ACAATTTCAAAAGCCTTAATAAAGATAGGCTGAGGGAAGCTTCTACAGGCAATATTC 1980  
Db 1921 ACAATTTCAAAAGCCTTAATAAAGATAGGCTGAGGGAAGCTTCTACAGGCAATATTC 1980  
Qy 1981 ATGCGCTTGAATAGTACAGTGAAGAAATCTAAGCCCACTAATTTGTAATTCGAAA 2040  
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Db 2041 TTGATAGTTGTTCTAGCAGTGAAGATTAAGAAAAAAGTACAAACCAATGCGAGTCA 2100  
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Qy 2821 TTGAATGTGAACAAAAGGAAGAAATCAAGGAAGATGAGTCTAATATCAAGCCTGTAC 2880  
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Qy 3121 AAAAATTTGAGGAACCTTCATGTCACCTGAAAGAAATGGGAAATGAGAACCTTCGA 3180  
Db 3121 AAAAATTTGAGGAACCTTCATGTCACCTGAAAGAAATGGGAAATGAGAACCTTCGA 3180  
Qy 3181 GTACAGTGAACCAATTTAGCCGTAAATACATTAAGAAAAATGTTTAAAGAACCCAGCT 3240  
Db 3181 GTACAGTGAACCAATTTAGCCGTAAATACATTAAGAAAAATGTTTAAAGAACCCAGCT 3240  
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Qy 3361 ATGCTATCTTGAATTTAGGGGTTTTCGCAACCTGAGGCTCATTAACAAAGTCTTCTGGA 3420  
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Db 3421 GTAAATTTGAGCATCTCGAAATTAAGAAACAGAAATGAAAGTTCAGACTGTA 3480  
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Qy 3541 ATGCAATCTCAGGTTGTTCTGAGACACCTGATGACCTGTTAGATGATGTAATTAAG 3600  
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Qy 3601 AAGATACTAGTTTGTCTGAAAAATGACATTAAGAAAGTCTGCTGTTTTCGCAAAAGC 3660  
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Qy 3721 GTTACCGAAGAGGCGCAAGAAATTAAGAGTCTCAGAAAGAACTTATCTAGTAGAGT 3780  
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Db 3781 AAGAGCTTCTGCTTCCAAACATTTGTTATTTGTTAAGTAAACATTAATCTTCTAGT 3840  
Qy 3841 CTACTAGGATAGCAACCTTCTACCAAGTCTGCTGTTAAGAAACAGAGAGGAAATTAAT 3900  
Db 3841 CTACTAGGATAGCAACCTTCTACCAAGTCTGCTGTTAAGAAACAGAGAGGAAATTAAT 3900

|    |      |  |      |
|----|------|--|------|
| OY | 3901 | TATCATTTGAAGAAATGCTTAAATATGCTCAGTAAACCAAGTAATTTGGCAAGGCAATCTC      | 3960 |
| Db | 3901 | TATCATTTGAAGAAATGCTTAAATATGCTCAGTAAACCAAGTAATTTGGCAAGGCAATCTC      | 3960 |
| OY | 3961 | AGGAACATCACCTTAGTAGAGAAAACAAATGTTCTGCTAGCTTGTTTCTTCAAGTGC          | 4020 |
| Db | 3961 | AGGAACATCACCTTAGTAGAGAAAACAAATGTTCTGCTAGCTTGTTTCTTCAAGTGC          | 4020 |
| OY | 4021 | GTGAATTTGAAAGACTTGACTGCAAAATACAAACACCAGAGATCTTTCTTGAATGGTCTT       | 4080 |
| Db | 4021 | GTGAATTTGAAAGACTTGACTGCAAAATACAAACACCAGAGATCTTTCTTGAATGGTCTT       | 4080 |
| OY | 4081 | CCAAACCAATGAGGATCAGTCTGTAAGCCAGGGAGTGGTCTGAGTACAAAGAAATTTGG        | 4140 |
| Db | 4081 | CCAAACCAATGAGGATCAGTCTGTAAGCCAGGGAGTGGTCTGAGTACAAAGAAATTTGG        | 4140 |
| OY | 4141 | TTTCAGATGATGAAGAAAAGAGAAACGGGCTTGGAAGAAAATATACAGAAAGCAAAAGCA       | 4200 |
| Db | 4141 | TTTCAGATGATGAAGAAAAGAGAAACGGGCTTGGAAGAAAATATACAGAAAGCAAAAGCA       | 4200 |
| OY | 4201 | TGGATTTCAAATTTAGGTAGAGCAGCATCTGGGTGTGAGATGAAAACAAAGCTTCTGAG        | 4260 |
| Db | 4201 | TGGATTTCAAATTTAGGTAGAGCAGCATCTGGGTGTGAGATGAAAACAAAGCTTCTGAG        | 4260 |
| OY | 4261 | ACTGCTCAGGGCTATCCTCTCAGAGTGCATTTTAAACCACTCAGAGGGGATACCATGC         | 4320 |
| Db | 4261 | ACTGCTCAGGGCTATCCTCTCAGAGTGCATTTTAAACCACTCAGAGGGGATACCATGC         | 4320 |
| OY | 4321 | AACATTAACCTATTAAGACTCCAGCAGAAATGGCTGAACCTAAGACTGTGTAAACACG         | 4380 |
| Db | 4321 | AACATTAACCTATTAAGACTCCAGCAGAAATGGCTGAACCTAAGACTGTGTAAACACG         | 4380 |
| OY | 4381 | ATGGAGCGCAGCCTTTCTAACAGCTACCCCTTCATCATTAAGTACTCTTTCGCCCTTAGG       | 4440 |
| Db | 4381 | ATGGAGCGCAGCCTTTCTAACAGCTACCCCTTCATCATTAAGTACTCTTTCGCCCTTAGG       | 4440 |
| OY | 4441 | ACCTGCCGAAATCCAGAACAAAGCACTATGAGAAAAAGCAGTATTAATCTTACAGAAAAGTA     | 4500 |
| Db | 4441 | ACCTGCCGAAATCCAGAACAAAGCACTATGAGAAAAAGCAGTATTAATCTTACAGAAAAGTA     | 4500 |
| OY | 4501 | GTGAATTAACCTATTAAGACTCCAGAAATCCAGAAAGGCTTTCTGCTGACAAGTTTCAAGTGTCTG | 4560 |
| Db | 4501 | GTGAATTAACCTATTAAGACTCCAGAAATCCAGAAAGGCTTTCTGCTGACAAGTTTCAAGTGTCTG | 4560 |
| OY | 4561 | CAGATAGTTCTTACCAATTAATAAAGAACCAAGAGTGGAAAGTCAATCCCTTCTAAAT         | 4620 |
| Db | 4561 | CAGATAGTTCTTACCAATTAATAAAGAACCAAGAGTGGAAAGTCAATCCCTTCTAAAT         | 4620 |
| OY | 4621 | GCCCATCTATTAGATGATAGTGGTGCATGCAAGTGTCTTGGGAGTCTTCAGAAATGAA         | 4680 |
| Db | 4621 | GCCCATCTATTAGATGATAGTGGTGCATGCAAGTGTCTTGGGAGTCTTCAGAAATGAA         | 4680 |
| OY | 4681 | ACTAACCCATCTCAAGAGAGGCTCATTTAAGTGTGATGTGAGAGAGCAACAGCTGGAG         | 4740 |
| Db | 4681 | ACTAACCCATCTCAAGAGAGGCTCATTTAAGTGTGATGTGAGAGAGCAACAGCTGGAG         | 4740 |
| OY | 4741 | AGTCTGGGCAACAGATTTGACGAAACATCTTACTTCCCAAGGCAAGATCTAGAGGAA          | 4800 |
| Db | 4741 | AGTCTGGGCAACAGATTTGACGAAACATCTTACTTCCCAAGGCAAGATCTAGAGGAA          | 4800 |
| OY | 4801 | CCCCCTTAACTTGAATCTGGAATCAAGCTCTTCTCTGATGACCTTGAAATCTGATCTCTG       | 4860 |
| Db | 4801 | CCCCCTTAACTTGAATCTGGAATCAAGCTCTTCTCTGATGACCTTGAAATCTGATCTCTG       | 4860 |
| OY | 4861 | AAGACAGAGCCCAAGAGTCAGTCTGCTGTGTCGCAACATCAATCTTCAACCTCTGCAATGA      | 4920 |
| Db | 4861 | AAGACAGAGCCCAAGAGTCAGTCTGCTGTGTCGCAACATCAATCTTCAACCTCTGCAATGA      | 4920 |
| OY | 4921 | AAGTTCCCAATTGAATTTGAGATTTGCCACAGATCCAGCTGCTGCTATATCTACTG           | 4980 |
| Db | 4921 | AAGTTCCCAATTGAATTTGAGATTTGCCACAGATCCAGCTGCTGCTATATCTACTG           | 4980 |
| OY | 4981 | ATACTGCTGGGTATATGCAATGGAAGAAAGTGTGAGCAGGAGAGACCAAGATTGACG          | 5040 |

|    |      |  |      |
|----|------|--|------|
| Db | 4981 | ATACTGCTGGGTATTAATGCAATGGAAGAAGTGTGACAGGAGAAACGAAATTGACAG    | 5040 |
| OY | 5041 | CTTCACAGAAAGGCTCAACAAAAGAAATGTCATGTGTGTCTGGCCTGACCCCAAG      | 5100 |
| Db | 5041 | CTTCACAGAAAGGCTCAACAAAAGAAATGTCATGTGTGTCTGGCCTGACCCCAAG      | 5100 |
| OY | 5101 | AATTTATGCTCGTACAGATTTGGCCGAAAACCAATCACTTAACTTAATTAATTA       | 5160 |
| Db | 5101 | AATTTATGCTCGTACAGATTTGGCCGAAAACCAATCACTTAACTTAATTAATTA       | 5160 |
| OY | 5161 | CTGAAGAGACTACTCATGTGTGTTATGAAAACAGATGCTGAGTTGTGTGTAACGAC     | 5220 |
| Db | 5161 | CTGAAGAGACTACTCATGTGTGTTATGAAAACAGATGCTGAGTTGTGTGTAACGAC     | 5220 |
| OY | 5221 | TGAAATATTTTCTAGGAATTTGGGAGAGAAAATGGGTAGTTAGCTATTTCTGGGTGACC  | 5280 |
| Db | 5221 | TGAAATATTTTCTAGGAATTTGGGAGAGAAAATGGGTAGTTAGCTATTTCTGGGTGACC  | 5280 |
| OY | 5281 | AGCTATTATTAAGAAAGAAAAATGCTGAATGAGCATGATTTTGAAGTCAGAGAGATGTGG | 5340 |
| Db | 5281 | AGCTATTATTAAGAAAGAAAAATGCTGAATGAGCATGATTTTGAAGTCAGAGAGATGTGG | 5340 |
| OY | 5341 | TCAAATGGAAGAACCAACCAAGTCCAAAGCAGCAGAGAATCCCAGAGCAAGAAATCT    | 5400 |
| Db | 5341 | TCAAATGGAAGAACCAACCAAGTCCAAAGCAGCAGAGAATCCCAGAGCAAGAAATCT    | 5400 |
| OY | 5401 | TCAGGGGGCTAAGAAATCTGTTGTAATGGGCCCTTCAACCAATGCCCCAGATCAACTGG  | 5460 |
| Db | 5401 | TCAGGGGGCTAAGAAATCTGTTGTAATGGGCCCTTCAACCAATGCCCCAGATCAACTGG  | 5460 |
| OY | 5461 | AATGATGATGACAGCTGTGTGTGCTTCTGTGTGAAGAGCTTTCATCAATTCACCTTG    | 5520 |
| Db | 5461 | AATGATGATGACAGCTGTGTGTGCTTCTGTGTGAAGAGCTTTCATCAATTCACCTTG    | 5520 |
| OY | 5521 | GCACAGGTGTCCACCCCAATTTGTGTTGTGACCCAGATGCTGTGACAGAGACAATGGCT  | 5580 |
| Db | 5521 | GCACAGGTGTCCACCCCAATTTGTGTTGTGACCCAGATGCTGTGACAGAGACAATGGCT  | 5580 |
| OY | 5581 | TCATATGCAATTTGGGCAATGTGTGAGGACCTGTGTGTGACCCCGAGATGGGTGTTGACA | 5640 |
| Db | 5581 | TCATATGCAATTTGGGCAATGTGTGAGGACCTGTGTGTGACCCCGAGATGGGTGTTGACA | 5640 |
| OY | 5641 | GTGTAGCACTTACCAAGTGCAGAGAGCTGGAACCTTACTGATATCCCAAGATCCCCACA  | 5700 |
| Db | 5641 | GTGTAGCACTTACCAAGTGCAGAGAGCTGGAACCTTACTGATATCCCAAGATCCCCACA  | 5700 |
| OY | 5701 | GCCACTACTGA 5711   |      |
| Db | 5701 | GCCACTACTGA 5711   |      |

RESULT 3  
 US-09-734-672-5  
 Sequence 5, Application US/09734672  
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 GENERAL INFORMATION:  
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 TITLE OF INVENTION: Coding Sequences of the Human  
 BRCA1 Gene  
 NUMBER OF SEQUENCES: 72  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Morgan Lewis & Bockius LLP  
 STREET: 1111 Pennsylvania Ave., N.W.  
 CITY: Washington  
 STATE: District of Columbia  
 COUNTRY: USA

ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
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INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5711 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: No. US20020183268A1 Relevant  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
STRAIN: BRCA1  
POSITION IN GENE:  
CHROMOSOME/SEGMENT: 17  
MAP POSITION: 17q21  
SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
US-09-734-672-5  
Query Match: 99.9%; Score 5703; DB 9; Length 5711;  
Best Local Similarity: 99.9%; Pred. No. 0;  
Matches 5706; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 AGCTCGTGAAGACTTCTGAGACCCGACACAGGCTGTGGGGTTTCTCAGATACTGGGCC 60  
Db 1 AGCTCGTGAAGACTTCTGAGACCCGACACAGGCTGTGGGGTTTCTCAGATACTGGGCC 60  
QY 61 CCTGGCTCAGAGAGGCTTCAACCTCTGCTCTGGGTTAAAGTTGTAACAGAAAGAA 120  
Db 61 CCTGGCTCAGAGAGGCTTCAACCTCTGCTCTGGGTTAAAGTTGTAACAGAAAGAA 120  
QY 121 TGGATTTATCTGCTCTGCGTTGAGAGTACAAAGTCAATTAATGCTATGCAAGAA 180  
Db 121 TGGATTTATCTGCTCTGCGTTGAGAGTACAAAGTCAATTAATGCTATGCAAGAA 180  
QY 181 TCTTAGAGTGTCCATCTGTCTGAGAGTTGATCAAGAACCTGTCTCACAAAGTGTACC 240  
Db 181 TCTTAGAGTGTCCATCTGTCTGAGAGTTGATCAAGAACCTGTCTCACAAAGTGTACC 240  
QY 181 TCTTAGAGTGTCCATCTGTCTGAGAGTTGATCAAGAACCTGTCTCACAAAGTGTACC 240  
Db 181 TCTTAGAGTGTCCATCTGTCTGAGAGTTGATCAAGAACCTGTCTCACAAAGTGTACC 240  
QY 241 ACATATTTTGAAGATTTTGCATGCTGAACCTTCTCAACAGAGAAAGGCTTCCACAGT 300  
Db 241 ACATATTTTGAAGATTTTGCATGCTGAACCTTCTCAACAGAGAAAGGCTTCCACAGT 300  
QY 301 GTCCCTTTATGTAAGATGATATTAACCAAGAGAGCTTACAGAAAGTACAGAGATTAGTC 360  
Db 301 GTCCCTTTATGTAAGATGATATTAACCAAGAGAGCTTACAGAAAGTACAGAGATTAGTC 360  
QY 361 AACTGTGTAAGAGCTATTAAGAAATCATTTGTGCTTTTTCAGCTTGAACAGGTTTGAGT 420  
Db 361 AACTGTGTAAGAGCTATTAAGAAATCATTTGTGCTTTTTCAGCTTGAACAGGTTTGAGT 420  
QY 421 ATGCAAAAGCTATTAATTTTGCAGAAAGAGAAATTAATCTCTGTAACATCTTAAAGATG 480  
Db 421 ATGCAAAAGCTATTAATTTTGCAGAAAGAGAAATTAATCTCTGTAACATCTTAAAGATG 480

QY 481 AGTTTCTATCATCCAAAGTATGGGCTACAGAAACCGTCCAAAGAAAGCTTTACAGAGTG 540  
Db 481 AGTTTCTATCATCCAAAGTATGGGCTACAGAAACCGTCCAAAGAAAGCTTTACAGAGTG 540  
QY 541 AACCCGAAATCTCTTCTTGCAGAGAAACCAAGTCTCAGTGTCCAACTCTTAACCTTGGAA 600  
Db 541 AACCCGAAATCTCTTCTTGCAGAGAAACCAAGTCTCAGTGTCCAACTCTTAACCTTGGAA 600  
QY 601 CTGTGAGAACTCTGAGACCAAGAGCGGATACAAACCTCAAAAGACGCTGTCTACACTTG 660  
Db 601 CTGTGAGAACTCTGAGACCAAGAGCGGATACAAACCTCAAAAGACGCTGTCTACACTTG 660  
QY 661 AATTGGAGTCTGATCTTCTGAGATACCGTTAAAGGCAACTTAATTCAGTGTGGAG 720  
Db 661 AATTGGAGTCTGATCTTCTGAGATACCGTTAAAGGCAACTTAATTCAGTGTGGAG 720  
QY 721 ATCAAGAAATTTGTAACAAATCACCCCTCAAGAACCGAGGATGAATATCAGTTGATCTG 780  
Db 721 ATCAAGAAATTTGTAACAAATCACCCCTCAAGAACCGAGGATGAATATCAGTTGATCTG 780  
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Db 781 CAAAAGAGCTGCTGTAATTTTCTGAGAGGATGTAACTAAATTAAGATCATCATCAAC 840  
QY 841 CCAGTAATTAATGATTTGAAACCACTGAGAGCGTGCAGCTGAGAGGATCCAGAAAGT 900  
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QY 901 ATCAGGGTATGTTCTGTTTCAAACTTGATGAGAGCCATGTGGCAAAATCTCATGCCA 960  
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QY 961 GCTCATTTACAGATAGAGAACGAGTTTAACTACTACATAAGACAGATGAATGTAGAA 1020  
Db 961 GCTCATTTACAGATAGAGAACGAGTTTAACTACTACATAAGACAGATGAATGTAGAA 1020  
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Db 1021 AGGCTGAATTTCTGTAATAAAGCAAAACAGCTGCTTACAGAGAGCCCAATTAACAGAT 1080  
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Db 1081 GGGCTGGAAGTAAAGAAACATGTAATGATGAGCGGACTCCAGACACAGAAAAAGGTAG 1140  
QY 1141 ATCTGAATGCTGATCCCTGCTGTGAGAGAAAGAAATGGAATGAGAAATGCGCATGCT 1200  
Db 1141 ATCTGAATGCTGATCCCTGCTGTGAGAGAAAGAAATGGAATGAGAAATGCGCATGCT 1200  
QY 1201 CAGAGATCTAGAGATCTGAGATGTTCTTGGATTAACATAATAGCAGATTGAGA 1260  
Db 1201 CAGAGATCTAGAGATCTGAGATGTTCTTGGATTAACATAATAGCAGATTGAGA 1260  
QY 1261 AAGTTAATGAGTGTGTTTCCAGAGATGTAACCTTGAAGTTCTGATGATCAATGATG 1320  
Db 1261 AAGTTAATGAGTGTGTTTCCAGAGATGTAACCTTGAAGTTCTGATGATCAATGATG 1320  
QY 1321 GGGAGTCTGAATCAAAATCCAAAGAGTGAATGATGAGAGCTTCTAATAGGTTAGTG 1380  
Db 1321 GGGAGTCTGAATCAAAATCCAAAGAGTGAATGATGAGAGCTTCTAATAGGTTAGTG 1380  
QY 1381 AATATTTCTGTTCTTCAAGAGAAATAGACTTACGCGCAGTATCTCATAGGCTTTAA 1440  
Db 1381 AATATTTCTGTTCTTCAAGAGAAATAGACTTACGCGCAGTATCTCATAGGCTTTAA 1440  
QY 1441 TATGTAAAGTGAAGAGTGAATCTCAAAATGATGAGAGTAAATTTGAGAGCAAAATAT 1500  
Db 1441 TATGTAAAGTGAAGAGTGAATCTCAAAATGATGAGAGTAAATTTGAGAGCAAAATAT 1500  
QY 1501 TTGGGAAACCTATGAGAGAGAGCAAGCCCTCCCACTTAAGCAGTAACTGAATC 1560  
Db 1501 TTGGGAAACCTATGAGAGAGAGCAAGCCCTCCCACTTAAGCAGTAACTGAATC 1560  
QY 1561 TAATTATAGAGACTTTGTTACTGAGCAGATTAATTAAGAGCGTCCCTCACAATA 1620



Db 1561 TAAATTATGAGAGCAATTTGTTACTGAGCCACAGATAAATAAGAGCCGCTCCCTCAAAATA 1620  
Qy 1621 AATTTAAAGCTTAAAGAGAGACCTACATCAGGCTTCTACCTGAGATTTTATCAAGAAAG 1680  
Db 1621 AATTTAAAGCTTAAAGAGAGACCTACATCAGGCTTCTACCTGAGATTTTATCAAGAAAG 1680  
Qy 1681 CAGATTTGCGAGTTCAAAAGACCTCTGAAAATGATTAATCAAGGAACTTACCAAACGAGAGC 1740  
Db 1681 CAGATTTGCGAGTTCAAAAGACCTCTGAAAATGATTAATCAAGGAACTTACCAAACGAGAGC 1740  
Qy 1741 AGAATGCTCAAGTGAATTAATTAATTAATGATGCTGATGGAATTAACAAAGGATGATT 1800  
Db 1741 AGAATGCTCAAGTGAATTAATTAATTAATGATGCTGATGGAATTAACAAAGGATGATT 1800  
Qy 1801 CTATTCAAGATGAGAAAATCTCTAACCCATATGATCCTGAAAAAGAAATCTGCTTTCA 1860  
Db 1801 CTATTCAAGATGAGAAAATCTCTAACCCATATGATCCTGAAAAAGAAATCTGCTTTCA 1860  
Qy 1861 AAAAGAAAGCTGAACCTATTAAGACAGATTAAGCAATATGAACTCGAAATTAATATCC 1920  
Db 1861 AAAAGAAAGCTGAACCTATTAAGACAGATTAAGCAATATGAACTCGAAATTAATATCC 1920  
Qy 1921 ACAATTTCAAAAGACCTTAAAAAGATTAAGCTGAGAGAAAGTCTTCTACAGGCAATATTC 1980  
Db 1921 ACAATTTCAAAAGACCTTAAAAAGATTAAGCTGAGAGAAAGTCTTCTACAGGCAATATTC 1980  
Qy 1981 ATGCGCTTGAACCTAGTATGATGAGAAATCTAAGCCACCTAATTTGATGATTCGAA 2040  
Db 1981 ATGCGCTTGAACCTAGTATGATGAGAAATCTAAGCCACCTAATTTGATGATTCGAA 2040  
Qy 2041 TTGATAGTTGTTTATGACAGTGAAGATTAAGAAAAAGAAAGTAAACCAATTCAGTCA 2100  
Db 2041 TTGATAGTTGTTTATGACAGTGAAGATTAAGAAAAAGTAAACCAATTCAGTCA 2100  
Qy 2101 GGCACAGCAGAAACCTTAACAATCATGGAAGTAAAGAACTGCACTGGAGCCAAAGAA 2160  
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Qy 2161 GTTAAAGCCAAATGAAAGACAGAAAGTAAAGAAAGTAAAGCAAGCAGTACTTTCCAGAGCTGA 2220  
Db 2161 GTTAAAGCCAAATGAAAGACAGAAAGTAAAGAAAGTAAAGCAAGCAGTACTTTCCAGAGCTGA 2220  
Qy 2221 AGTTAAACAATGCACTGCTGTTCTTTTACTTAAGTTCCTAAATACAGTGAATCTTAAAGAT 2280  
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Qy 2401 AAAAGATCTGAGAGATGAGAGATTTTCAATGTTGTTACCTGTTATGAGCACTCAGG 2460  
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Qy 2461 AAAAGTATCTGTTTACTGGAAGTTAGCACTCTAGGAAAGGCAAAAACAGAAACCAAAATTAAT 2520  
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Db 2521 GTGTGAGTCAAGTGTGAGCACTTGAAGAACCCCAAGGAGCTAATCTAGTGTGTTTCCAAAG 2580  
Qy 2581 ATAAATGAATGAACAGAGAGCTTTAAGTATCATTTGGGACATGAAGTAAACCAAGTGC 2640  
Db 2581 ATAAATGAATGAACAGAGAGCTTTAAGTATCATTTGGGACATGAAGTAAACCAAGTGC 2640  
Qy 2641 GGGAAACAAAGCATGAAGAAATGGAAGAAAGTGAACCTTATGCTCAGTATTTTGCAGAAATCAAT 2700  
Db 2641 GGGAAACAAAGCATGAAGAAATGGAAGAAAGTGAACCTTATGCTCAGTATTTTGCAGAAATCAAT 2700

Db 2641 GGGAAACAAAGCATGAAGAAATGGAAGAAAGTGAACCTTATGCTCAGTATTTTGCAGAAATCAAT 2700  
Qy 2701 TCAAGGTTTCAAAAGCCCAATGCTTGTCTGTTTCAATCCAGAAATGCAAGAGG 2760  
Db 2701 TCAAGGTTTCAAAAGCCCAATGCTTGTCTGTTTCAATCCAGAAATGCAAGAGG 2760  
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Db 2761 AATGTCGAACATTTCTGCTCCACCTGCGGTCTTTAAAGAAACAAATCCAAAGTCACTT 2820  
Qy 2821 TTGAATGTGAACAAAGAGAAAGAAATCAAGAAAGAAATGAGTAAATATCAAGCTGTAC 2880  
Db 2821 TTGAATGTGAACAAAGAGAAAGAAATCAAGAAAGAAATGAGTAAATATCAAGCTGTAC 2880  
Qy 2881 AGACAGTTAATATCACTGCAAGCTTCTGCTGTTGTGTCAGAAAGTAAAGCCAGTGAAT 2940  
Db 2881 AGACAGTTAATATCACTGCAAGCTTCTGCTGTTGTGTCAGAAAGTAAAGCCAGTGAAT 2940  
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Qy 3001 AGGAAACCTGACTATTAATCTCCAAATTAACATGAGCTTTTACAAACCAATATCTATAC 3060  
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Qy 3181 GTACAGTGAACCAATTAACCTGTAATTAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGT 3240  
Db 3181 GTACAGTGAACCAATTAACCTGTAATTAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGT 3240  
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Qy 3481 ATACAGATTTCTCTCATATCTGATTTTCAAGTAACTTGAAGACAGCTTATGGAAGTAAAGT 3540  
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Qy 3601 AAGATATCTAGTTTGTCTGAGAAATGACATTAAGAAAGTGTCTGTTTATGCAAAAGG 3660  
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Qy 3661 TCCAGAAAGAGAGCTTATGAGAGAGCTTACAGCTTCAACCATACACATTTGGCTCAGG 3720  
Db 3661 TCCAGAAAGAGAGCTTATGAGAGAGCTTACAGAGAGCTTACAGCTTCAACCATACACATTTGGCTCAGG 3720  
Qy 3721 GTTACCGAAAGAGGAGGCAAGAAATTAAGTCTCAGAAAGAACTTATCTAGTGAAGT 3780  
Db 3721 GTTACCGAAAGAGGAGGCAAGAAATTAAGTCTCAGAAAGAACTTATCTAGTGAAGT 3780

QY 3781 AAGAGCTCCGCTTCCACACCTTGTATTTGTAAGTAACAATATACCTTCAGT 3840  
 DB 3781 AAGAGCTCCGCTTCCACACCTTGTATTTGTAAGTAACAATATACCTTCAGT 3840  
 QY 3841 CTACTAGGACATAGACCCGTTGCTACGAGTGTCTGTCTAAGAACACAGAGGAAATTTAT 3900  
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 DB 3901 TATCATTTGAAGATAGCTTAATATGACTGCAATACAGGTAATATTTGGCAAGGATCTC 3960  
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 DB 4021 GTGAATTTGGAAGACTTGAATGCAAAATACAAACCCAGAGATCCTTTCTTGATTGTTCTT 4080  
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 DB 4081 CCAAAACAATGAGGATCAGTCTGAAAGCCAGGAGTTGCTGAGTGAACAAGAAATGG 4140  
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 DB 4141 TTTGAGATGATGAAGAAAGAGAAAGGCTTGGAAAGAAATATCAAGAAAGCAAGGA 4200  
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 QY 4261 ACTGCTCAGGGCTATCTCTCAGAGTGAATTTTAACCACTCAGCAGAGGAAATCATGC 4320  
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 DB 4321 AACATTAACCTGATTAAGCTCCAGCAGGAAATGCTGAATGAAGCTGTGTTAGAACAG 4380  
 QY 4381 ATGGAGCCAGGCTTCTAAGCAGTACCTTCCATCAATAGTGAATCTTCTGCTTGAAG 4440  
 DB 4381 ATGGAGCCAGGCTTCTAAGCAGTACCTTCCATCAATAGTGAATCTTCTGCTTGAAG 4440  
 QY 4441 ACCTGCGAAATCCAGAACAAAGCAGTCAAGAAAGAGATTTAATTCAAGAAAGTA 4500  
 DB 4441 ACCTGCGAAATCCAGAACAAAGCAGTCAAGAAAGAGATTTAATTCAAGAAAGTA 4500  
 QY 4501 GTGAATACCTTAAAGCCAGAAATCCAGAAAGGCTTCTGCTGAACAAGTTGAGGTCTG 4560  
 DB 4501 GTGAATACCTTAAAGCCAGAAATCCAGAAAGGCTTCTGCTGAACAAGTTGAGGTCTG 4560  
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 DB 4561 CAGATAGTCTTCAAGATAAATAAAGAACACAGAGTGAAGAGTATCCCTCTTAAAT 4620  
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RESULT 4  
 US-09-982-828-3  
 ; Sequence 3, Application US/09982828  
 ; Publication No. US20030022184A1  
 ; GENERAL INFORMATION:  
 APPLICANT: Murphy, Patricia D.  
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 Olson, Sheri J.  
 Thurber, Denise  
 Zeng, Bin

TITLE OF INVENTION: Coding Sequences of the Human  
BRCA1 Gene  
NUMBER OF SEQUENCES: 72  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Morgan Lewis & Bockius LLP  
STREET: 1111 Pennsylvania Avenue N. W.  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/982,828  
FILING DATE: 22-Oct-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 09/074,453  
FILING DATE: 1998-05-06  
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FILING DATE: 1997-02-12  
APPLICATION NUMBER: US 08/598,591  
FILING DATE: 1996-02-12  
ATTORNEY/AGENT INFORMATION:  
NAME: Michael S. Tuscan  
REGISTRATION NUMBER: 43,210  
REFERENCE/DOCKET NUMBER: 44921-5053-01-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-739-3000  
TELEFAX: 202-739-3001  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5711 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
ORGANISM SOURCE:  
ORGANISM: Homo sapiens  
STRAIN: BRCA1 (om12)  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: 17  
MAP POSITION: 17q21  
SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
US-09-982-828-3  
Query Match 99.9%; Score 5703; DB 9; Length 5711;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 5706; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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QY 4261 ACTGCTCAGGGCTATCTCTCAGAGTGAATTTTAACTCACTCAGCAGAGGATACCATGC 4320  
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QY 5641 GTGTAGCACTTACAGATGACAGAGCTGTGACACCTGATATCCAGATCTCCGACAG 5700  
Db 5641 GTGTAGCACTTACAGATGACAGAGCTGTGACACCTGATATCCAGATCTCCGACAG 5700  
QY 5701 GCCACTACTGA 5711  
Db 5701 GCCACTACTGA 5711





QY 1261 AAGTTAATGAGTGTTCAGAAAGTGAATGTTAGGTTCTGATGACTCATGATG 1320  
Db 1261 AAGTTAATGAGTGTTCAGAAAGTGAATGTTAGGTTCTGATGACTCATGATG 1320  
QY 1321 GGGAGTCTGAATCAATGCCAAAGTGTGATGATTTGACGTTCTTAATGAGTGTG 1380  
Db 1321 GGGAGTCTGAATCAATGCCAAAGTGTGATGATTTGACGTTCTTAATGAGTGTG 1380  
QY 1381 AATATCTGGTCTTCAAGAGAAATGACTTACTGGCCAGTATCCCTAGAGGCTTTA 1440  
Db 1381 AATATCTGGTCTTCAAGAGAAATGACTTACTGGCCAGTATCCCTAGAGGCTTTA 1440  
QY 1441 TATGTAAAGTGAAGAGTTCCTCCAAATCAGTAGAGTAATATTGAAGACAAATAT 1500  
Db 1441 TATGTAAAGTGAAGAGTTCCTCCAAATCAGTAGAGTAATATTGAAGACAAATAT 1500  
QY 1501 TTGGGAAAACCTTATCGAAGAGGCAAGCCTCCCACTTAAGCCATGTAACTGAAATC 1560  
Db 1501 TTGGGAAAACCTTATCGAAGAGGCAAGCCTCCCACTTAAGCCATGTAACTGAAATC 1560  
QY 1561 TAATTAAGAGCATTTGTACTGAGCCAGATTAATACAGAGCGTCCCTCACAATA 1620  
Db 1561 TAATTAAGAGCATTTGTACTGAGCCAGATTAATACAGAGCGTCCCTCACAATA 1620  
QY 1621 AATTAAGCGTAAAGGAGACCTACATCAGGCTTCATCCTGAGATTTTATCAAGAAAG 1680  
Db 1621 AATTAAGCGTAAAGGAGACCTACATCAGGCTTCATCCTGAGATTTTATCAAGAAAG 1680  
QY 1681 CAGATTGGCAGTTCAAAAGACTCTGAAATGATTAATCAGGAACTAACCAAGCGAGC 1740  
Db 1681 CAGATTGGCAGTTCAAAAGACTCTGAAATGATTAATCAGGAACTAACCAAGCGAGC 1740  
QY 1741 AGAATGCTCAAGTGAATATTAATAGTGTGATGAGTAATAAACAAAGTGAT 1800  
Db 1741 AGAATGCTCAAGTGAATATTAATAGTGTGATGAGTAATAAACAAAGTGAT 1800  
QY 1801 CTATTCAGATGAGAAAAATCTTACCCATAGATACACTCGAAAAAGAACTGCTTTCA 1860  
Db 1801 CTATTCAGATGAGAAAAATCTTACCCATAGATACACTCGAAAAAGAACTGCTTTCA 1860  
QY 1861 AAAAGAAAGTGAATCTATAGCAGAGATTAAGCAATATGAACTCGAATTAATATCC 1920  
Db 1861 AAAAGAAAGTGAATCTATAGCAGAGATTAAGCAATATGAACTCGAATTAATATCC 1920  
QY 1921 ACAATTCAAAAGCCTTAATAAAGTGTGAGGAGGAAAGTCTTACAGGCAATATC 1980  
Db 1921 ACAATTCAAAAGCCTTAATAAAGTGTGAGGAGGAAAGTCTTACAGGCAATATC 1980  
QY 1981 ATGCGCTTGAATAGTACAGTGAAGATTAAGCCACCTAATTTGATGAAATGCA 2040  
Db 1981 ATGCGCTTGAATAGTACAGTGAAGATTAAGCCACCTAATTTGATGAAATGCA 2040  
QY 2041 TTGATAGTGTCTTACAGTGAAGATTAAGAAAAAGTACCAACCAATGCGAGTCA 2100  
Db 2041 TTGATAGTGTCTTACAGTGAAGATTAAGAAAAAGTACCAACCAATGCGAGTCA 2100  
QY 2101 GGGACGCGAAAACTTCAACATCATGAAAGTAAACCTGCACTGAGGCCAAMAA 2160  
Db 2101 GGGACGCGAAAACTTCAACATCATGAAAGTAAACCTGCACTGAGGCCAAMAA 2160  
QY 2161 GTAAACGCAATGAAGACAAAGTAAAGACATGACAGCGATACCTTCCAGAGCTGA 2220  
Db 2161 GTAAACGCAATGAAGACAAAGTAAAGACATGACAGCGATACCTTCCAGAGCTGA 2220  
QY 2221 AGTTAAACAATGACCTGTGTTCTTTACTAGTGTTCAAATACAGTGAACCTTAAGAA 2280  
Db 2221 AGTTAAACAATGACCTGTGTTCTTTACTAGTGTTCAAATACAGTGAACCTTAAGAA 2280  
QY 2281 TTGTCAATCTGAGCTTCCAGAGGAAAGAAAGAAAGAAAGAAAGAAAGAAAGTAA 2340  
Db 2281 TTGTCAATCTGAGCTTCCAGAGGAAAGAAAGAAAGAAAGAAAGAAAGTAA 2340

QY 2341 CTAAATATCTGAGAACCCCAAGATCTCATGTAAATGAGAAAGGTTTCCAACTG 2400  
Db 2341 CTAAATATCTGAGAACCCCAAGATCTCATGTAAATGAGAAAGGTTTCCAACTG 2400  
QY 2401 AAAAGTCTGTAGAGTACAGATTTTCAATGGTACCTGTACTGATTTATGCACTCAG 2460  
Db 2401 AAAAGTCTGTAGAGTACAGATTTTCAATGGTACCTGTACTGATTTATGCACTCAG 2460  
QY 2461 AAAAGTCTGTACTGAGAAAGTTAGACCTGAGGAAAGGCAAAACAGAAACCAATTA 2520  
Db 2461 AAAAGTCTGTACTGAGAAAGTTAGACCTGAGGAAAGGCAAAACAGAAACCAATTA 2520  
QY 2521 GTGTAGTCAAGTGTGACAGATTTGAAACCCAGAGCAATTAATCAATGTTTCCAAAG 2580  
Db 2521 GTGTAGTCAAGTGTGACAGATTTGAAACCCAGAGCAATTAATCAATGTTTCCAAAG 2580  
QY 2581 ATATATGAATGACACAGAAAGCTTAAATATCATTTGGACATGAAGTTAACCAAGTC 2640  
Db 2581 ATATATGAATGACACAGAAAGCTTAAATATCATTTGGACATGAAGTTAACCAAGTC 2640  
QY 2641 GGGAAACAGCATAGAAATGAAAGAAAGTGAATGATGCTCAGATTTTGCAGAAATCAT 2700  
Db 2641 GGGAAACAGCATAGAAATGAAAGAAAGTGAATGATGCTCAGATTTTGCAGAAATCAT 2700  
QY 2701 TCAAGGTTCAAGGCGCAGTCAATTTGCTCTGTTTCAATCCAGAAATGAGAAAGAG 2760  
Db 2701 TCAAGGTTCAAGGCGCAGTCAATTTGCTCTGTTTCAATCCAGAAATGAGAAAGAG 2760  
QY 2761 AATGTGCAACATTTCTGCCCACCTGCGGCTCTTAAAGAAACAAAGTCCAAAGTCACT 2820  
Db 2761 AATGTGCAACATTTCTGCCCACCTGCGGCTCTTAAAGAAACAAAGTCCAAAGTCACT 2820  
QY 2821 TTGAATGTGAACAAAGAAAGAAATCAAGSAAAGATGATTAATCAAGCCGTATC 2880  
Db 2821 TTGAATGTGAACAAAGAAAGAAATCAAGSAAAGATGATTAATCAAGCCGTATC 2880  
QY 2881 AGACAGTTAATATCACTGAGGCTTCTGTGTGTGTGAGAAAGTAAAGCCAGTTGATA 2940  
Db 2881 AGACAGTTAATATCACTGAGGCTTCTGTGTGTGTGAGAAAGTAAAGCCAGTTGATA 2940  
QY 2941 ATGCCAAATGTATCAAAAGAGGCTTGAAGTTTGTCTATCATCTCAGTTGAGGCA 3000  
Db 2941 ATGCCAAATGTATCAAAAGAGGCTTGAAGTTTGTCTATCATCTCAGTTGAGGCA 3000  
QY 3001 ACGAAACGAGCTCAATTAATCCAAATTAACAGGACTTTTACAAACCAATTCGATATC 3060  
Db 3001 ACGAAACGAGCTCAATTAATCCAAATTAACAGGACTTTTACAAACCAATTCGATATC 3060  
QY 3061 CACCACTTTTCCATCAAGTCAATTTGTTTAAATGTAAGAAAAATCTGCTAGAG 3120  
Db 3061 CACCACTTTTCCATCAAGTCAATTTGTTTAAATGTAAGAAAAATCTGCTAGAG 3120  
QY 3121 AAAACTTTGAGGAACTTCATGCAATGTCAGTGAAGAAATGGAACATTTCCAA 3180  
Db 3121 AAAACTTTGAGGAACTTCATGCAATGTCAGTGAAGAAATGGAACATTTCCAA 3180  
QY 3181 GTACAGTGAACCAATTTAGCCCTTAATTAACATTAAGAAATGTTTAAAGAACAGCT 3240  
Db 3181 GTACAGTGAACCAATTTAGCCCTTAATTAACATTAAGAAATGTTTAAAGAACAGCT 3240  
QY 3241 CAAGCAATTTAATGAAGTGTCCAGTACATTAAGAAAGTGGCTCCAGTATTAATGA 3300  
Db 3241 CAAGCAATTTAATGAAGTGTCCAGTACATTAAGAAAGTGGCTCCAGTATTAATGA 3300  
QY 3301 TAGGTTCCAGTATGAAGAAACATTTCAAGCAAACTAGTGAAGAAAGAGGCAAAATGA 3360  
Db 3301 TAGGTTCCAGTATGAAGAAACATTTCAAGCAAACTAGTGAAGAAAGAGGCAAAATGA 3360  
QY 3361 ATGCTATGCTTAATTAAGGAGTTTTCAGACCTGAGAGTCTAATAAAGTCTTCCGGA 3420  
Db 3361 ATGCTATGCTTAATTAAGGAGTTTTCAGACCTGAGAGTCTAATAAAGTCTTCCGGA 3420  
QY 3421 GTAATTTGATGATCTGTAATTAAGAAAGCAAGATATGAAGAAAGTATGAGATGTTA 3480

|    |  |      |   |      |
|----|--|------|---|------|
| Dd |  | 3421 | GTAATTGTAAGCATCCTGAAATAAAAAGCAAGAATATGAAGAACTTACACTGTTTA          | 3480 |
| Oy |  | 3481 | ATACAGATTTCTCTCCATATCTGATTTAGATACTTGAAACAGCTTATGGGAATAGTC         | 3540 |
| Dd |  | 3481 | ATACAGATTTCTCTCCATATCTGATTTAGATACTTGAAACAGCTTATGGGAATAGTC         | 3540 |
| Oy |  | 3541 | ATGCATCTCAGGTTGTTCTCGAGACACTGATGACCTTGATGATGATGATGTAATTAAGG       | 3600 |
| Dd |  | 3541 | ATGCATCTCAGGTTGTTCTCGAGACACTGATGACCTTGATGATGATGTAATTAAGG          | 3600 |
| Oy |  | 3601 | AAGATACTAGTTTTCTGAAAAATGACATTAAGSAAAGTCTGCTGTTTTTGCAAAAAGCG       | 3660 |
| Dd |  | 3601 | AAGATACTAGTTTTCTGAAAAATGACATTAAGSAAAGTCTGCTGTTTTTGCAAAAAGCG       | 3660 |
| Oy |  | 3661 | TCCAGAAAGAGAGAGCTTAGCAGAGAGTCTAGCCCTTTACACCATACATTTGGCTCAGG       | 3720 |
| Dd |  | 3661 | TCCAGAGAGAGAGAGCTTAGCAGAGAGTCTAGCCCTTTACACCATACATTTGGCTCAGG       | 3720 |
| Oy |  | 3721 | GTTACCGAAGAGGGGCCAAAGAAATTAGAGTCTCGAAGAGAACTTAATCTAGAGATG         | 3780 |
| Dd |  | 3721 | GTTACCGAAGAGGGGCCAAAGAAATTAGAGTCTCGAAGAGAACTTAATCTAGAGATG         | 3780 |
| Oy |  | 3781 | AAGAGCTTCCCTGCTTCCAACACTTGTTATTTGGTAAGTAAACAATTAACCTTCTCAGT       | 3840 |
| Dd |  | 3781 | AAGAGCTTCCCTGCTTCCAACACTTGTTATTTGGTAAGTAAACAATTAACCTTCTCAGT       | 3840 |
| Oy |  | 3841 | CTACTAGGACATPAGCACCGGTGCTACCGAGTGTCTGTCTPAAGAACACAGAGAGAAATTAT    | 3900 |
| Dd |  | 3841 | CTACTAGGACATPAGCACCGGTGCTACCGAGTGTCTGTCTPAAGAACACAGAGAGAAATTAT    | 3900 |
| Oy |  | 3901 | TATCATTTAAGAAATAGCTTAAATGACTGACAGTAAACAGGTAAATTTGGCAAAGGCATCTC    | 3960 |
| Dd |  | 3901 | TATCATTTAAGAAATAGCTTAAATGACTGACAGTAAACAGGTAAATTTGGCAAAGGCATCTC    | 3960 |
| Oy |  | 3961 | AGGAACATCACCTTAGTAGAGAAACAAATGTTCTGCTAGCTGTTGTTTCCTCAACAGTGA      | 4020 |
| Dd |  | 3961 | AGGAACATCACCTTAGTAGAGAAACAAATGTTCTGCTAGCTGTTGTTTCCTCAACAGTGA      | 4020 |
| Oy |  | 4021 | GTTGAATTTGGAAGACTTGAACGCAATPACAAACACCCAGAGATCCCTTCTTGATTTGGTCTT   | 4080 |
| Dd |  | 4021 | GTTGAATTTGGAAGACTTGAACGCAATPACAAACACCCAGAGATCCCTTCTTGATTTGGTCTT   | 4080 |
| Oy |  | 4081 | CCAAACAAATGAAGGCATGCTGTGAAGCCAGGGAGTTGCTGTAGTGACAAAGAAATYGG       | 4140 |
| Dd |  | 4081 | CCAAACAAATGAAGGCATGCTGTGAAGCCAGGGAGTTGCTGTAGTGACAAAGAAATYGG       | 4140 |
| Oy |  | 4141 | TTTTCAGATGATGAAGAAAGAGAACGGGCTTGGAAAGAAATATATCAGAGAGCAAAAGCA      | 4200 |
| Dd |  | 4141 | TTTTCAGATGATGAAGAAAGAGAACGGGCTTGGAAAGAAATATATCAGAGAGCAAAAGCA      | 4200 |
| Oy |  | 4201 | TGSATTTCAAACITTAGGTGAGAGAGCATGCTGGGTGTGAGAGTGAACAAAGGCTCTGTAAG    | 4260 |
| Dd |  | 4201 | TGSATTTCAAACITTAGGTGAGAGAGCATGCTGGGTGTGAGAGTGAACAAAGGCTCTGTAAG    | 4260 |
| Oy |  | 4261 | ACTGCTCAGGGGCTATCTCTCAGATGTGACATTTTAACCACTCAGCAGAGGGATACCATGC     | 4320 |
| Dd |  | 4261 | ACTGCTCAGGGGCTATCTCTCAGATGTGACATTTTAACCACTCAGCAGAGGGATACCATGC     | 4320 |
| Oy |  | 4321 | AACATTAACCTGTATAAGCTCCAGCAGAAATGGCTGAACCTAGAAAGCTGTGTTAGAACGC     | 4380 |
| Dd |  | 4321 | AACATTAACCTGTATAAGCTCCAGCAGAAATGGCTGAACCTAGAAAGCTGTGTTAGAACGC     | 4380 |
| Oy |  | 4381 | ATGGGAGCAGGCTTTCTAAGAGCTACCTTCCATATATAGTACCTCTTCCCTTGAAG          | 4440 |
| Dd |  | 4381 | ATGGGAGCAGGCTTTCTAAGAGCTACCTTCCATATATAGTACCTCTTCCCTTGAAG          | 4440 |
| Oy |  | 4441 | ACCTGCGAAATTCAGAACAAAGCAATCAGAAAAAGCAGTATTAATTCACAGAAAAAGTA       | 4500 |
| Dd |  | 4441 | ACCTGCGAAATTCAGAACAAAGCAATCAGAAAAAGCAGTATTAATTCACAGAAAAAGTA       | 4500 |
| Oy |  | 4501 | GTTGAATACCTTATAAGCCAGAAATCCAGAAAGGCTTTTCTGCTGACAAAGTTTGAAGGTGTCTG | 4560 |

|    |      |  |      |
|----|------|--|------|
| Db | 4501 | GTGAATACCCTTAATAGCCAGAAATCCAGAAGCCCTTTCTGCTGACAAAGTTTAGAGTCTG  | 4550 |
| Qy | 4561 | CAGATAGTTCTACGAGTAAAAATAAAGAACGAGAGTGGAAAGTCATCCCTCTTAAT       | 4620 |
| Db | 4561 | CAGATAGTTCTACGAGTAAAAATAAAGAACGAGAGTGGAAAGTCATCCCTCTTAAT       | 4620 |
| Qy | 4621 | GGCCATCATTAATATATAGTGTGTCAATGCACAGTGTCTCTGGAGTCTTCAGAAATGAA    | 4680 |
| Db | 4621 | GGCCATCATTAATATATAGTGTGTCAATGCACAGTGTCTCTGGAGTCTTCAGAAATGAA    | 4680 |
| Qy | 4681 | ACTACCCACTCTCAAGAGAGCGCTCATTTAAGTGTGTTGATGTGGAGAGCAACAGCTGAAG  | 4740 |
| Db | 4681 | ACTACCCACTCTCAAGAGAGCGCTCATTTAAGTGTGTTGATGTGGAGAGCAACAGCTGAAG  | 4740 |
| Qy | 4741 | AGTCTGGGCGACACGATTTGACGGAAACATCTTACTTGCCAAAGCAAGATCTTAAGGGAA   | 4800 |
| Db | 4741 | AGTCTGGGCGACACGATTTGACGGAAACATCTTACTTGCCAAAGCAAGATCTTAAGGGAA   | 4800 |
| Qy | 4801 | CCCCCTTACCTGGAATCTGGAATCAGCCCTCTCTCTGATGAGACCTTGAAATCTATCCTCTG | 4860 |
| Db | 4801 | CCCCCTTACCTGGAATCTGGAATCAGCCCTCTCTCTGATGAGACCTTGAAATCTATCCTCTG | 4860 |
| Qy | 4861 | AAGACAGAGCCCCACAGATCAGCTGTGTGGCAACATCCATCTTCAACTCTGATTTGA      | 4920 |
| Db | 4861 | AAGACAGAGCCCCACAGATCAGCTGTGTGGCAACATCCATCTTCAACTCTGATTTGA      | 4920 |
| Qy | 4921 | AAGTTCGCCCAATTGGAAGTTGCAGAAATCTGCCACAGAGTCACAGCTGCTGCTATACTG   | 4980 |
| Db | 4921 | AAGTTCGCCCAATTGGAAGTTGCAGAAATCTGCCACAGAGTCACAGCTGCTGCTATACTG   | 4980 |
| Qy | 4981 | ATACTGCTGGGTATATATCAATGCAAGAAAGTGTGACGAGGAGAGCCAGAAATTTGACAG   | 5040 |
| Db | 4981 | ATACTGCTGGGTATATATCAATGCAAGAAAGTGTGACGAGGAGAGCCAGAAATTTGACAG   | 5040 |
| Qy | 5041 | CTTCAACAGAAAAGGCTCAACAAAAGAAATGTCATGAGTGTCTGCGCCCTGACCCCAAG    | 5100 |
| Db | 5041 | CTTCAACAGAAAAGGCTCAACAAAAGAAATGTCATGAGTGTCTGCGCCCTGACCCCAAG    | 5100 |
| Qy | 5101 | AATTATGCTGCTGTACAAAGTTTGGCCAAAAAACACACATCACTTTAATCTAATTA       | 5160 |
| Db | 5101 | AATTATGCTGCTGTACAAAGTTTGGCCAAAAAACACACATCACTTTAATCTAATTA       | 5160 |
| Qy | 5161 | CTGAAGAGACTACTCATGTGTTATGAAAACAGATGCTGAAGTTGTGTGTGAACGGACAC    | 5220 |
| Db | 5161 | CTGAAGAGACTACTCATGTGTTATGAAAACAGATGCTGAAGTTGTGTGTGAACGGACAC    | 5220 |
| Qy | 5221 | TGAAATATTTCTAGAAATCCGGGAGGAAAATGGGTAGTTAGCTAATTTCTGGGGTACC     | 5280 |
| Db | 5221 | TGAAATATTTCTAGAAATCCGGGAGGAAAATGGGTAGTTAGCTAATTTCTGGGGTACC     | 5280 |
| Qy | 5281 | AGTCAATTAAAGAAAAGAAAATGCTGAATGAGCATGATTTTGAAGTCAGAGAGATGTGG    | 5340 |
| Db | 5281 | AGTCAATTAAAGAAAAGAAAATGCTGAATGAGCATGATTTTGAAGTCAGAGAGATGTGG    | 5340 |
| Qy | 5341 | TCATATGAGAAACCCACCAAGGTCCAAGCGAGCAAGAAATCCACAGACAGAAAGATCT     | 5400 |
| Db | 5341 | TCATATGAGAAACCCACCAAGGTCCAAGCGAGCAAGAAATCCACAGACAGAAAGATCT     | 5400 |
| Qy | 5401 | TCAGGGGGCTGGAATCTGTTGCTATGAGGCCCTTCAACAATATGCCACAGATCAACTGG    | 5460 |
| Db | 5401 | TCAGGGGGCTGGAATCTGTTGCTATGAGGCCCTTCAACAATATGCCACAGATCAACTGG    | 5460 |
| Qy | 5461 | AATGATATGTACAGCTGTGTGTGCTTCTGTGTGTAAGAGACTTTCATCAATCCCTTG      | 5520 |
| Db | 5461 | AATGATATGTACAGCTGTGTGTGCTTCTGTGTGTAAGAGACTTTCATCAATCCCTTG      | 5520 |
| Qy | 5521 | GCACAGTGTCCACCCCAATTGTGTTGTGACGACAGATGCTCTGACAGAGCAATGGCT      | 5580 |
| Db | 5521 | GCACAGTGTCCACCCCAATTGTGTTGTGACGACAGATGCTCTGACAGAGCAATGGCT      | 5580 |
| Qy | 5581 | TCATATGCAATTGGGCAAGTGTGTGAGGCACTGTGTGTGACCCGAGAGTGGGTGTGGACA   | 5640 |
| Db | 5581 | TCATATGCAATTGGGCAAGTGTGTGAGGCACTGTGTGTGACCCGAGAGTGGGTGTGGACA   | 5640 |

QY 5641 GTGTAGACTCTTACAGTGGCCAGAGCTGTGACACCTTATACCCAGATCCCCACA 5700  
| | | | |  
Db 5641 GTGTAGACTCTTACAGTGGCCAGAGCTGTGACACCTTATACCCAGATCCCCACA 5700  
| | | | |  
QY 5701 GCCACTACTGA 5711  
| | | | |  
Db 5701 GCCACTACTGA 5711  
| | | | |  
RESULT 6  
US-09-734-672-1  
Sequence 1, Application US/09734672  
Publication No. US20020183268A1  
GENERAL INFORMATION:  
APPLICANT: Murphy, Patricia D.  
Allen, Antoinette C.  
Alvares, Christopher P.  
Critz, Brenda S.  
Olson, Sheri J.  
Schelter, Denise B.  
Zeng, Bin  
TITLE OF INVENTION: Coding Sequences of the Human  
BRCAL Gene  
NUMBER OF SEQUENCES: 72  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Morgan Lewis & Bockius LLP  
STREET: 1111 Pennsylvania Ave., N.W.  
CITY: Washington  
STATE: District of Columbia  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/734,672  
FILING DATE: 03-Dec-2000  
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APPLICATION NUMBER: US 08/966,436  
FILING DATE: 07-No. US20020183268A1-97  
APPLICATION NUMBER: US 08/598,591  
FILING DATE: 12-Feb-96  
ATTORNEY/AGENT INFORMATION:  
NAME: Michael S. Tuscan  
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TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-739-3000  
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INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5711 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: No. US20020183268A1 Relevant  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
STRAIN: BRCAL  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: 17  
MAP POSITION: 17q21  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-734-672-1  
Query Match 99.8%; Score 5701.4; DB 9; Length 5711;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 5705; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
QY 1 AGCTCGCTGAGACTTCTGTGAGCCCGCACAGGCTGTGGGGTTTTCAGATAACTGGGCC 60

Db 1 AGCTCGCTGAGACTTCTGTGAGCCCGCACAGGCTGTGGGGTTTTCAGATAACTGGGCC 60  
| | | | |  
QY 61 CCTGGCCTCAGAGAGGCTTACCCCTGTCTGTGGTAAAGTTCATTGGAAACAGAAAGAA 120  
| | | | |  
Db 61 CCTGGCCTCAGAGAGGCTTACCCCTGTCTGTGGTAAAGTTCATTGGAAACAGAAAGAA 120  
| | | | |  
QY 121 TGGATTTATCTGCTCTTGGCTTGAAGAGTACAAATATGCTAATTAATGATGACAGAAA 180  
| | | | |  
Db 121 TGGATTTATCTGCTCTTGGCTTGAAGAGTACAAATATGCTAATTAATGATGACAGAAA 180  
| | | | |  
QY 181 TCTTAAGTGTCCCATCTGTCTGAGATTGATCAAGGAACCTGTCTCACAAAGTGTACC 240  
| | | | |  
Db 181 TCTTAAGTGTCCCATCTGTCTGAGATTGATCAAGGAACCTGTCTCACAAAGTGTACC 240  
| | | | |  
QY 241 ACATATTTTGGCAATTTTGCATGCTGAAACTTCTCAACAGAAAGAAAGGCTTTCACAGT 300  
| | | | |  
Db 241 ACATATTTTGGCAATTTTGCATGCTGAAACTTCTCAACAGAAAGAAAGGCTTTCACAGT 300  
| | | | |  
QY 301 GTCTTTATGTAAAGATGATATACCAAAAGAGCCTACAAAGAAAGTACAGATTTAGTC 360  
| | | | |  
Db 301 GTCTTTATGTAAAGATGATATACCAAAAGAGCCTACAAAGAAAGTACAGATTTAGTC 360  
| | | | |  
QY 361 AACTGTTGAAGAGCTATTGAAATCATTTGTGCTTTTACGCTTGCACAGGTTTGAAGT 420  
| | | | |  
Db 361 AACTGTTGAAGAGCTATTGAAATCATTTGTGCTTTTACGCTTGCACAGGTTTGAAGT 420  
| | | | |  
QY 421 ATGCACAACGCTATATTTTGCAGAAAAGAAATTAATCTCTCTGAACATCTAAAGATG 480  
| | | | |  
Db 421 ATGCACAACGCTATATTTTGCAGAAAAGAAATTAATCTCTCTGAACATCTAAAGATG 480  
| | | | |  
QY 481 AAGTTTCTATCATCCAAAGTATGGGCTACAGAAACCGTCCAAAGACTTCTACAGAGTG 540  
| | | | |  
Db 481 AAGTTTCTATCATCCAAAGTATGGGCTACAGAAACCGTCCAAAGACTTCTACAGAGTG 540  
| | | | |  
QY 541 AACCCGAAAATCTTCTCTTGCAGAAAACCAAGTCTCAGTGTCCAACTCTTAACTTTGAA 600  
| | | | |  
Db 541 AACCCGAAAATCTTCTCTTGCAGAAAACCAAGTCTCAGTGTCCAACTCTTAACTTTGAA 600  
| | | | |  
QY 601 CTGTGAAAGCTGTGAGAGCAAAAGCAGCGGATACAACTTAAAGAGCTGTGTACATTG 660  
| | | | |  
Db 601 CTGTGAAAGCTGTGAGAGCAAAAGCAGCGGATACAACTTAAAGAGCTGTGTACATTG 660  
| | | | |  
QY 661 AATTGGAGTCTATCTTCTGAAAGATACCGTAAATTAAGGCACTTATTCAGATGGGAG 720  
| | | | |  
Db 661 AATTGGAGTCTATCTTCTGAAAGATACCGTAAATTAAGGCACTTATTCAGATGGGAG 720  
| | | | |  
QY 721 ATCAAGAAATTTTGAACAATCACCCCTCAAGAAACAGGATGAAATCACTTTGATTTCTG 780  
| | | | |  
Db 721 ATCAAGAAATTTTGAACAATCACCCCTCAAGAAACAGGATGAAATCACTTTGATTTCTG 780  
| | | | |  
QY 781 CAAAAAGAGCTCTTGTGAATTTTCTGAGACGAGTGAACAAATCTGAACATCATCAAC 840  
| | | | |  
Db 781 CAAAAAGAGCTCTTGTGAATTTTCTGAGACGAGTGAACAAATCTGAACATCATCAAC 840  
| | | | |  
QY 841 CAGTAATATGATTTGAACACCACTGAGAACGCTGAGGCTGAGGCAATCCAGAAAGT 900  
| | | | |  
Db 841 CAGTAATATGATTTGAACACCACTGAGAACGCTGAGGCTGAGGCAATCCAGAAAGT 900  
| | | | |  
QY 901 ATCAGGGTATGTTCTGTTTCAAACTTGCAATGTGAGACCATGTGGCAAAATCTCATGCGCA 960  
| | | | |  
Db 901 ATCAGGGTATGTTCTGTTTCAAACTTGCAATGTGAGACCATGTGGCAAAATCTCATGCGCA 960  
| | | | |  
QY 961 GCTCATTCAGATGAGAACAGCACTTTTACTCATTAAGACGAATGATGAGAA 1020  
| | | | |  
Db 961 GCTCATTCAGATGAGAACAGCACTTTTACTCATTAAGACGAATGATGAGAA 1020  
| | | | |  
QY 1021 AGGCTGAATTCGTATATAAAGCAAGCCTGCTTACAGAGGCAAGCAATACAGAT 1080  
| | | | |  
Db 1021 AGGCTGAATTCGTATATAAAGCAAGCCTGCTTACAGAGGCAAGCAATACAGAT 1080  
| | | | |  
QY 1081 GGGCTGAAGTAAAGAAACATGTAATGATAGCGGACTCCAGCAAGAAAAAGGTAG 1140  
| | | | |

Db 1081 GGGCTGAAGTAAGGAAACATGTAATGATAGGCGGACTCCAGACACAGAAAAAAGTAGT 1140  
Qy 1141 ATCTGATGCTGATCCCTGCTGTGAGAGAAAGAAATGGAATAAGCAGAAACTGCCATGCT 1200  
Db 1141 ATCTGAAATGCTGATCCCTGCTGTGAGAGAAAGAAATGGAATAAGCAGAAACTGCCATGCT 1200  
Qy 1201 CAGAGAAATCTAGAGATACCTGAAAGTGTCTCTGGATACACTAAATATAGCACATTCAGA 1260  
Db 1201 CAGAGAAATCTAGAGATACCTGAAAGTGTCTCTGGATACACTAAATATAGCACATTCAGA 1260  
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QY 3781 AAGAGCTTCCCTGCTTCAACACTGTTATTTGGTAAATTAACATATACCTTCAGT 3840  
DB 3781 AAGAGCTTCCCTGCTTCAACACTGTTATTTGGTAAATTAACATATACCTTCAGT 3840  
QY 3841 CTACTAGGCATAGCACCGTGTCTACGAGTGTCTGTCTAAGAACACAGAGAGAAATTA 3900  
DB 3841 CTACTAGGCATAGCACCGTGTCTACGAGTGTCTGTCTAAGAACACAGAGAGAAATTA 3900  
QY 3901 TATCTTTGAAGAAATAGCTTAATTAAGTCTGAGTAACTAGGTAATTTGGCAAGGCACT 3960  
DB 3901 TATCTTTGAAGAAATAGCTTAATTAAGTCTGAGTAACTAGGTAATTTGGCAAGGCACT 3960  
QY 3961 AGGAACATCACCTTAGTGAAGAAACAAATGTTCTGCTAGCTGTTTCTTCAAGTGA 4020  
DB 3961 AGGAACATCACCTTAGTGAAGAAACAAATGTTCTGCTAGCTGTTTCTTCAAGTGA 4020  
QY 4021 GTGAATTGGAAGACTTGACTGCAATACAAACACCCAGGATCTTTCTTGAATGGTCTT 4080  
DB 4021 GTGAATTGGAAGACTTGACTGCAATACAAACACCCAGGATCTTTCTTGAATGGTCTT 4080  
QY 4081 CCAAAACAATGAGGATCATGCTGAAAGCCAGGAGTGTGTGAGTGAACAAGAAATGG 4140  
DB 4081 CCAAAACAATGAGGATCATGCTGAAAGCCAGGAGTGTGTGAGTGAACAAGAAATGG 4140  
QY 4141 TTTGAGATGATGAAGAAAGAGGACGGGCTTGGAGAAATTAATCAAGAAAGCAAGGA 4200  
DB 4141 TTTGAGATGATGAAGAAAGAGGACGGGCTTGGAGAAATTAATCAAGAAAGCAAGGA 4200  
QY 4201 TGAATTCAAACCTTAGTGAGAGCATCTGGGTGTGAGAGTGAACAAAGCTCTCTGAG 4260

DB 4201 TGAATTCAAACCTTAGTGAGAGCATCTGGGTGTGAGAGTGAACAAAGCTCTCTGAG 4260  
QY 4261 ACTGCTCAGGCTATACCTCTCAGAGTGAATTTTAAACCACTCAGCAGAGGATACATG 4320  
DB 4261 ACTGCTCAGGCTATACCTCTCAGAGTGAATTTTAAACCACTCAGCAGAGGATACATG 4320  
QY 4321 AACATTAACCTGATTAAGCTCCAGAGAGAAATGAGTGAATTAAGTGTGTAAGACAG 4380  
DB 4321 AACATTAACCTGATTAAGCTCCAGAGAGAAATGAGTGAATTAAGTGTGTAAGACAG 4380  
QY 4381 ATGGAGCCAGCTTCTAAGCTACCTTCAATCAATAGTACTTTCTGCTTGAAG 4440  
DB 4381 ATGGAGCCAGCTTCTAAGCTACCTTCAATCAATAGTACTTTCTGCTTGAAG 4440  
QY 4441 ACCGCGAAATCCAGAAACAAAGCATCAGAGAAAGAGATTAAGTCTCAGAGAAAGTA 4500  
DB 4441 ACCGCGAAATCCAGAAACAAAGCATCAGAGAAAGAGATTAAGTCTCAGAGAAAGTA 4500  
QY 4501 GTGAATACCTTAATAGCAGAAATCCAGAGGCTTTCTGCTGACAAAGTGTGCTG 4560  
DB 4501 GTGAATACCTTAATAGCAGAAATCCAGAGGCTTTCTGCTGACAAAGTGTGCTG 4560  
QY 4561 CAGATAGTTCTACCAATTAATTAAGAACAGAGTGAAGAGTCAATCCCTTTTAAT 4620  
DB 4561 CAGATAGTTCTACCAATTAATTAAGAACAGAGTGAAGAGTCAATCCCTTTTAAT 4620  
QY 4621 GCCCATCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4680  
DB 4621 GCCCATCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4680  
QY 4681 ACTACCATCTCAAGAGAGGCTCATTAAGTGTGTAATGAGAGAGCAACAGCTGAG 4740  
DB 4681 ACTACCATCTCAAGAGAGGCTCATTAAGTGTGTAATGAGAGAGCAACAGCTGAG 4740  
QY 4741 AGTCTGGCCACAGATTTGACGAAACATTTACTTCCAGAGCAAGATCTAGAGGAA 4800  
DB 4741 AGTCTGGCCACAGATTTGACGAAACATTTACTTCCAGAGCAAGATCTAGAGGAA 4800  
QY 4801 CCCCTTACCTGGAATCTGGAATCAGCCCTCTCTGATGACCCGATCTGATCCTCTG 4860  
DB 4801 CCCCTTACCTGGAATCTGGAATCAGCCCTCTCTGATGACCCGATCTGATCCTCTG 4860  
QY 4861 AAGACAGAGCCCAAGAGTCAAGTCTGTTGCAACATACATCTTCAACCTCTGATTA 4920  
DB 4861 AAGACAGAGCCCAAGAGTCAAGTCTGTTGCAACATACATCTTCAACCTCTGATTA 4920  
QY 4921 AAGTCCCAATTTGAAGTTGCAAGATCTGCCAGAGTCCAGCTGCTCATCTACTG 4980  
DB 4921 AAGTCCCAATTTGAAGTTGCAAGATCTGCCAGAGTCCAGCTGCTCATCTACTG 4980  
QY 4981 ATACTGCTGGGATTAATGCAATGGAAGAAATGAGACAGAGGAGAGCAGAAATTAAG 5040  
DB 4981 ATACTGCTGGGATTAATGCAATGGAAGAAATGAGACAGAGGAGAGCAGAAATTAAG 5040  
QY 5041 CTTCAACGAAAGGCTCAACAAAGAAATGTCATGCTGCTGCTGCTGCTGCTGCTG 5100  
DB 5041 CTTCAACGAAAGGCTCAACAAAGAAATGTCATGCTGCTGCTGCTGCTGCTGCTG 5100  
QY 5101 AATTTATGCTGCTGCAAGTTTCCAGAGAAACCAATCACTTAATTAATTAATTA 5160  
DB 5101 AATTTATGCTGCTGCAAGTTTCCAGAGAAACCAATCACTTAATTAATTAATTA 5160  
QY 5161 CTGAAGAACATCACTATCTGTTATGAAACAGATGCTGAGTGTGTAAGAGGACAC 5220  
DB 5161 CTGAAGAACATCACTATCTGTTATGAAACAGATGCTGAGTGTGTAAGAGGACAC 5220  
QY 5221 TGAATATTTTCTAGGAATTCGGGAGGAAATGGTATGATTTTCTGAGTGAAG 5280  
DB 5221 TGAATATTTTCTAGGAATTCGGGAGGAAATGGTATGATTTTCTGAGTGAAG 5280  
QY 5281 AGTCTATTAAGAAAGAAATGCTGAATGATGATTTTGAAGTCAAGAGAGATGAG 5340



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SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 4552
; LENGTH: 424
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO L78833.1
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.4
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.1
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.3
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.9
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.9
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.4
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 2.3
; US-09-864-761-4552

Query Match          3.1%; Score 175.4; DB 10; Length 424;
Best Local Similarity 94.3%; Pred. No. 2e-34; Mismatches 11; Indels 0; Gaps 0;
Matches 182; Conservative 0;

QY 4303 AGCAGAGGATACCATGACATTAACCTGATTAAGCTCCAGAGGAAATGGCTGAAGTAG 4362
    |||||
DB 232 AGCAGAGGATACCATGACATTAACCTGATTAAGCTCCAGAGGAAATGGCTGAAGTAG 291
    |||||
QY 4363 AAGCTGTATTGAAACAGCATGGGAGCCAGCTTTTAAACGCTTACCTTCATCATTAAGTG 4422
    |||||
DB 292 AAGCTGTATTGAAACAGCATGGGAGCCAGCTTTTAAACGCTTACCTTCATCATTAAGTG 351
    |||||
QY 4423 ACTCTTGCCCTTGGAGGACCTGCGAATCCAGAACAAAGCATCAGAAAAAGCAGTAT 4482
    |||||
DB 352 ACTCTTGCCCTTGGAGGACCTGCGAATCCAGAACAAAGCATCAGAAAAAGCAGTAT 411
    |||||
QY 4483 TAACCTTCACAGAA 4495
    |||||
DB 412 ATGTGTGCCAA 424

RESULT 10
US-09-864-761-21299
; Sequence 21299, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecmice-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 21299
; LENGTH: 147
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO L78833.1
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.4
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.1
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.3
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.9
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.9
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.4
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 2.3
; OTHER INFORMATION: EST HUMAN HIT: AUI25312.1, EVALUE 2.00e-77
; OTHER INFORMATION: SWISSPROT HIT: P38398, EVALUE 4.00e-12
; OTHER INFORMATION: NT HIT: g11424969, EVALUE 1.00e-77
; US-09-864-761-21299

Query Match          2.6%; Score 147; DB 10; Length 147;
Best Local Similarity 100.0%; Pred. No. 1.8e-27; Mismatches 0; Indels 0; Gaps 0;
Matches 147; Conservative 0;

QY 4330 TGATTAAGCTCCAGAGGAATGGCTGACATGAGAGCTGTAGACACATGGAGGCC 4389
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DB 1 TGATTAAGCTCCAGAGGAATGGCTGACATGAGAGCTGTAGACACATGGAGGCC 60
    |||||
QY 4390 AGCCTTCTAAGCAGTACCTTCCATCATTAAGTGAAGTCTTCTGACCTTGAGACCTGGAA 4449
    |||||
DB 61 AGCCTTCTAAGCAGTACCTTCCATCATTAAGTGAAGTCTTCTGACCTTGAGACCTGGAA 120
    |||||
QY 4450 ATCCAGAACAAAGCATCAGAAAAAG 4476
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DB 121 ATCCAGAACAAAGCATCAGAAAAAG 147

RESULT 11
US-09-818-875-653
; Sequence 653, Application US/0981875
; Publication No. US20030051270A1
; GENERAL INFORMATION:
; APPLICANT: Kmiec, Eric B.
; APPLICANT: Gampert, Howard B.
; APPLICANT: Rice, Michael C.
; TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single
; FILE REFERENCE: Napro-4
; CURRENT APPLICATION NUMBER: US/09/818,875
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: US 60/192,176
; PRIOR FILING DATE: 2000-03-27
; PRIOR APPLICATION NUMBER: US 60/192,179
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2000

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; SOFTWARE: Friedman macro Napro4
; SEQ ID NO 658

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LENGTH: 121  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-818-875-658

Query Match 2.1%; Score 121; DB 9; Length 121;  
Best Local Similarity 100.0%; Pred. No. 7.1e-21;  
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 91 CTGGGTAAGTTCATTGGACGAGAAATGATTTATCTGCTCTTCGCGTTGAAG 150  
DB 121 CTGGGTAAGTTCATTGGACGAGAAATGATTTATCTGCTCTTCGCGTTGAAG 62  
QY 151 TACAAATGCTCATTAATGCTATGACGAAATCTTAGAGTGTCCCATCTGCTGAGTTGA 210  
DB 61 TACAAATGCTCATTAATGCTATGACGAAATCTTAGAGTGTCCCATCTGCTGAGTTGA 2

QY 211 T 211  
DB 1 T 1

RESULT 15  
US-09-818-875-661  
Sequence 661, Application US/09818875  
Publication No. US20030051270A1  
GENERAL INFORMATION:  
APPLICANT: Kmiec, Eric B.  
APPLICANT: Gamper, Howard B.  
APPLICANT: Rice, Michael C.  
TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single  
FILE REFERENCE: Napro-4  
CURRENT APPLICATION NUMBER: US/09/818,875  
CURRENT FILING DATE: 2001-03-27  
PRIOR APPLICATION NUMBER: US 60/192,176  
PRIOR FILING DATE: 2000-03-27  
PRIOR APPLICATION NUMBER: US 60/208,538  
PRIOR FILING DATE: 2000-06-01  
PRIOR APPLICATION NUMBER: US 60/244,989  
PRIOR FILING DATE: 2000-10-30  
NUMBER OF SEQ ID NOS: 4385  
SOFTWARE: Friedmann macro Napro4  
SEQ ID NO 661  
LENGTH: 121  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-818-875-661

Query Match 2.1%; Score 121; DB 9; Length 121;  
Best Local Similarity 100.0%; Pred. No. 7.1e-21;  
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 120 ATGATTTATCTGCTTGGCGTTGAAGTACAAATGCTATTAATGCTATGCAAGAA 179  
DB 1 ATGATTTATCTGCTTGGCGTTGAAGTACAAATGCTATTAATGCTATGCAAGAA 60  
QY 180 ATCTTAGAGTGTCCATCTGTCTGAGTTGATCAAGAACTGTCTCCAAAGTGTGAC 239  
DB 61 ATCTTAGAGTGTCCATCTGTCTGAGTTGATCAAGAACTGTCTCCAAAGTGTGAC 120  
QY 240 C 240  
DB 121 C 121

Search completed: June 13, 2003, 12:45:45  
Job time : 727.5 secs



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 12, 2003, 23:09:35 ; Search time 14037.5 Seconds

(without alignments)  
11840.151 Million cell updates/sec

Title: US-09-734-672-3

Perfect score: 5711

Sequence: 1 AGCTCCGCTAGACTCTCTG3.....TCCCCACAGCAGCTACTGA 5711

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

GenEmbl:\*

- 1: gb\_ba:\*
- 2: gb\_hcg:\*
- 3: gb\_in:\*
- 4: gb\_ov:\*
- 5: gb\_ov:\*
- 6: gb\_ov:\*
- 7: gb\_ph:\*
- 8: gb\_pl:\*
- 9: gb\_pl:\*
- 10: gb\_ro:\*
- 11: gb\_ro:\*
- 12: gb\_ro:\*
- 13: gb\_ro:\*
- 14: gb\_ro:\*
- 15: gb\_ro:\*
- 16: gb\_ro:\*
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- 27: gb\_ro:\*
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- 33: gb\_ro:\*
- 34: gb\_ro:\*
- 35: gb\_ro:\*
- 36: gb\_ro:\*
- 37: gb\_ro:\*
- 38: gb\_ro:\*
- 39: gb\_ro:\*
- 40: gb\_ro:\*
- 41: gb\_ro:\*

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score  | Query Match | Length | DB | ID       | Description          |
|------------|--------|-------------|--------|----|----------|----------------------|
| 1          | 5711   | 100.0       | 5711   | 6  | AR007334 | AR007334 Sequence    |
| 2          | 5711   | 100.0       | 5711   | 6  | AR112810 | AR112810 Sequence    |
| 3          | 5709.4 | 100.0       | 5711   | 6  | AR033056 | AR033056 Sequence    |
| 4          | 5709.4 | 100.0       | 5711   | 9  | HSU14680 | U14680 Homo sapien   |
| 5          | 5709.4 | 100.0       | 5712   | 6  | AR070223 | AR070223 Sequence    |
| 6          | 5709.4 | 100.0       | 5712   | 6  | AR118507 | AR118507 Sequence    |
| 7          | 5709.4 | 100.0       | 5712   | 6  | AR125601 | AR125601 Sequence    |
| 8          | 5709.4 | 100.0       | 5712   | 6  | AR184044 | AR184044 Sequence    |
| 9          | 5709.4 | 100.0       | 5914   | 6  | AR004673 | AR004673 Sequence    |
| 10         | 5709.4 | 100.0       | 5914   | 6  | AR008159 | AR008159 Sequence    |
| 11         | 5709.4 | 100.0       | 5914   | 6  | AR136942 | AR136942 Sequence    |
| 12         | 5709.4 | 100.0       | 5914   | 6  | 176943   | 176943 Sequence 1    |
| 13         | 5709.4 | 100.0       | 5914   | 6  | 180938   | 180938 Sequence 1    |
| 14         | 5709.4 | 100.0       | 5914   | 6  | 181034   | 181034 Sequence 1    |
| 15         | 5707.8 | 99.9        | 5711   | 6  | AR048660 | AR048660 Sequence    |
| 16         | 5707.8 | 99.9        | 5711   | 6  | AR048666 | AR048666 Sequence    |
| 17         | 5707.8 | 99.9        | 5711   | 6  | 140795   | 140795 Sequence 4    |
| 18         | 5707.8 | 99.9        | 5711   | 6  | 140801   | 140801 Sequence 4    |
| 19         | 5703   | 99.9        | 5711   | 6  | AR007335 | AR007335 Sequence    |
| 20         | 5703   | 99.9        | 5711   | 6  | AR112809 | AR112809 Sequence    |
| 21         | 5701.4 | 99.8        | 5711   | 6  | AR007333 | AR007333 Sequence    |
| 22         | 5701.4 | 99.8        | 5711   | 6  | AR112808 | AR112808 Sequence    |
| 23         | 5701.4 | 99.8        | 5711   | 6  | 159546   | 159546 Sequence 1    |
| 24         | 5698.4 | 99.8        | 5712   | 6  | AR048668 | AR048668 Sequence 1  |
| 25         | 5698.4 | 99.8        | 5712   | 6  | 140803   | 140803 Sequence 12   |
| 26         | 5697.4 | 99.8        | 5710   | 6  | AR048662 | AR048662 Sequence 6  |
| 27         | 5697.4 | 99.8        | 5710   | 6  | 140797   | 140797 Sequence 6    |
| 28         | 5695.4 | 99.7        | 5709   | 6  | AR048658 | AR048658 Sequence    |
| 29         | 5695.4 | 99.7        | 5709   | 6  | AR048663 | AR048663 Sequence    |
| 30         | 5695.4 | 99.7        | 5709   | 6  | AR048664 | AR048664 Sequence    |
| 31         | 5695.4 | 99.7        | 5709   | 6  | AR048665 | AR048665 Sequence    |
| 32         | 5695.4 | 99.7        | 5709   | 6  | 140793   | 140793 Sequence 2    |
| 33         | 5695.4 | 99.7        | 5709   | 6  | 140798   | 140798 Sequence 7    |
| 34         | 5695.4 | 99.7        | 5709   | 6  | 140799   | 140799 Sequence 8    |
| 35         | 5695.4 | 99.7        | 5709   | 6  | 140800   | 140800 Sequence 9    |
| 36         | 5691.4 | 99.7        | 5707   | 6  | AR048667 | AR048667 Sequence 11 |
| 37         | 5691.4 | 99.7        | 5707   | 6  | 140802   | 140802 Sequence 11   |
| 38         | 5659.4 | 99.1        | 5709   | 6  | AX281859 | AX281859 Sequence    |
| 39         | 5655.4 | 99.0        | 5689   | 6  | AR048659 | AR048659 Sequence    |
| 40         | 5655.4 | 99.0        | 5689   | 6  | 140794   | 140794 Sequence 3    |
| 41         | 5629.2 | 98.6        | 5770   | 6  | AR048661 | AR048661 Sequence    |
| 42         | 5629.2 | 98.6        | 5770   | 6  | 140796   | 140796 Sequence 5    |
| 43         | 5590.4 | 97.9        | 5656   | 6  | AR048657 | AR048657 Sequence    |
| 44         | 5590.4 | 97.9        | 5656   | 6  | 140792   | 140792 Sequence 1    |
| 45         | 5532.4 | 96.9        | 5693   | 9  | AF005068 | AF005068 Homo sapi   |

#### ALIGNMENTS

RESULT 1  
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LOCUS AR007334 5711 bp DNA linear PAT 04-DEC-1998  
DEFINITION Sequence 3 from patent US 5750400.  
ACCESSION AR007334  
VERSION AR007334.1 GI:3966818  
KEYWORDS  
SOURCE  
ORGANISM  
Unknown.  
Unclassified.  
REFERENCE  
1 (bases 1 to 5711)  
Murphy,P.D., Allen,A.C., Alvares,C.P., Critz,B.S., Olson,S.J.,  
Schelter,D.B. and Zeng,B.  
TITLE  
Coding sequences of the human BRCA1 gene  
JOURNAL  
Patent: US 5750400-A 3 12-MAY-1998;

Pred. No. is the number of results predicted by chance to have a

FEATURES  
Location/Qualifiers  
source 1..5711  
/organism="unknown"  
BASE COUNT 1956 a 1098 c 1274 g 1383 t  
ORIGIN

Query Match 100.0%; Score 5711; DB 6; Length 5711;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 5711; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 AGCTGCTGAGACTCTTCGGAACCCGCAACAGGCTGTGGGGTTTCTCAGATACCTGGCC 60  
QY 61 CCTGGCTCAGAGAGGCTTCAACCTCTGCTGCGGTTAAAGTTCATGGAAAGAAAGAA 120  
DB 61 CCTGGCTCAGAGAGGCTTCAACCTCTGCTGCGGTTAAAGTTCATGGAAAGAAAGAA 120  
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DB 121 TGGATTATCTGCTCTTCGCGTTGAAGAAATGTCATTAATGCTATGCAAGAAA 180  
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DB 181 TCTTAGAGTGTCCCATCTGTCTGGAAGTTGATCAGGAACCTGTCCCAAAAGTGTACC 240  
QY 241 ACATATTTTGGCAATTTTGCATGCTGGAACCTCTCAACAGAAAGAGGCTTCACAGT 300  
DB 241 ACATATTTTGGCAATTTTGCATGCTGGAACCTCTCAACAGAAAGAGGCTTCACAGT 300  
QY 301 GTCTTTATGTAGAAGATATTAACCAAAAGAGCTTAACAGAAAGTACGAGATTAGTC 360  
DB 301 GTCTTTATGTAGAAGATATTAACCAAAAGAGCTTAACAGAAAGTACGAGATTAGTC 360  
QY 361 AACTGTGTGAAGAGTATGGAATAATCATTTTGTCTTTCAGCTTACACAGTTGGAGT 420  
DB 361 AACTGTGTGAAGAGTATGGAATAATCATTTTGTCTTTCAGCTTACACAGTTGGAGT 420  
QY 421 ATGCAACAGCTATTAATTTGCAAAAGAAATTAATCTCTGAAACATCTTAAAGATG 480  
DB 421 ATGCAACAGCTATTAATTTGCAAAAGAAATTAATCTCTGAAACATCTTAAAGATG 480  
QY 481 AAGTTTCTATCATCCAAAGTATGGGCTACAGAAACCGTGCCAAAGACTTCTACAGAGT 540  
DB 481 AAGTTTCTATCATCCAAAGTATGGGCTACAGAAACCGTGCCAAAGACTTCTACAGAGT 540  
QY 541 AACCAGAAATCCCTTCTCTGCAAGAAACCAAGTCTAGAGTCCAACTCTCTAACCTTGGAA 600  
DB 541 AACCAGAAATCCCTTCTCTGCAAGAAACCAAGTCTAGAGTCCAACTCTCTAACCTTGGAA 600  
QY 601 CTGTGAGAACTCTGAGGCAAGACGCGGATACAACTCTCAAAAGCGTCTGTCAATTG 660  
DB 601 CTGTGAGAACTCTGAGGCAAGACGCGGATACAACTCTCAAAAGCGTCTGTCAATTG 660  
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Db 1861 AAACGAAAGCTGAACCTTATAGCAGACGATTAAGCAATATGGAATCCGAATTAATCC 1920  
QY 1921 ACAATTTCAAAAGCAGCTTAAAAAGAAATAGGCTGAGAGAAAGTCTTCAACAGCATATTC 1980  
Db 1921 ACAATTTCAAAAGCAGCTTAAAAAGAAATAGGCTGAGAGAAAGTCTTCAACAGCATATTC 1980  
QY 1981 ATGCGCTTGAATAGTAGTAGTAGTAAGAAATCTTAAGCCCACTTAATTTGATCTGAAA 2040  
Db 1981 ATGCGCTTGAATAGTAGTAGTAGTAAGAAATCTTAAGCCCACTTAATTTGATCTGAAA 2040  
QY 2041 TTGATAGTTGTTCTGACGTGAAGATTAAGAAAAAAGTAAACCAATGCCAGTCA 2100  
Db 2041 TTGATAGTTGTTCTGACGTGAAGATTAAGAAAAAAGTAAACCAATGCCAGTCA 2100  
QY 2101 GGCACAGCAGAAACCTTCAACTCATGGAAGGTAAAGAACTGCACTGAGCCAGAAAGA 2160  
Db 2101 GGCACAGCAGAAACCTTCAACTCATGGAAGGTAAAGAACTGCACTGAGCCAGAAAGA 2160  
QY 2161 GTTAAACGCCAAATGAACAGACAACTAAAGACATGACAGCGATACCTTCCAGAGCTGA 2220  
Db 2161 GTTAAACGCCAAATGAACAGACAACTAAAGACATGACAGCGATACCTTCCAGAGCTGA 2220  
QY 2221 AGTTAAACAAATGCACTGCTGTTTCTTACTAAGTGTCAAAATACAGTGAATCTTAAAGAT 2280  
Db 2221 AGTTAAACAAATGCACTGCTGTTTCTTACTAAGTGTCAAAATACAGTGAATCTTAAAGAT 2280  
QY 2281 TTGTCATCTTACGCTTCCAGAGAAAGAAAGAGAACTTAAAGACAGTTAAAGT 2340  
Db 2281 TTGTCATCTTACGCTTCCAGAGAAAGAAAGAGAACTTAAAGACAGTTAAAGT 2340  
QY 2341 CTAAATATGCTGAGAGACCCCAAGATCTCATGTTAAGTGAAGAAAGGTTTGAACCTG 2400  
Db 2341 CTAAATATGCTGAGAGACCCCAAGATCTCATGTTAAGTGAAGAAAGGTTTGAACCTG 2400  
QY 2401 AAAGATCTGTAGAGTACAGTATTTCAATTTGATCTCTGATCTGATTAAGCACTACAG 2460  
Db 2401 AAAGATCTGTAGAGTACAGTATTTCAATTTGATCTCTGATCTGATTAAGCACTACAG 2460

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|----|------|--|------|
| QY | 2461 | AAAAGTATCTCGTTACTCTGGAAGTTAGCACTCTAGGAAAGCCAAAACGAAACCAATTAAT  | 2520 |
| Db | 2461 | AAAAGTATCTCGTTACTCTGGAAGTTAGCACTCTAGGAAAGCCAAAACGAAACCAATTAAT  | 2520 |
| QY | 2521 | GGTGTGCTGAGTGTGAGCATTTTGAAAACCCCAAGGGAGCTTAATCAATGGTGTTCAAAG   | 2580 |
| Db | 2521 | GGTGTGCTGAGTGTGAGCATTTTGAAAACCCCAAGGGAGCTTAATCAATGGTGTTCAAAG   | 2580 |
| QY | 2581 | ATPATTAAGAAATGACACAGAAAGGCTTTAAGTATCCATTGGGACATGAAGTTAACCAAGTC | 2640 |
| Db | 2581 | ATPATTAAGAAATGACACAGAAAGGCTTTAAGTATCCATTGGGACATGAAGTTAACCAAGTC | 2640 |
| QY | 2641 | GGGAAACAAGCATAGAAATGGAAGAAAGTGAATTGATGCTCAGTATTTTGCAGAAATCAT   | 2700 |
| Db | 2641 | GGGAAACAAGCATAGAAATGGAAGAAAGTGAATTGATGCTCAGTATTTTGCAGAAATCAT   | 2700 |
| QY | 2701 | TCAAGGTTTCAAGGCGCAGTCAATTTGCTCTGTGTTTCAAAATCCAGAAATGCAGAAAGG   | 2760 |
| Db | 2701 | TCAAGGTTTCAAGGCGCAGTCAATTTGCTCTGTGTTTCAAAATCCAGAAATGCAGAAAGG   | 2760 |
| QY | 2761 | AATGTGCAACATTTCTGTCCCACTGTGGGTCTTTAAAGAAACAAAGTCCAAAAGTCACTT   | 2820 |
| Db | 2761 | AATGTGCAACATTTCTGTCCCACTGTGGGTCTTTAAAGAAACAAAGTCCAAAAGTCACTT   | 2820 |
| QY | 2821 | TTGAATGTGAACAAAAGGAAGAAATATACGAAAGAAATGAGTCTAATATCAAGCCTGTAC   | 2880 |
| Db | 2821 | TTGAATGTGAACAAAAGGAAGAAATATACGAAAGAAATGAGTCTAATATCAAGCCTGTAC   | 2880 |
| QY | 2881 | AGACAGTTAATATCAGTCGAGGCTTCTGTGGTGTGTCAGAAAGATTAAGCAGTTGATA     | 2940 |
| Db | 2881 | AGACAGTTAATATCAGTCGAGGCTTCTGTGGTGTGTCAGAAAGATTAAGCAGTTGATA     | 2940 |
| QY | 2941 | ATGCCAAATGTAGTATCAAGAGAGGCTCTAAGTTTGTCTATCATCTCAGTTCCAGAGCA    | 3000 |
| Db | 2941 | ATGCCAAATGTAGTATCAAGAGAGGCTCTAAGTTTGTCTATCATCTCAGTTCCAGAGCA    | 3000 |
| QY | 3001 | ACGAAACTGAGCATCTATTACTCCAAATTAACATGACCTTTTACAAACCCCATATGCTATAC | 3060 |
| Db | 3001 | ACGAAACTGAGCATCTATTACTCCAAATTAACATGACCTTTTACAAACCCCATATGCTATAC | 3060 |
| QY | 3061 | CACCACTTTTCCCATCAAGTCAATTTGTGTAAACCTAATGTAAAGAAATCTGCTAGAG     | 3120 |
| Db | 3061 | CACCACTTTTCCCATCAAGTCAATTTGTGTAAACCTAATGTAAAGAAATCTGCTAGAG     | 3120 |
| QY | 3121 | AAAACCTTTGAGGAACATTCATATGCTGAAAGAGAAATGGGAAATGAGAACATTTCCAA    | 3180 |
| Db | 3121 | AAAACCTTTGAGGAACATTCATATGCTGAAAGAGAAATGGGAAATGAGAACATTTCCAA    | 3180 |
| QY | 3181 | GTACAGTAGGACAAATTAAGCCGTAAATTAACCTTAGAGAAATGTTTTTAAAGAACCGACT  | 3240 |
| Db | 3181 | GTACAGTAGGACAAATTAAGCCGTAAATTAACCTTAGAGAAATGTTTTTAAAGAACCGACT  | 3240 |
| QY | 3241 | CAAGCAATATTAATGAAGTAGTTCAGTACTAATGAAGTGGGCTCCAGATTTAATGAAA     | 3300 |
| Db | 3241 | CAAGCAATATTAATGAAGTAGTTCAGTACTAATGAAGTGGGCTCCAGATTTAATGAAA     | 3300 |
| QY | 3301 | TAGGTTCCAGTGATGAAAACATTCAGACAGAACTAGGTAGAAAACAGAGGCGCAAAATTTGA | 3360 |
| Db | 3301 | TAGGTTCCAGTGATGAAAACATTCAGACAGAACTAGGTAGAAAACAGAGGCGCAAAATTTGA | 3360 |
| QY | 3361 | ATGCTATGCTTAGATTAAAGGGTTTTTGCAACCTGAGGTCTATTAACAAAGTCTTCTGTGAA | 3420 |
| Db | 3361 | ATGCTATGCTTAGATTAAAGGGTTTTTGCAACCTGAGGTCTATTAACAAAGTCTTCTGTGAA | 3420 |
| QY | 3421 | GTAAATGTAGCAATCCGTGAATAAAAAAGCAAGATATGAAGAAGTATGCTCAGCTGTAA    | 3480 |
| Db | 3421 | GTAAATGTAGCAATCCGTGAATAAAAAAGCAAGATATGAAGAAGTATGCTCAGCTGTAA    | 3480 |
| QY | 3481 | ATACAGATTTCCTCCATATCTGATTTCAAGTAACTTAGAAACAGCCTATGGAAGTATGTC   | 3540 |
| Db | 3481 | ATACAGATTTCCTCCATATCTGATTTCAAGTAACTTAGAAACAGCCTATGGAAGTATGTC   | 3540 |
| QY | 3541 | ATGCATCTCAGGTTTGTCTGAGACACTGATGACCTGTTAGATGATGTGAAATTAAGG      | 3600 |

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|----|------|---|------|
| Db | 3541 | ATGCACTCAGAGTTTGTTCTGAGACACCTGATGACCTGTTTAGATGATGGTAAATTAAGC    | 3600 |
| Qy | 3601 | AAGATACTAGTGTTCGTGAAAATACATTTAGAAAGTTCGTGTTTTAGCAAAAGCG         | 3660 |
| Db | 3601 | AAGATACTAGTGTTCGTGAAAATACATTTAGAAAGTTCGTGTTTTAGCAAAAGCG         | 3660 |
| Qy | 3661 | TCGAAAGAGAGCTTAGCAGAGAGTCTAGCCCTTTCAACCATAKACTTTGGCTCAGG        | 3720 |
| Db | 3661 | TCGAAAGAGAGCTTAGCAGAGAGTCTAGCCCTTTCAACCATAKACTTTGGCTCAGG        | 3720 |
| Qy | 3721 | GTTACCGAAGAGGGGCCAAGAAATTTAGAGTCTCAGAAAGAACTTATCTTAGAGAGTGG     | 3780 |
| Db | 3721 | GTTACCGAAGAGGGGCCAAGAAATTTAGAGTCTCAGAAAGAACTTATCTTAGAGAGTGG     | 3780 |
| Qy | 3781 | AAGAGCTTCCCTGCTCCACACCTGTTATTTGGTAAAGTAAACAATAATACCTTCAGT       | 3840 |
| Db | 3781 | AAGAGCTTCCCTGCTCCACACCTGTTATTTGGTAAAGTAAACAATAATACCTTCAGT       | 3840 |
| Qy | 3841 | CTACTAGGCATAGCACCGTTCCTACCGAGTCTGCTTAAGAAACAGAGAGAAATTTAT       | 3900 |
| Db | 3841 | CTACTAGGCATAGCACCGTTCCTACCGAGTCTGCTTAAGAAACAGAGAGAAATTTAT       | 3900 |
| Qy | 3901 | TATCATTTGAAGAAATAGCTTAATATGACTGAGATAACCGAGTAAATTTGGCAAGGCACTCTC | 3960 |
| Db | 3901 | TATCATTTGAAGAAATAGCTTAATATGACTGAGATAACCGAGTAAATTTGGCAAGGCACTCTC | 3960 |
| Qy | 3961 | AGGAACATCACCTTAGTAGAGAAACAAATGTTCTGCTAGCTGTTTTCTTCAACAGTGA      | 4020 |
| Db | 3961 | AGGAACATCACCTTAGTAGAGAAACAAATGTTCTGCTAGCTGTTTTCTTCAACAGTGA      | 4020 |
| Qy | 4021 | GTTGAATTGGAAGACTTGACTGCAAAATACAAACCCAGAGATCCTTTCTTGATTTGGTCTT   | 4080 |
| Db | 4021 | GTTGAATTGGAAGACTTGACTGCAAAATACAAACCCAGAGATCCTTTCTTGATTTGGTCTT   | 4080 |
| Qy | 4081 | CCAAACAAATAGGCACTAGCTGTAAGAGCCAGGAGTTGGTCTGAGTGAACAAGAAATTTGG   | 4140 |
| Db | 4081 | CCAAACAAATAGGCACTAGCTGTAAGAGCCAGGAGTTGGTCTGAGTGAACAAGAAATTTGG   | 4140 |
| Qy | 4141 | TTTCAGATGATGAAGAAAGAGAAACGGGCTTTGGAAGAAATTAATCAAGAAAGCAAGCA     | 4200 |
| Db | 4141 | TTTCAGATGATGAAGAAAGAGAAACGGGCTTTGGAAGAAATTAATCAAGAAAGCAAGCA     | 4200 |
| Qy | 4201 | TGGAATTCAACTTAGTGAAGACACAGACTGTGGGTGTGAGAGTGAACAAGCTCTCTGAAG    | 4260 |
| Db | 4201 | TGGAATTCAACTTAGTGAAGACACAGACTGTGGGTGTGAGAGTGAACAAGCTCTCTGAAG    | 4260 |
| Qy | 4261 | ACTGTCAGGGCTATCCTCTCAGAGTACATTTTAACAACCTCAGCAGAGGGATTCACATGC    | 4320 |
| Db | 4261 | ACTGTCAGGGCTATCCTCTCAGAGTACATTTTAACAACCTCAGCAGAGGGATTCACATGC    | 4320 |
| Qy | 4321 | AACATTAACCTGATAAAGCTCCAGCAGGAAATGSCITGAATAGAAAGCTGTGTTGAACAGC   | 4380 |
| Db | 4321 | AACATTAACCTGATAAAGCTCCAGCAGGAAATGSCITGAATAGAAAGCTGTGTTGAACAGC   | 4380 |
| Qy | 4381 | ATGGAGGCTAGCTTTAACAAGCTTACACCTTCCATCAATAAGTACCTTCTGCGCCCTTAGG   | 4440 |
| Db | 4381 | ATGGAGGCTAGCTTTAACAAGCTTACACCTTCCATCAATAAGTACCTTCTGCGCCCTTAGG   | 4440 |
| Qy | 4441 | ACCTGCGGAATTCAGAAACAAAGCAATTCAGAAAGAGATTAATTACTTCCAGAAAGTA      | 4500 |
| Db | 4441 | ACCTGCGGAATTCAGAAACAAAGCAATTCAGAAAGAGATTAATTACTTCCAGAAAGTA      | 4500 |
| Qy | 4501 | GTTGAATACCTATAGCAGAAATCCAGAAAGGCTTTTCTGTCGACAAATTTGAGGTGCTG     | 4560 |
| Db | 4501 | GTTGAATACCTATAGCAGAAATCCAGAAAGGCTTTTCTGTCGACAAATTTGAGGTGCTG     | 4560 |
| Qy | 4561 | CAGATAGTTCACAGATTAATAAAGAACAGAGAGTGAAGAGTCAATCCCTCTTAAT         | 4620 |
| Db | 4561 | CAGATAGTTCACAGATTAATAAAGAACAGAGAGTGAAGAGTCAATCCCTCTTAAT         | 4620 |
| Qy | 4621 | GCCCATCTTTAGATGATAGTGGTGAATGCAATGCAAGTTCCTCTGGAGTCTTCAAGATTGA   | 4680 |
| Db | 4621 | GCCCATCTTTAGATGATAGTGGTGAATGCAATGCAAGTTCCTCTGGAGTCTTCAAGATTGA   | 4680 |



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| Db | 4621 | GCACATCATTTGATGATAGTGGTGCATGCAACAGTGGCTCTGGGAGTCTTACGATTTGAA   | 4680 |
| OY | 4681 | ACTACCCATCTCCAGAGAGGCTCATTTAAGTTGTTGATGTGGAGAGCAACGCTGGAA      | 4740 |
| Db | 4681 | ACTACCCATCTCCAGAGAGGCTCATTTAAGTTGTTGATGTGGAGAGCAACGCTGGAA      | 4740 |
| OY | 4741 | AGTCGGGGCCACACGATTTGACGGAAACATCTTACTGGCCAAAGGCAGAACTTAAAGGAA   | 4800 |
| Db | 4741 | AGTCGGGGCCACACGATTTGACGGAAACATCTTACTGGCCAAAGGCAGAACTTAAAGGAA   | 4800 |
| OY | 4801 | CCCCCTTACTGGAATCTGGAATACAGCCCTCTCTGATGACCCCTGAATCTGATCCTTCTG   | 4860 |
| Db | 4801 | CCCCCTTACTGGAATCTGGAATACAGCCCTCTCTGATGACCCCTGAATCTGATCCTTCTG   | 4860 |
| OY | 4861 | AAGACAGAGCCCCACAGAGTCACTGGTGGGCAACATCCATCTTCAACCTCTGCATTTGA    | 4920 |
| Db | 4861 | AAGACAGAGCCCCACAGAGTCACTGGTGGGCAACATCCATCTTCAACCTCTGCATTTGA    | 4920 |
| OY | 4921 | AAGTTTCCCCAATTGAAAGTTGACAGATCTGCCACAGAGTCAGCTGCTCATCTCTCTG     | 4980 |
| Db | 4921 | AAGTTTCCCCAATTGAAAGTTGACAGATCTGCCACAGAGTCAGCTGCTCATCTCTCTG     | 4980 |
| OY | 4981 | ATATCGCTGGGATPATATGATTCATGGAAGAAAGTGGAGCAGGAGAGACAGAAATTGACAG  | 5040 |
| Db | 4981 | ATATCGCTGGGATPATATGATTCATGGAAGAAAGTGGAGCAGGAGAGACAGAAATTGACAG  | 5040 |
| OY | 5041 | CTTCAACAGAAAGGCTCAACAAAAGATGTCATGTGGTGTCTGGCTGACCCACAGAG       | 5100 |
| Db | 5041 | CTTCAACAGAAAGGCTCAACAAAAGATGTCATGTGGTGTCTGGCTGACCCACAGAG       | 5100 |
| OY | 5101 | AATTTATGCTGTGTGATCAAGTTTGCAGAAAACACACATCATCTTAACTTAATCTAAATTA  | 5160 |
| Db | 5101 | AATTTATGCTGTGTGATCAAGTTTGCAGAAAACACACATCATCTTAACTTAATCTAAATTA  | 5160 |
| OY | 5161 | CTGAAGAGACTACTCATGTTGTTATGAAAACAGATGCTGAATTTGTGGTGAAGGCAAC     | 5220 |
| Db | 5161 | CTGAAGAGACTACTCATGTTGTTATGAAAACAGATGCTGAATTTGTGGTGAAGGCAAC     | 5220 |
| OY | 5221 | TGAATATATTTTCTAGGAATTCGGGAGAGAAATGGGTAGTTAGCTATTTCTGGGTGACCC   | 5280 |
| Db | 5221 | TGAATATATTTTCTAGGAATTCGGGAGAGAAATGGGTAGTTAGCTATTTCTGGGTGACCC   | 5280 |
| OY | 5281 | AGTCTATTTAAAGAAAGAAAATGCTGAATGACATGATTTTGAAGTCAAGAGAGATGTGG    | 5340 |
| Db | 5281 | AGTCTATTTAAAGAAAGAAAATGCTGAATGACATGATTTTGAAGTCAAGAGAGATGTGG    | 5340 |
| OY | 5341 | TCATATGGAAGAAACCAACAGTCCAAAGCAGACGAAGAATCCCAAGACAGAAAGATCT     | 5400 |
| Db | 5341 | TCATATGGAAGAAACCAACAGTCCAAAGCAGACGAAGAATCCCAAGACAGAAAGATCT     | 5400 |
| OY | 5401 | TCAGGGGGGCTTGAATCTGTGCTATGAGGGCCCTTCAACCAATGCCACAGATCAATCGG    | 5460 |
| Db | 5401 | TCAGGGGGGCTTGAATCTGTGCTATGAGGGCCCTTCAACCAATGCCACAGATCAATCGG    | 5460 |
| OY | 5461 | AATGATATGTAACAGCTGTGTGTGCTTGTGTGTAAGAGAGCTTTCATCAATCCCTTG      | 5520 |
| Db | 5461 | AATGATATGTAACAGCTGTGTGTGCTTGTGTGTAAGAGAGCTTTCATCAATCCCTTG      | 5520 |
| OY | 5521 | GCAACAGGTGTCCACCCCAATTTGGTGTGTGACCCAGATGCTGTGACACAGAGCAATGGCT  | 5580 |
| Db | 5521 | GCAACAGGTGTCCACCCCAATTTGGTGTGTGACCCAGATGCTGTGACACAGAGCAATGGCT  | 5580 |
| OY | 5581 | TCATATGCAATTGGGACAGATGTGTAGAGGCACTGTGTGTGACCCGAGAGTGGGTGTGGACA | 5640 |
| Db | 5581 | TCATATGCAATTGGGACAGATGTGTAGAGGCACTGTGTGTGACCCGAGAGTGGGTGTGGACA | 5640 |
| OY | 5641 | GTTGATGACCTTACACAGTCCAGAGAGCTGACACACTACCTGATACCCACAGATCCCCACA  | 5700 |
| Db | 5641 | GTTGATGACCTTACACAGTCCAGAGAGCTGACACACTACCTGATACCCACAGATCCCCACA  | 5700 |
| OY | 5701 | GCACACTACTGA   | 5711 |
| Db | 5701 | GCACACTACTGA   | 5711 |

| LOCUS                      | AR033056  | 5711 bp    | DNA | linear | PAT 29-SEP-1992 |
|----------------------------|---|------------|-----|--------|-----------------|
| DEFINITION                 | Sequence 1 from patent US 5869245.  |            |     |        |                 |
| ACCESSION                  | AR033056  |            |     |        |                 |
| VERSION                    | AR033056.1  | GI:5948661 |     |        |                 |
| KEYWORDS                   |   |            |     |        |                 |
| SOURCE                     | Unknown.  |            |     |        |                 |
| ORGANISM                   | Unknown.  |            |     |        |                 |
| REFERENCE                  | Unclassified.   |            |     |        |                 |
| AUTHORS                    | 1 (bases 1 to 5711)   |            |     |        |                 |
| TITLE                      | Yeung,A.T.  |            |     |        |                 |
| JOURNAL                    | Mismatch endonuclease and its use in identifying mutations in targeted polynucleotide strands |            |     |        |                 |
| FEATURES                   | Patent: US 5869245-A 1 09-FEB-1999;   |            |     |        |                 |
| source                     | location/Qualifiers   |            |     |        |                 |
|                            | 1..5711   |            |     |        |                 |
| BASE COUNT                 | 1956 a 1099 c 1274 g 1382 t   |            |     |        |                 |
| ORIGIN                     |   |            |     |        |                 |
| Query Match                | 100.0%; Score 5709.4; DB 6; Length 5711;  |            |     |        |                 |
| Best Local Similarity      | 100.0%; Pred. No. 0;  |            |     |        |                 |
| Matches 5710; Conservative | 0; Mismatches 1; Indels 0; Gaps 0;  |            |     |        |                 |
| 1                          | AGCTCGCTGAGACTCTCTGACACCCCGACACGAGCTGTGGGGTTCTCAGATTACTGGGCC                                  | 60         |     |        |                 |
| 1                          | AGCTCGCTGAGACTCTCTGACACCCCGACACGAGCTGTGGGGTTCTCAGATTACTGGGCC                                  | 60         |     |        |                 |
| 61                         | CTGCGCTCAGAGAGGCTTCACTCTGCTCTGGGTAAAGTTCAATTGGACACAAAGAAA                                     | 120        |     |        |                 |
| 61                         | CTGCGCTCAGAGAGGCTTCACTCTGCTCTGGGTAAAGTTCAATTGGACACAAAGAAA                                     | 120        |     |        |                 |
| 121                        | TGGAATTAATCGCTCTTCGCGGTTGAAGAGTACAAAATGTCATTAATGCTATGACAGAAA                                  | 180        |     |        |                 |
| 121                        | TGGAATTAATCGCTCTTCGCGGTTGAAGAGTACAAAATGTCATTAATGCTATGACAGAAA                                  | 180        |     |        |                 |
| 181                        | TCTTAGAGTGTCCCATGTGTCTGGAGTTGATCAAGAAACCTGTCCACAAAGTGTGACC                                    | 240        |     |        |                 |
| 181                        | TCTTAGAGTGTCCCATGTGTCTGGAGTTGATCAAGAAACCTGTCCACAAAGTGTGACC                                    | 240        |     |        |                 |
| 241                        | ACATATTTTGGAAATTTTGCATGCTGAACTTCTCAACACAGAGAAAGGGCTTCAAGT                                     | 300        |     |        |                 |
| 241                        | ACATATTTTGGAAATTTTGCATGCTGAACTTCTCAACACAGAGAAAGGGCTTCAAGT                                     | 300        |     |        |                 |
| 301                        | GTCCTTATGTAAGATGATTAATCAACAAAGAGAGCTTACAAAGAAAGTACGAGATTTAGTC                                 | 360        |     |        |                 |
| 301                        | GTCCTTATGTAAGATGATTAATCAACAAAGAGAGCTTACAAAGAAAGTACGAGATTTAGTC                                 | 360        |     |        |                 |
| 361                        | AACCTGTTGAAGAGCTATTGAAATCAATTTGTGCTTTTACGTTTGACACAGGTTGGAGT                                   | 420        |     |        |                 |
| 361                        | AACCTGTTGAAGAGCTATTGAAATCAATTTGTGCTTTTACGTTTGACACAGGTTGGAGT                                   | 420        |     |        |                 |
| 421                        | ATGGAACAGGTAAATTTTGGCAAAAAGGAAATTAATCTCTCCGAACATTTAAAGATG                                     | 480        |     |        |                 |
| 421                        | ATGGAACAGGTAAATTTTGGCAAAAAGGAAATTAATCTCTCCGAACATTTAAAGATG                                     | 480        |     |        |                 |
| 481                        | AAGTTTCTATCATCAAAAGTATGGGCTACAGAAACCGTGCACAAAGACTTCTACAGAGT                                   | 540        |     |        |                 |
| 481                        | AAGTTTCTATCATCAAAAGTATGGGCTACAGAAACCGTGCACAAAGACTTCTACAGAGT                                   | 540        |     |        |                 |
| 541                        | AACCCGAAATCCTTCTCTTGACGAAACCAAGTCTCAAGTGTCCAACTCTTAACCTTGAA                                   | 600        |     |        |                 |
| 541                        | AACCCGAAATCCTTCTCTTGACGAAACCAAGTCTCAAGTGTCCAACTCTTAACCTTGAA                                   | 600        |     |        |                 |
| 601                        | CTGTGAAACCTCTGAGACAAAGAGCGGATPACAACCTCAAAAGAGCTGTGTACACTTG                                    | 660        |     |        |                 |
| 601                        | CTGTGAAACCTCTGAGACAAAGAGCGGATPACAACCTCAAAAGAGCTGTGTACACTTG                                    | 660        |     |        |                 |
| 661                        | AATGGGATCGATTTCTTGAAGATACCGTTAATAAGCACTTATGGCAGTGTGGAG  | 720        |     |        |                 |

Db 661 AATTGGATCTGATCTTCTGTGAAGATACGGTTAATAGCACTTATTGTCAGTGTGGAG 720  
Qy 721 ATCAAGATTTGTACAAATCAACCCCTCAAGGAACCAAGGATGGAATCACTTTGGATTCTG 780  
Db 721 ATCAAGATTTGTACAAATCAACCCCTCAAGGAACCAAGGATGGAATCACTTTGGATTCTG 780  
Qy 781 CAAAAAGGCTGCTGTGAAATTTTCTGAGACGGATGTAACTAATCTGAACTCATCAAC 840  
Db 781 CAAAAAGGCTGCTGTGAAATTTTCTGAGACGGATGTAACTAATCTGAACTCATCAAC 840  
Qy 841 CCAGTAAATGATTTGAAACACACTGAGAAAGCTGACAGCTGAGAGCATCCAGAAAGT 900  
Db 841 CCAGTAAATGATTTGAAACACACTGAGAAAGCTGACAGCTGAGAGCATCCAGAAAGT 900  
Qy 901 ATCAGGAGTCTGTTCTTCAAACTTGTGATGATGAGGACCAATGAGCACTTCTGCA 960  
Db 901 ATCAGGAGTCTGTTCTTCAAACTTGTGATGATGAGGACCAATGAGCACTTCTGCA 960  
Qy 961 GCTCATTTACAGCATGAGAAACAGCACTTATTACTCACTTAAAGACAAATGATGAGAA 1020  
Db 961 GCTCATTTACAGCATGAGAAACAGCACTTATTACTCACTTAAAGACAAATGATGAGAA 1020  
Qy 1021 AGGCTGAATCTGTATATAAAGCAACAGCTGCTTACAGAGCAACCAATTAACAGAT 1080  
Db 1021 AGGCTGAATCTGTATATAAAGCAACAGCTGCTTACAGAGCAACCAATTAACAGAT 1080  
Qy 1081 GGGCTGAGTAAAGGAACATGTAATGAGGCGAATCCCGACAGAAAAAAGGTAG 1140  
Db 1081 GGGCTGAGTAAAGGAACATGTAATGAGGCGAATCCCGACAGAAAAAAGGTAG 1140  
Qy 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAAAAGATGAAATGAGAGAACTGCCATGCT 1200  
Db 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAAAAGATGAAATGAGAGAACTGCCATGCT 1200  
Qy 1201 CAGAGATCTTAGAGATCTGAAAGATGTTCTTGTGATTAACATAATGACAGATTGAGA 1260  
Db 1201 CAGAGATCTTAGAGATCTGAAAGATGTTCTTGTGATTAACATAATGACAGATTGAGA 1260  
Qy 1261 AAGTTAATGAGTGGTTTCCAGAAATGAGTGAATCTTGGTCTGATGATCTGATGATG 1320  
Db 1261 AAGTTAATGAGTGGTTTCCAGAAATGAGTGAATCTTGGTCTGATGATCTGATGATG 1320  
Qy 1321 GGGAGTCTGAATCAAAATGCCAAAGTAGATGATATTTGACCTTAAATGAGTGAATG 1380  
Db 1321 GGGAGTCTGAATCAAAATGCCAAAGTAGATGATATTTGACCTTAAATGAGTGAATG 1380  
Qy 1381 AATATTTCTGTTCTTCAAGAAATAGACTTAATGAGGATGATCTCTCAATGAGCTTTAA 1440  
Db 1381 AATATTTCTGTTCTTCAAGAAATAGACTTAATGAGGATGATCTCTCAATGAGCTTTAA 1440  
Qy 1441 TATGTAAAGTGAAGAGTCTCTCAATCAGTAGAGTAAATTTGAAAGCAAAATAT 1500  
Db 1441 TATGTAAAGTGAAGAGTCTCTCAATCAGTAGAGTAAATTTGAAAGCAAAATAT 1500  
Qy 1501 TTGGAAAACTTATGGAAGAGGCAAGCTTCCCACTTAAAGCATGTAATCTGAATATC 1560  
Db 1501 TTGGAAAACTTATGGAAGAGGCAAGCTTCCCACTTAAAGCATGTAATCTGAATATC 1560  
Qy 1561 TAAATTTAGAGACATTTGTACTGAGCCACAGATTAATACAGAGGTCCTCCCTCAATA 1620  
Db 1561 TAAATTTAGAGACATTTGTACTGAGCCACAGATTAATACAGAGGTCCTCCCTCAATA 1620  
Qy 1621 AATTAAAGCTTAAAGAGACCTACATCAGGCTTCACTGAGGATTTTATCAAGAAAG 1680  
Db 1621 AATTAAAGCTTAAAGAGACCTACATCAGGCTTCACTGAGGATTTTATCAAGAAAG 1680  
Qy 1681 CAGATTTGGCAGTTCAAAAAGACTCTGGAATGATTAATCAAGGAACTAAACAAAGGAGC 1740  
Db 1681 CAGATTTGGCAGTTCAAAAAGACTCTGGAATGATTAATCAAGGAACTAAACAAAGGAGC 1740  
Qy 1741 AGAATGCTCAAGTGAATATTAATAGTGTGATGAGATTAACAAAGGCTGAT 1800  
Db 1741 AGAATGCTCAAGTGAATATTAATAGTGTGATGAGATTAACAAAGGCTGAT 1800

Qy 1801 CTATTCAAGATGAGAAAAATCTTAACCAATAGAAATCACTGAAAAAAGAAATCTGCTTTCA 1860  
Db 1801 CTATTCAAGATGAGAAAAATCTTAACCAATAGAAATCACTGAAAAAAGAAATCTGCTTTCA 1860  
Qy 1861 AAAGGAAAGCTGAACCTATTAAGCAGATATTAAGCAATATGAACTGAAATTAATATCC 1920  
Db 1861 AAAGGAAAGCTGAACCTATTAAGCAGATATTAAGCAATATGAACTGAAATTAATATCC 1920  
Qy 1921 ACAATTTCAAAAGCACCTTAATAAAGATAGGCTGAGAGAGAAAGTCTTCAACAGGATATTC 1980  
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| Qy         | 5161  | CTGAAGAGACTACTAGTGTGTTATGAAAACAGATGCTGAGTTTGTGTGAACGACAC       | 5220 |
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| Qy         | 5281  | AGCTATTTAAAGAAAAGAAAATGCTGANTGAGCATGATTTTGAAGTCAAGAGAGATGGG    | 5340 |
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| Qy         | 5461  | AATGATGATGTCAGAGTGTGTGGTCTTCTGTGTGAAGAGCTTTCATTCATCCCTTG       | 5520 |
| Db         | 5461  | AATGATGATGTCAGAGTGTGTGGTCTTCTGTGTGAAGAGCTTTCATTCATCCCTTG       | 5520 |
| Qy         | 5521  | GCACAGGTGTCCACCCAAATGTTGTTGTGACCGACAGATGCCGTGACAGACAAATGGCT    | 5580 |
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| Qy         | 5581  | TCCATGCAATTTGGGCGAGATGTGTAGGAGACCTGTGGTGAACCGAGAGGGGTGTGGACA   | 5640 |
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| Qy         | 5641  | GTGTAGCACTCTACCAAGTCCAGAGAGCTGAGACACCTACTGATATACCCAGATCCCCACA  | 5700 |
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| Db         | 5701  | GCCACTACTGA 5711   |      |
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| HSU14680   |   |  |      |
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| DEFINITION | Homo sapiens breast and ovarian cancer susceptibility (BRCA1) mRNA.   |  |      |
| ACCESSION  | U14680  |  |      |
| VERSION    | U14680.1 GI:555931  |  |      |
| KEYWORDS   |   |  |      |
| SOURCE     | human.  |  |      |
| ORGANISM   | Homo sapiens  |  |      |
| REFERENCE  | Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  |  |      |
| AUTHORS    | Miki,Y., Swensen,J., Shattuck-Eidens,D., Futreal,P.A., Harshman,K., Tavtigian,S., Liu,Q., Cochran,C., Bennett,L.M., Ding,W., Bell,R., Rosenthal,J., Hussey,C., Tran,T., McClure,M., Frye,C., Hattier,T., Phelps,R., Haugen-Strano,A., Katcher,H., Yakuno,K., Gholami,Z., Shafer,D., Stone,S., Bayer,S., Wray,C., Bogden,R., Dayananth,P., Ward,J., Tonin,P., Narod,S., Bristow,P.K., Norris,F.H., Helvering,L., Morrison,P., Roseleck,P., Lai,M., Barrett,D.C., Lewis,C., Neuhausen,S., Cannon-Albright,L., Goldgar,D., Wiseman,R., Kamb,A. and Skolnick,M.H. |  |      |
| TITLE      | A strong candidate for the breast and ovarian cancer susceptibility gene BRCA1  |  |      |
| JOURNAL    | Science 266 (5182), 66-71 (1994)  |  |      |
| MEDLINE    | 95025896  |  |      |

PUBMED 7545954  
REFERENCE 2 (bases 1 to 5711)  
AUTHORS Skolnick, M.H.  
TITLE Direct Submission  
JOURNAL Submitted (14-SEP-1994) Mark H. Skolnick, Myriad Genetics Inc. and the University of Utah, 421 Wakara Way, Suite 201, Salt Lake City, UT 84108, USA

FEATURES  
SOURCE location/qualifiers  
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| Qy | 181  | TCTTAGAGTGTCCCATCTGTCTGAGTTGATCAAGAACTGTCTCCACAAGTGTGACC        | 240  |
| Db | 181  | TCTTAGAGTGTCCCATCTGTCTGAGTTGATCAAGAACTGTCTCCACAAGTGTGACC        | 240  |
| Qy | 241  | ACATATTTTGGCAATTTTGGCATGTGCTGAAACTTCTCAACCGAAGAAAGGGCTTCCACAGT  | 300  |
| Db | 241  | ACATATTTTGGCAATTTTGGCATGTGCTGAAACTTCTCAACCGAAGAAAGGGCTTCCACAGT  | 300  |
| Qy | 301  | GTCCCTTTATGTAAAGATGATATTAACCAAAAGAGCTCAAGAAAGTACGATATTAGTC      | 360  |
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| Qy | 601  | CTGTGAGAACTCTGAGGACAAAGCAGCGGATACAACCTCAAAAGACGTCTGTCTACATTG    | 660  |
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| Qy | 661  | AATTGGGATCTGATCTTCTCTGAAGATACCGTTAATPAAGCAACTTATGCACTGTGGGAG    | 720  |
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| Qy | 721  | ATCAAGATTTGTTAACAAATCAACCCCTCAAGGAAACGAGGATGAATCAAGTTGATTCG     | 780  |
| Db | 721  | ATCAAGATTTGTTAACAAATCAACCCCTCAAGGAAACGAGGATGAATCAAGTTGATTCG     | 780  |
| Qy | 781  | CAAAAAAGGCTGCTTGATATTTTCTGAGACGAGTGAACAAATACGTAACATCATCAAC      | 840  |
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| Qy | 841  | CCAGTAAATATGATTTTGAACACCACTGGAAGCGTGTCACTGAGAGGCATCCAGAAAGT     | 900  |
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| Qy | 901  | ATCAGGGATGTTCTGTTCAAACTTGACATGTGGAGCCATGTGGCAACAATATCTCATGCCA   | 960  |
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| Qy | 1081 | GGGCTGGAAGTAAGSAAACATGTAATGTATAGCGGACCTCCAGCAACAATAAAAAAGGTAG   | 1140 |
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| Qy | 1141 | ATCTGAATGTGATCTCCCTGTGTGAGAGAAAAGATGGAATPAAGCAGAACTGCCATCT      | 1200 |
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DEFINITION AR070223  
ACCESSION AR070223  
VERSION AR070223.1 GI:7221111  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 5712)  
AUTHORS Holte,J.T., Jensen,R.A., King,M.-C., Page,D.L., Szabo,C.I.,  
Jettison,T.L., Robinson-Benion,C.L. and Thompson,M.E.  
TITLE Characterized BRCA1 and BRCA2 proteins and screening and  
therapeutic methods based on characterized BRCA1 and BRCA2 proteins  
JOURNAL Patent: US 5891857-A 1 06-APR-1999;  
FEATURES  
source location/Qualifiers  
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BASE COUNT 1956 a 1099 c 1274 g 1383 t  
ORIGIN

Query Match 100.0%; Score 5709.4; DB 6; Length 5712;  
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Qy 2401 AAGATCTGTAGAGATGACAGATTTCAATGGTACCTGTACTGATTTATGGCAGCTCAG 2460  
Dh 2401 AAGATCTGTAGAGATGACAGATTTCAATGGTACCTGTACTGATTTATGGCAGCTCAG 2460  
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|    |      |  |      |
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| OY | 3841 | CTACAGGCAATAGCAACCGTGTACCGAGTGTCTCTTAAGAACAACAAGAGAAATTTAT     | 3900 |
| Db | 3841 | CTACTAGGCATAGCAACCGTGTCTACCGAGTGTCTGTCTTAAGAACAACAAGAGAAATTTAT | 3900 |
| OY | 3901 | TATCATTTAAGAAATAGCTTTAAATGACTCAGTAAACAGATTAATATGGCAAGCATCTC    | 3960 |
| Db | 3901 | TATCATTTGAAGATATGCTTTAAATGACTCAGTAAACAGATTAATATGGCAAGCATCTC    | 3960 |
| OY | 3961 | AGGAACATCACCTTAGTAGAGAAACAAATGTTCTGTAGCTGTGTTTCTTCAACGTGCA     | 4020 |
| Db | 3961 | AGGAACATCACCTTAGTAGAGAAACAAATGTTCTGTAGCTGTGTTTCTTCAACGTGCA     | 4020 |
| OY | 4021 | GTGAATTGGAAAGACTTGACTGCAATTAACAAACACCAGAGATCCCTTCTGTAGTGGTCTT  | 4080 |
| Db | 4021 | GTGAATTGGAAAGACTTGACTGCAATTAACAAACACCAGAGATCCCTTCTGTAGTGGTCTT  | 4080 |
| OY | 4081 | CCAAACAATGAGAGCATCATGTCGAAAGCCAGGAGTGTGTCGTAGTACAAGAAATTTGG    | 4140 |
| Db | 4081 | CCAAACAATGAGAGCATCATGTCGAAAGCCAGGAGTGTGTCGTAGTACAAGAAATTTGG    | 4140 |
| OY | 4141 | TTTCAGATGATGAAAGAAAGAGAACGGGCTTGGAAAGAAATATACAAAGAGCAACACA     | 4200 |
| Db | 4141 | TTTCAGATGATGAAAGAAAGAGAACGGGCTTGGAAAGAAATATACAAAGAGCAACACA     | 4200 |
| OY | 4201 | TGGATTCAAACTTAGTGAAGAGACATCTGGGTGTGAAGATGAACAAAGCCTCTCTGAAG    | 4260 |
| Db | 4201 | TGGATTCAAACTTAGTGAAGAGACATCTGGGTGTGAAGATGAACAAAGCCTCTCTGAAG    | 4260 |
| OY | 4261 | ACTGCTCAGGGCTATCTCTCTCAGAGTGAACATTTAACCACTCAGACAGGGATACCATGC   | 4320 |
| Db | 4261 | ACTGCTCAGGGCTATCTCTCTCAGAGTGAACATTTAACCACTCAGACAGGGATACCATGC   | 4320 |
| OY | 4321 | AACATTAACCTGATAAAAGCTCCAGCAGAAATGCTGAACTGAAAGCTGTGTAGAACAGC    | 4380 |
| Db | 4321 | AACATTAACCTGATAAAAGCTCCAGCAGAAATGCTGAACTGAAAGCTGTGTAGAACAGC    | 4380 |
| OY | 4381 | ATGGAGGACAGCTCTCTTAACAGCTACCTTCATATAGTAGACTCTTCTGCTTGAAG       | 4440 |
| Db | 4381 | ATGGAGGACAGCTCTCTTAACAGCTACCTTCATATAGTAGACTCTTCTGCTTGAAG       | 4440 |
| OY | 4441 | ACCTGCGAAATCCAGAACAAAGCAATCAGAAAAAGCAGTATTAACTTCACAGAAAAAGTA   | 4500 |
| Db | 4441 | ACCTGCGAAATCCAGAACAAAGCAATCAGAAAAAGCAGTATTAACTTCACAGAAAAAGTA   | 4500 |
| OY | 4501 | GTGAATACCTATAAAGCCAGAAATCCAGAAAGGCTTCTGTCTACAGATTTGAGGTCTG     | 4560 |
| Db | 4501 | GTGAATACCTATAAAGCCAGAAATCCAGAAAGGCTTCTGTCTACAGATTTGAGGTCTG     | 4560 |
| OY | 4561 | CAGATAGTCTTAACAGTAAATAAAGAACCAAGAGGTGAAGAAAGTCAATCCCTCTTAAT    | 4620 |
| Db | 4561 | CAGATAGTCTTAACAGTAAATAAAGAACCAAGAGGTGAAGAAAGTCAATCCCTCTTAAT    | 4620 |
| OY | 4621 | GCCCATCTTATAGATATAGTGTGATACATGACAGTGTCTGTGGAGCTTTCAGAAATAGAA   | 4680 |
| Db | 4621 | GCCCATCTTATAGATATAGTGTGATACATGACAGTGTCTGTGGAGCTTTCAGAAATAGAA   | 4680 |
| OY | 4681 | ACTACCATCTTCAGAGAGAGCTCATTTAAGTGTGTGATGTGGAGAGCAACGCTGGAAG     | 4740 |
| Db | 4681 | ACTACCATCTTCAGAGAGAGCTCATTTAAGTGTGTGATGTGGAGAGCAACGCTGGAAG     | 4740 |
| OY | 4741 | AGTCTGGGCCACAGATTTAGCGGAAACATCTTACTTCCAAAGCAAGATCTAGAGGGAA     | 4800 |
| Db | 4741 | AGTCTGGGCCACAGATTTAGCGGAAACATCTTACTTCCAAAGCAAGATCTAGAGGGAA     | 4800 |
| OY | 4801 | CCCCTTACTTGAAGTCTGGAATCAGGCTCTTCTGTGAAGCCCTGAATCTGATCCTTCTG    | 4860 |
| Db | 4801 | CCCCTTACTTGAAGTCTGGAATCAGGCTCTTCTGTGAAGCCCTGAATCTGATCCTTCTG    | 4860 |
| OY | 4861 | AAGACAGAGCCCAAGAGTCAAGTCTGTGTGGCAATACATCTTCAACTCTGCAATTGA      | 4920 |
| Db | 4861 | AAGACAGAGCCCAAGAGTCAAGTCTGTGTGGCAATACATCTTCAACTCTGCAATTGA      | 4920 |
| OY | 4921 | AAATTCCCAATTGAAGTTGCAGATCTGCCAGAGTCCAGCTGCTGCTATACTG           | 4980 |

| Db         | Accession   | Sequence  | Length |
|------------|---|---|--------|
| Db         | 4921  | AAGTTCGCCAATTGAAAGTTCAGAAATGTGCCAGAGTCCAGCTGCTCTATCTACTG      | 4980   |
| Qy         | 4981  | ATACTGCTGGGTATTAATGCAATGGAAAGGTGTGACGAGGAGAGACAGAAATTGACAG    | 5040   |
| Db         | 4981  | ATACTGCTGGGTATTAATGCAATGGAAAGGTGTGACGAGGAGAGACAGAAATTGACAG    | 5040   |
| Qy         | 5041  | CTTCACAGAAAGGTCACAAACAAAGATATGTCATGTGTGTCTGTGGCTTACCCACAGAG   | 5100   |
| Db         | 5041  | CTTCACAGAAAGGTCACAAACAAAGATATGTCATGTGTGTGTGGCTTACCCACAGAG     | 5100   |
| Qy         | 5101  | AATTATATCTGTGTGACAAAGTTGTGCCAGAAAACCAACATCATTAACTAATTA        | 5160   |
| Db         | 5101  | AATTATATCTGTGTGACAAAGTTGTGCCAGAAAACCAACATCATTAACTAATTA        | 5160   |
| Qy         | 5161  | CTGAAGAGACTACTCATATTGTTATGAAGACAGATGCTGAATTTGTGTGAACGACAC     | 5220   |
| Db         | 5161  | CTGAAGAGACTACTCATATTGTTATGAAGACAGATGCTGAATTTGTGTGAACGACAC     | 5220   |
| Qy         | 5221  | TGAAATATTTTCTAGAAATTCGGGAGGAGAAAATGGTATAGTATTTCTGGGTGACCC     | 5280   |
| Db         | 5221  | TGAAATATTTTCTAGAAATTCGGGAGGAGAAAATGGTATAGTATTTCTGGGTGACCC     | 5280   |
| Qy         | 5281  | AGTCATATTAAGAAAGAAAATGCTGATGATGACATGATTTGAAGTCCAGAGATGTGG     | 5340   |
| Db         | 5281  | AGTCATATTAAGAAAGAAAATGCTGATGATGACATGATTTGAAGTCCAGAGATGTGG     | 5340   |
| Qy         | 5341  | TCAATGGAAGAAACACCAACAGGTCCAAAGCGAGCAGAGAGATCCACAGACAGAAAGATCT | 5400   |
| Db         | 5341  | TCAATGGAAGAAACACCAACAGGTCCAAAGCGAGCAGAGAGATCCACAGACAGAAAGATCT | 5400   |
| Qy         | 5401  | TCAGGGGGCTTGAAATCTGTGCTATGAGGCCCTTCACCAACATGCCCACAGATCACTGG   | 5460   |
| Db         | 5401  | TCAGGGGGCTTGAAATCTGTGCTATGAGGCCCTTCACCAACATGCCCACAGATCACTGG   | 5460   |
| Qy         | 5461  | AATGATGTGTGACAGTGTGTGTCTCTGTGTGTGAAGAGACTTTCATCATTCACCCCTTG   | 5520   |
| Db         | 5461  | AATGATGTGTGACAGTGTGTGTCTCTGTGTGTGAAGAGACTTTCATCATTCACCCCTTG   | 5520   |
| Qy         | 5521  | GCACAGGTGTCCACCCCAATGTGTGTGTGACAGCCAGATGCTGTGACAGAGACATGGCT   | 5580   |
| Db         | 5521  | GCACAGGTGTCCACCCCAATGTGTGTGTGACAGCCAGATGCTGTGACAGAGACATGGCT   | 5580   |
| Qy         | 5581  | TCATATGCAATGTGGCAGATGTGTGAGGACCTGTGTGTGACCCGAGAGGGGTGTGAGCA   | 5640   |
| Db         | 5581  | TCATATGCAATGTGGCAGATGTGTGAGGACCTGTGTGTGACCCGAGAGGGGTGTGAGCA   | 5640   |
| Qy         | 5641  | GTTGATGACCTTACACAGTGCAGAGAGCTGACACCTTCTGTATPACCCAGATCCCCACA   | 5700   |
| Db         | 5641  | GTTGATGACCTTACACAGTGCAGAGAGCTGACACCTTCTGTATPACCCAGATCCCCACA   | 5700   |
| Qy         | 5701  | GCCACTACTGA 5711  |        |
| Db         | 5701  | GCCACTACTGA 5711  |        |
| RESULT 6   | AR118507  | 5712 bp   | Linear |
| LOCUS      | AR118507  |   |        |
| DEFINITION | Sequence 1 from patent US 6149903.                                  |   |        |
| ACCESSION  | AR118507  |   |        |
| VERSION    | AR118507.1  | GI:14100417   |        |
| KEYWORDS   |   |   |        |
| SOURCE     | Unknown.  |   |        |
| ORGANISM   | Unclassified.   |   |        |
| REFERENCE  | 1 (bases 1 to 5712)   |   |        |
| AUTHORS    | Holt,J.T., Jensen,R.A., King,M.-C., Page,D.L., Szabo,C.I.,          |   |        |
| TITLE      | Jetton,T.L., Robinson-Benton,C.L., and Thompson,M.E.                |   |        |
| JOURNAL    | Characterized BRCA1 and BRCA2 proteins and screening and            |   |        |
| FEATURES   | therapeutic methods based on characterized BRCA1 and BRCA2 proteins |   |        |
|            | Patent: US 6149903-A 1.21-NOV-2000;                                 |   |        |
|            | Location/Qualifiers   |   |        |

source 1. .5712  
/organism="unknown"  
BASE COUNT 1956 a 1099 c 1274 g 1383 t  
ORIGIN

Query Match 100.0%; Score 5709.4; DB 6; Length 5712;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 5710; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 AGCTGCTAGACTTCTGGAACCCGACACAGGCTTGCGTTTCTCAGATTAACGGGC 60  
1 AGCTGCTAGACTTCTGGAACCCGACACAGGCTTGCGTTTCTCAGATTAACGGGC 60  
61 CCTGCGCTAGAGAGGCTTCAACCTCTGCTGGTAAAGTTCAATGGAACAGAAAGAA 120  
61 CCTGCGCTAGAGAGGCTTCAACCTCTGCTGGTAAAGTTCAATGGAACAGAAAGAA 120  
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VERSION AR125601.1 GI:14111663
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 5712)
AUTHORS Holt,J.T., Jensen,R.A., King,M.-C., Steiner,M.S.,
Robinson-Benion,C.L. and Thompson,M.E.
TITLE Therapeutic methods for prostate cancer
JOURNAL Patent: US 6177410-A 1 23-JAN-2001;
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location/Qualifiers
source 1..5712
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VERSION AR004673.1 GI:3965552  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 5914)  
AUTHORS Skolnick,M.H., Goldgar,D.E., Miki,Y., Swenson,J., Kamb,A.,  
Hairston,K.D., Shattuck-Bidens,D.M., Tavilgian,S.V., Wiseman,R.W.  
and Futreal,P.Andrew.  
TITLE 17Q-linked breast and ovarian cancer susceptibility gene  
JOURNAL Patent: US 5747282-A 1 05-MAY-1998;  
FEATURES  
source location/Qualifiers  
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ORIGIN  
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DB 4681 ACTACCATCTCAAGAGAGGCTCATTAAGTGTGATGATGAGAGGACAAAGCTGGAAG 4740  
QY 4741 AGTCTGGGCGCACAGATTTGAGAGGAAACATCTTACTGCGCAAGGAAAGATCTAGAGGGA 4800  
DB 4741 AGTCTGGGCGCACAGATTTGAGAGGAAACATCTTACTGCGCAAGGAAAGATCTAGAGGGA 4800

QY 4801 CCCCTTACCTGGAATCTGGAATCAGAGCTCTTCTCTGATGACCCGTGAATCTGATCTTCTG 4860  
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QY 4861 AAGACAGAGCCCGAGAGTCAAGCTGTGTGGCAACATACATCTTCAACTCTGCAATGA 4920  
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QY 4981 ATACTGCTGGGTATATGCAATGGAAGAAAGTGTGACAGAGGAGAAACAGAAATGACAG 5040  
DB 4981 ATACTGCTGGGTATATGCAATGGAAGAAAGTGTGACAGAGGAGAAACAGAAATGACAG 5040  
QY 5041 CTTCAACAGAAAGGCTCAACAAAGAAATGTCATGCTGTGTCTGCTGAGTCAAGAGAG 5100  
DB 5041 CTTCAACAGAAAGGCTCAACAAAGAAATGTCATGCTGTGTCTGCTGAGTCAAGAGAG 5100  
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DB 5101 AATTATGCTGTGTACAGAGTGTGCGAAGAAACCAATCACTTAATCTAATTA 5160  
QY 5161 CTGAAGAGACTACTCATGTTGTTATGAAACACAGATGCTGAGTGTGTGTGAACGAGCAC 5220  
DB 5161 CTGAAGAGACTACTCATGTTGTTATGAAACACAGATGCTGAGTGTGTGTGAACGAGCAC 5220  
QY 5221 TGAATATTTTCTAGAGATTTGCGGAGAGAAATGGTATGTTAGTATTTCTGGGTGACC 5280  
DB 5221 TGAATATTTTCTAGAGATTTGCGGAGAGAAATGGTATGTTAGTATTTCTGGGTGACC 5280  
QY 5281 AGCTATTTAAAGAAAGAAATGCTGAATGAGATGTTTGAAGTGAAGAGAGATGAG 5340  
DB 5281 AGCTATTTAAAGAAAGAAATGCTGAATGAGATGTTTGAAGTGAAGAGAGATGAG 5340  
QY 5341 TCAATGGAAGAAACCAACAGGTCGCAAGAGGAGAGAGATCCAGAGAGAGAAAGTCT 5400  
DB 5341 TCAATGGAAGAAACCAACAGGTCGCAAGAGGAGAGAGATCCAGAGAGAGAAAGTCT 5400  
QY 5401 TCAGGGGCTTGAATCTGTTGCTATGAGGCTTCAACCAATGCTGAGATCAACTG 5460  
DB 5401 TCAGGGGCTTGAATCTGTTGCTATGAGGCTTCAACCAATGCTGAGATCAACTG 5460  
QY 5461 AATGATGATGAGCTGTGTGCTCTGAGTGAAGAGGCTTCAATCACTGACCCTTG 5520  
DB 5461 AATGATGATGAGCTGTGTGCTCTGAGTGAAGAGGCTTCAATCACTGACCCTTG 5520  
QY 5521 GCACAGGTGTCCACCAATTTGTTGTGACAGGAGTGCCTGACAGAGAGAAATGCT 5580  
DB 5521 GCACAGGTGTCCACCAATTTGTTGTGACAGGAGTGCCTGACAGAGAGAAATGCT 5580  
QY 5581 TCATGCAATTTGGGAGATGTGTGAGGCACTGTGTGACCCGAGAGTGGTGTGGACA 5640  
DB 5581 TCATGCAATTTGGGAGATGTGTGAGGCACTGTGTGACCCGAGAGTGGTGTGGACA 5640  
QY 5641 GTGTAGCACTTACAGAGGCGAGAGGCTGAGACCTGATGATACCCAGATCCCGACA 5700  
DB 5641 GTGTAGCACTTACAGAGGCGAGAGGCTGAGACCTGATGATACCCAGATCCCGACA 5700  
QY 5701 GCCACTACTGA 5711  
DB 5701 GCCACTACTGA 5711

RESULT 11  
ARI36942  
LOCUS ARI36942 5914 bp DNA linear PAT 16-JUN-2001  
DEFINITION Sequence 1 from patent US 616897.  
ACCESSION ARI36942  
VERSION ARI36942.1 GI:14478192  
KEYWORDS  
SOURCE Unknown.



ORGANISM Unknown.  
 Unclassified.  
 1 (bases 1 to 5914)  
 REFERENCE Skolnick, M.H., Goldgar, D.E., Miki, Y., Swenson, J., Kamb, A.,  
 AUTHORS Harshman, K.D., Shattuck-Eidens, D.M., Tavtigian, S.V., Wiseman, R.W.  
 and Futreal, P. Andrew.  
 TITLE 17q-linked breast and ovarian cancer susceptibility gene  
 JOURNAL Patent: US 6162897-A 1 19-DEC-2000;  
 FEATURES location/Qualifiers  
 source 1..5914  
 /organism="unknown"  
 BASE COUNT 2006 a 1156 c 1316 g 1436 t  
 ORIGIN

Query Match 100.0%; Score 5709.4; DB 6; Length 5914;  
 Best Local Similarity 100.0%; Pred. No.0;  
 Matches 5710; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGCTCGCTGAGACTTCCTGAGACCCGACACGAGCTGGGGTTTCTCAGATTAACGTGGCC 60  
 Db 1 AGCTCGCTGAGACTTCCTGAGACCCGACACGAGCTGGGGTTTCTCAGATTAACGTGGCC 60

QY 61 CCTGCGCTCAGAGGCGCTTACCTCTGCTCTGGGTAAAGTTGATGGAAACAGAAAGAA 120  
 Db 61 CCTGCGCTCAGAGGCGCTTACCTCTGCTCTGGGTAAAGTTGATGGAAACAGAAAGAA 120

QY 121 TGGATTATATGCTGCTTCGCGGTGAAGAAGTACAAAATGCTAATAGCTTATGSCAGAAA 180  
 Db 121 TGGATTATATGCTGCTTCGCGGTGAAGAAGTACAAAATGCTAATAGCTTATGSCAGAAA 180

QY 181 TCTTAAGTGTCCCATCTGCTGAGAGTTGATCAAGAACTGCTCTCACAAGAGTGTACC 240  
 Db 181 TCTTAAGTGTCCCATCTGCTGAGAGTTGATCAAGAACTGCTCTCACAAGAGTGTACC 240

QY 241 ACATATTTTGGCAATTTTGGATGCTGAAACTTCTCAACAGAAAGAGGCGCTTCAAGT 300  
 Db 241 ACATATTTTGGCAATTTTGGATGCTGAAACTTCTCAACAGAAAGAGGCGCTTCAAGT 300

QY 301 GTCCTTATATGTAAGTAATGATATTAACAAAAGAGCCTACAGAAAGTACAGATTTAAGTC 360  
 Db 301 GTCCTTATATGTAAGTAATGATATTAACAAAAGAGCCTACAGAAAGTACAGATTTAAGTC 360

QY 361 AACTTGTGAAGACTTATGAAATCATTTTGTCTTTTACAGTTGACACAGGTTTGGAGT 420  
 Db 361 AACTTGTGAAGACTTATGAAATCATTTTGTCTTTTACAGTTGACACAGGTTTGGAGT 420

QY 421 ATGCAAAACAGCTATTAATTTTGGCAAAAAGGAAATTAATCTCTCTGAACATCTAAAAGATG 480  
 Db 421 ATGCAAAACAGCTATTAATTTTGGCAAAAAGGAAATTAATCTCTCTGAACATCTAAAAGATG 480

QY 481 AAGTTCTATCATCCAAAGATGGGCTACAGAAACCGTGCCAAAAGACTTTCTACAGAGT 540  
 Db 481 AAGTTCTATCATCCAAAGATGGGCTACAGAAACCGTGCCAAAAGACTTTCTACAGAGT 540

QY 541 AACCCGAAAATCCTTCTCTGACAGAAACAGTCTCAGTGTCCAACTCTTAACTTTGAA 600  
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QY 601 CTGTGGAACCTGTGAGACAAAGACGAGATACACCTCAAAAAGAGTCTGTCTACATTG 660  
 Db 601 CTGTGGAACCTGTGAGACAAAGACGAGATACACCTCAAAAAGAGTCTGTCTACATTG 660

QY 661 AATTGGATCTGATTTCTTCTGAAAGATACGGTTAATTAAGCACTTATTCAGAGTGGAG 720  
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QY 721 ATCAAGATTTGTACAAATCACCCCTCAAGAAACGAGATGAATCAGTTGGATTCTG 780  
 Db 721 ATCAAGATTTGTACAAATCACCCCTCAAGAAACGAGATGAATCAGTTGGATTCTG 780

QY 781 CAAAAAAGCTGTTGTGAATTTTCTGAGACGAGATTAACAAATCTGAACATCATCAAC 840  
 Db 781 CAAAAAAGCTGTTGTGAATTTTCTGAGACGAGATTAACAAATCTGAACATCATCAAC 840

QY 841 CCAGTATATATGATTTTGAACACCACTGAGAGGCTGACGTGAGAGGATCCAGAAAGT 900  
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QY 901 ATCAGGGATGTTCTGTTTTCMAACTGATGAGAGCCATGTGGCACTCAATCTCATGCCA 960  
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QY 961 GCTCATTAACAGATGAGAAACAGCAGTTTATCTCACTTAAAGACAGATGATGTGAAA 1020  
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QY 1021 AGGCTGAATTCGTATATTAACCAACACCTGGGCTTAGCAAGAGGCCAATACAGAT 1080  
 Db 1021 AGGCTGAATTCGTATATTAACCAACACCTGGGCTTAGCAAGAGGCCAATACAGAT 1080

QY 1081 GGGCTGGAAGTAAGGAACATGTAATGATAGCGGACCTCCAGACAGAAAAAAGGTAG 1140  
 Db 1081 GGGCTGGAAGTAAGGAACATGTAATGATAGCGGACCTCCAGACAGAAAAAAGGTAG 1140

QY 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAAATGAATTAAGCAAACTGCCATGCT 1200  
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QY 1201 CAGAGAACTCTAGAGTACTGAAGATGTTCTTGATTAACACTTAATACAGATTCACA 1260  
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QY 1261 AAGTTAATGAGTGTGTTTCCAGAAAGTATGAACCTGTTAGTCTGTATGACTCATATGAT 1320  
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QY 1321 GGGAGTCTGAATCAAAATGCAAAAGTACTGATGATTTGAGAGTTCTTAAATGAGTATG 1380  
 Db 1321 GGGAGTCTGAATCAAAATGCAAAAGTACTGATGATTTGAGAGTTCTTAAATGAGTATG 1380

QY 1381 AATATTTGGTCTTCAAGAAATAGACTTCTGCGCAGATATCTCAAGGCTTTTA 1440  
 Db 1381 AATATTTGGTCTTCAAGAAATAGACTTCTGCGCAGATATCTCAAGGCTTTTA 1440

QY 1441 TATGTAAAGTGAAGAGAGTTCACTCCAAATCAGTGAAGATTAATTTGAAGCAAAATAT 1500  
 Db 1441 TATGTAAAGTGAAGAGAGTTCACTCCAAATCAGTGAAGATTAATTTGAAGCAAAATAT 1500

QY 1501 TTGGAAAACTATCGGAAAGGCAAGCTTCCCACTTAAGCCATGTAACTGAAAAATC 1560  
 Db 1501 TTGGAAAACTATCGGAAAGGCAAGCTTCCCACTTAAGCCATGTAACTGAAAAATC 1560

QY 1561 TAAATATAGGACATTTGTTACTGAGCAAGATTAATCAAGAGGTCCTCCACAAAAT 1620  
 Db 1561 TAAATATAGGACATTTGTTACTGAGCAAGATTAATCAAGAGGTCCTCCACAAAAT 1620

QY 1621 AATTAAGGCTTAAAGAGACCTACATGAGGCTTCATCTGAGATTTTATCAAGAAAG 1680  
 Db 1621 AATTAAGGCTTAAAGAGACCTACATGAGGCTTCATCTGAGATTTTATCAAGAAAG 1680

QY 1681 CAGATTTGGCACTTCAAAAAGCTCTGAAATGATTAATCAAGGAACTTAAACGAGAC 1740  
 Db 1681 CAGATTTGGCACTTCAAAAAGCTCTGAAATGATTAATCAAGGAACTTAAACGAGAC 1740

QY 1741 AGAATGTCAGTGAATTAATTAATTAATGATGATGAGAAATTAACAAAGTGTAT 1800  
 Db 1741 AGAATGTCAGTGAATTAATTAATTAATTAATGATGATGAGAAATTAACAAAGTGTAT 1800

QY 1801 CTATTCAGATGAGAAAAATCTTAACCAATAGATCACTCGAAAAAAGATGTGTTTCA 1860  
 Db 1801 CTATTCAGATGAGAAAAATCTTAACCAATAGATCACTCGAAAAAAGATGTGTTTCA 1860

QY 1861 AAACGAAGCTGAACCTTATTAAGCAGATTAATGAGCAATATGGAATCGAATTAATATCC 1920  
 Db 1861 AAACGAAGCTGAACCTTATTAAGCAGATTAATGAGCAATATGGAATCGAATTAATATCC 1920

|    |      |   |      |
|----|------|---|------|
| QY | 1921 | ACAAATTCAAAGCACCCTAAAGAAATAGGCTGAGGAGGAGTCTTCTACAGGCATATTC    | 1980 |
| Db | 1921 | ACAAATTCAAAGCACCCTAAAGAAATAGGCTGAGGAGGAGTCTTCTACAGGCATATTC    | 1980 |
| QY | 1981 | ATGGCCTTGAACCTAGTACGTAGCAAAATCTTAAGCCCACTAATGTGACTGAATTGGCAA  | 2040 |
| Db | 1981 | ATGCCCTTGAACCTAGTACGTAGCAAAATCTTAAGCCCACTAATGTGACTGAATTGGCAA  | 2040 |
| QY | 2041 | TTGATAGTGTGTTCTAGCAGTGAGAGATTAAGAAAAAAGATCAACCAATATGCGAGTCA   | 2100 |
| Db | 2041 | TTGATAGTGTGTTCTAGCAGTGAGAGATTAAGAAAAAAGATCAACCAATATGCGAGTCA   | 2100 |
| QY | 2101 | GGCAGCAGCAAAACCTTCAACTCATGGAAGGTAAAGAACTTGCAACTGGAGCCAAAGAA   | 2160 |
| Db | 2101 | GGCAGCAGCAAAACCTTCAACTCATGGAAGGTAAAGAACTTGCAACTGGAGCCAAAGAA   | 2160 |
| QY | 2161 | GTTAAACAGCCAAATGATCAAGATTAAGAAAGCATGACAGGGATCTTTCCAGAGCTGA    | 2220 |
| Db | 2161 | GTTAAACAGCCAAATGATCAAGATTAAGAAAGCATGACAGGGATCTTTCCAGAGCTGA    | 2220 |
| QY | 2221 | AGTTAAACAAATGACACCTGGTTCCTTTTAACTAAGTGTTCAAATACAGTAACTTAAAGAT | 2280 |
| Db | 2221 | AGTTAAACAAATGACACCTGGTTCCTTTTAACTAAGTGTTCAAATACAGTAACTTAAAGAT | 2280 |
| QY | 2281 | TTGTCAATCTTACCTTCCAGAGAAAGAAAGAGAAACTAGAAACAGTTAAAGTGT        | 2340 |
| Db | 2281 | TTGTCAATCTTACCTTCCAGAGAAAGAAAGAGAAACTAGAAACAGTTAAAGTGT        | 2340 |
| QY | 2341 | CTAATATATGCTGAGAACCCCAAGATCTCATGTTAAGTGGAGAAAGGTTTTGGCAATCG   | 2400 |
| Db | 2341 | CTAATATATGCTGAGAACCCCAAGATCTCATGTTAAGTGGAGAAAGGTTTTGGCAATCG   | 2400 |
| QY | 2401 | AAAGATCTGTAGAGAGTAGACATATTTCAATTTGCTACTGTAATATGGAAGTGGCACTCAG | 2460 |
| Db | 2401 | AAAGATCTGTAGAGAGTAGACATATTTCAATTTGCTACTGTAATATGGAAGTGGCACTCAG | 2460 |
| QY | 2461 | AAAGTATCTGTTACTGGAAGTTAGCACTTACGGAAGGCCAAAAACAGAACCAATTAAT    | 2520 |
| Db | 2461 | AAAGTATCTGTTACTGGAAGTTAGCACTTACGGAAGGCCAAAAACAGAACCAATTAAT    | 2520 |
| QY | 2521 | GTGTAGTCAAGTGCACAGATTTTGAAACCCCAAGGCTAATTAAGTGTGCCAAG         | 2580 |
| Db | 2521 | GTGTAGTCAAGTGCACAGATTTTGAAACCCCAAGGCTAATTAAGTGTGTGCCAAG       | 2580 |
| QY | 2581 | ATAATAGAAATATACACAGAGGCTTTAAGTATCCAATGGGACATGAATTAACACACATC   | 2640 |
| Db | 2581 | ATAATAGAAATATACACAGAGGCTTTAAGTATCCAATGGGACATGAATTAACACACATC   | 2640 |
| QY | 2641 | GGGAAACAAAGCATTAAGAAATGGAAGAAAGTGAATGATGCTCAGATTTTGCAATATCAT  | 2700 |
| Db | 2641 | GGGAAACAAAGCATTAAGAAATGGAAGAAAGTGAATGATGCTCAGATTTTGCAATATCAT  | 2700 |
| QY | 2701 | TCAAGTTTCAAGGGCCAGTATTTGCTCGTGTTCAAATCAGAGAAATGACAGAGGG       | 2760 |
| Db | 2701 | TCAAGTTTCAAGGGCCAGTATTTGCTCGTGTTCAAATCAGAGAAATGACAGAGGG       | 2760 |
| QY | 2761 | AATGTGCAACATTTCTGCGCCACTCGGGTCTTAAAGAAACAAAGTCCAAAAGTCACTT    | 2820 |
| Db | 2761 | AATGTGCAACATTTCTGCGCCACTCGGGTCTTAAAGAAACAAAGTCCAAAAGTCACTT    | 2820 |
| QY | 2821 | TTGAATGTGACAAAAAGAGAAATCAAGAAAGATAGTCTAATATCAAGCTGTAC         | 2880 |
| Db | 2821 | TTGAATGTGACAAAAAGAGAAATCAAGAAAGATAGTCTAATATCAAGCTGTAC         | 2880 |
| QY | 2881 | AGACAGTTAATATCACTGACAGCTTTCTGTGTGTTGTCAAGAAATAGCCAGTTGATA     | 2940 |
| Db | 2881 | AGACAGTTAATATCACTGACAGCTTTCTGTGTGTTGTCAAGAAATAGCCAGTTGATA     | 2940 |
| QY | 2941 | ATGCCAAATGTATATCAAGAGGCTCTAAGTTTTGTCTATCATCTCAAGTTCAAGGCA     | 3000 |
| Db | 2941 | ATGCCAAATGTATATCAAGAGGCTCTAAGTTTTGTCTATCATCTCAAGTTCAAGGCA     | 3000 |
| QY | 3001 | ACGAAATCTGACTTACTTCCAAATTAACATGAGCTTTTACAAAAACCATATGCTATAC    | 3060 |

|   |      |             |           |            |          |          |          |        |         |      |
|---|------|-------------|-----------|------------|----------|----------|----------|--------|---------|------|
| D | 3001 | ACGAAACTGGA | CTCAATTA  | CTCCAAATAA | CACTGAC  | CTTTTAC  | CAAAACC  | CAATTC | GTATAC  | 3060 |
| Q | 3061 | CACCACTTTT  | CCCCATCA  | AGTCATTT   | GTAAAA   | CTAATGT  | AAGAAAA  | ATCTG  | CTAGAG  | 3120 |
| D | 3061 | CACCACTTTT  | CCCCATCA  | AGTCATTT   | GTAAAA   | CTAATGT  | AAGAAAA  | ATCTG  | CTAGAG  | 3120 |
| Q | 3121 | AAAACTTTGA  | GAACAATT  | CAATGTGC   | CTGAGAG  | AAATGG   | CAATGACA | CTTCCA | 3180    |      |
| D | 3121 | AAAACTTTGA  | GAACAATT  | CAATGTGC   | CTGAGAG  | AAATGG   | CAATGACA | CTTCCA | 3180    |      |
| Q | 3181 | GTACAGTGA   | CAACAATT  | AGCGTAA    | TAACATTA | SAGAAAA  | TGTTTTAA | GAAGCC | AGCT    | 3240 |
| D | 3181 | GTACAGTGA   | CAACAATT  | AGCGTAA    | TAACATTA | SAGAAAA  | TGTTTTAA | GAAGCC | AGCT    | 3240 |
| Q | 3241 | CAAGCAATAT  | TAATGAAG  | TAGTTC     | CAAGTAC  | TAAATGA  | AGTGGG   | CTCCAG | TATTA   | 3300 |
| D | 3241 | CAAGCAATAT  | TAATGAAG  | TAGTTC     | CAAGTAC  | TAAATGA  | AGTGGG   | CTCCAG | TATTA   | 3300 |
| Q | 3301 | TAGGTTCCAG  | TGATGAAAA | CAATTC     | CAAGCAGA | CTAGT    | TAGAA    | CAGGGG | CAAAAT  | 3360 |
| D | 3301 | TAGGTTCCAG  | TGATGAAAA | CAATTC     | CAAGCAGA | CTAGT    | TAGAA    | CAGGGG | CAAAAT  | 3360 |
| Q | 3361 | ATGCTATG    | CTAGATTT  | AGGGGTTT   | GGCA     | CCTGAGG  | CTTAA    | CAAAAG | CTTC    | 3420 |
| D | 3361 | ATGCTATG    | CTAGATTT  | AGGGGTTT   | GGCA     | CCTGAGG  | CTTAA    | CAAAAG | CTTC    | 3420 |
| Q | 3421 | GTAATTTGA   | ACATTC    | CTGAATA    | TAATAAAA | AGCAGAA  | TAATGA   | AAAGT  | AGTTC   | 3480 |
| D | 3421 | GTAATTTGA   | ACATTC    | CTGAATA    | TAATAAAA | AGCAGAA  | TAATGA   | AAAGT  | AGTTC   | 3480 |
| Q | 3481 | ATAAGATTT   | CTCTCC    | ATATCTG    | ATTTG    | AGATTA   | CTTAGA   | CAACG  | CTTAG   | 3540 |
| D | 3481 | ATAAGATTT   | CTCTCC    | ATATCTG    | ATTTG    | AGATTA   | CTTAGA   | CAACG  | CTTAG   | 3540 |
| Q | 3541 | ATGCATCTC   | AGTTTGT   | CTTGAGA    | CACCTGA  | TGACCTG  | TAGATG   | ATGAGT | GGAAAT  | 3600 |
| D | 3541 | ATGCATCTC   | AGTTTGT   | CTTGAGA    | CACCTGA  | TGACCTG  | TAGATG   | ATGAGT | GGAAAT  | 3600 |
| Q | 3601 | AAGATTA     | CTAGTTT   | GTCTGA     | AAATACAT | TAAGAA   | AAATTTG  | CTGT   | TTTTAG  | 3660 |
| D | 3601 | AAGATTA     | CTAGTTT   | GTCTGA     | AAATACAT | TAAGAA   | AAATTTG  | CTGT   | TTTTAG  | 3660 |
| Q | 3661 | TCCAGAAA    | GAGAGC    | TTAG       | CAGAG    | AGTCCT   | TAAC     | CCATCA | CACTTTG | 3720 |
| D | 3661 | TCCAGAAA    | GAGAGC    | TTAG       | CAGAG    | AGTCCT   | TAAC     | CCATCA | CACTTTG | 3720 |
| Q | 3721 | GTATCCGA    | AGAGGGG   | CCAA       | GAATAAT  | TAAAGT   | CCCTG    | AGAA   | AGAGATG | 3780 |
| D | 3721 | GTATCCGA    | AGAGGGG   | CCAA       | GAATAAT  | TAAAGT   | CCCTG    | AGAA   | AGAGATG | 3780 |
| Q | 3781 | AAGAGCTT    | CCCTGCTT  | CCAA       | CACTTGT  | TATTTG   | GTAAAGT  | AAACA  | TATAC   | 3840 |
| D | 3781 | AAGAGCTT    | CCCTGCTT  | CCAA       | CACTTGT  | TATTTG   | GTAAAGT  | AAACA  | TATAC   | 3840 |
| Q | 3841 | CTACTAGG    | CAATAGA   | CCGTTG     | CTTAC    | CGATGT   | CTGTCT   | TAAAG  | ACACAG  | 3900 |
| D | 3841 | CTACTAGG    | CAATAGA   | CCGTTG     | CTTAC    | CGATGT   | CTGTCT   | TAAAG  | ACACAG  | 3900 |
| Q | 3901 | TATCTTGA    | AGATTA    | AGCTTAA    | TATG     | ATCTG    | CAATA    | CCAGT  | AAATTA  | 3960 |
| D | 3901 | TATCTTGA    | AGATTA    | AGCTTAA    | TATG     | ATCTG    | CAATA    | CCAGT  | AAATTA  | 3960 |
| Q | 3961 | AGGAACAT    | CACCTT    | AGTGA      | GAACA    | CAAAAT   | TTCTG    | TAC    | CTTGT   | 4020 |
| D | 3961 | AGGAACAT    | CACCTT    | AGTGA      | GAACA    | CAAAAT   | TTCTG    | TAC    | CTTGT   | 4020 |
| Q | 4021 | GTGAATGGA   | AGACTT    | GA         | CTGCA    | AAATACAA | CA       | CCAG   | ATC     | 4080 |
| D | 4021 | GTGAATGGA   | AGACTT    | GA         | CTGCA    | AAATACAA | CA       | CCAG   | ATC     | 4080 |
| Q | 4081 | CCAAACAA    | ATGAG     | CACTAG     | CTTGA    | AAACCA   | GGAGT    | TGCT   | GTAGT   | 4140 |
| D | 4081 | CCAAACAA    | ATGAG     | CACTAG     | CTTGA    | AAACCA   | GGAGT    | TGCT   | GTAGT   | 4140 |

Db 4081 CCAAAAGATGAGCATCACTGTGAAAGCCAGGAGTTGGTCTGATGACAAAGAAATGG 4140  
 QY 4141 TTTCAGATGATGAAGAAGAGAACGGGCTTTGGAGAAATTAATCAAGAGACCAAGCA 4200  
 Db 4141 TTTCAGATGATGAAGAAGAGAACGGGCTTTGGAGAAATTAATCAAGAGACCAAGCA 4200  
 QY 4201 TGGATTCAAACTTAGGTGAAGACAGCATCTGGGTGTGAGAGTGAACAAGAGCTCTGAAG 4260  
 Db 4201 TGGATTCAAACTTAGGTGAAGACAGCATCTGGGTGTGAGAGTGAACAAGAGCTCTGAAG 4260  
 QY 4261 ACTGCTCAGGGCTTACTCTCAAGATGACATTTTAACTCAAGAGAGGATACCATGC 4320  
 Db 4261 ACTGCTCAGGGCTTACTCTCAAGATGACATTTTAACTCAAGAGAGGATACCATGC 4320  
 QY 4321 AACATTAACCTGATTAAGCTCAGAGGAAATGGCTGTAACATGAGGCTGTTAGAACAGC 4380  
 Db 4321 AACATTAACCTGATTAAGCTCAGAGGAAATGGCTGTAACATGAGGCTGTTAGAACAGC 4380  
 QY 4381 ATGGAGCCAGCCTTTCAACAGTACCTTCATCAATTAAGTGAATCTTCTGCCCTTGAGG 4440  
 Db 4381 ATGGAGCCAGCCTTTCAACAGTACCTTCATCAATTAAGTGAATCTTCTGCCCTTGAGG 4440  
 QY 4441 ACTCGGAAATCCAGAACAAAGACATCAGAAAAAGCATTAATTAACCTCAAGAAAAATGA 4500  
 Db 4441 ACTCGGAAATCCAGAACAAAGACATCAGAAAAAGCATTAATTAACCTCAAGAAAAATGA 4500  
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 QY 4621 GCCCATCAATTAGATGATAGGTGTACATGACAGTTGCTCTGGAGCTTTCAGATAGAA 4680  
 Db 4621 GCCCATCAATTAGATGATAGGTGTACATGACAGTTGCTCTGGAGCTTTCAGATAGAA 4680  
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 Db 4681 ACTACCATCTCAAGAGAGCTCATTAAGGTGTGATAGTGGAGGACCAAGCTGGAG 4740  
 QY 4741 AGTCTGGGACCAACGATTTGACGGAACATCTTACTTGGCAAGCAAGTCTAGAGGAA 4800  
 Db 4741 AGTCTGGGACCAACGATTTGACGGAACATCTTACTTGGCAAGCAAGTCTAGAGGAA 4800  
 QY 4801 CCCCTTACCTGGAATCTGGAATCAGCTCTTCTGTATGACCTGGAATCTGATCCTTCTG 4860  
 Db 4801 CCCCTTACCTGGAATCTGGAATCAGCTCTTCTGTATGACCTGGAATCTGATCCTTCTG 4860  
 QY 4861 AAGACAGAGCCCGAGTCAAGCTCGTGTGGCAACATCACTTCAACCTCTGCAATTA 4920  
 Db 4861 AAGACAGAGCCCGAGTCAAGCTCGTGTGGCAACATCACTTCAACCTCTGCAATTA 4920  
 QY 4921 AAGTCCCAATTGAAGTTGACAGATCTGCCAGAGTCAGGTGTGCTCATACTAG 4980  
 Db 4921 AAGTCCCAATTGAAGTTGACAGATCTGCCAGAGTCAGGTGTGCTCATACTAG 4980  
 QY 4981 ATATCTGCTGGTATTAATGCAATGGAAGAGTGTGACAGGAGAGACAGAAATTAACAG 5040  
 Db 4981 ATATCTGCTGGTATTAATGCAATGGAAGAGTGTGTGACAGGAGAGACAGAAATTAACAG 5040  
 QY 5041 CTTCACAGAAAGGGTCAACAAAGAGTGTGATGAGTGTGCTGCAAGCCCAAGG 5100  
 Db 5041 CTTCACAGAAAGGGTCAACAAAGAGTGTGATGAGTGTGCTGCAAGCCCAAGG 5100  
 QY 5101 AATTTATGCTGCTGATCAAGTTTGCAGAAAAACACCAATCACTTAACTTAATTA 5160  
 Db 5101 AATTTATGCTGCTGATCAAGTTTGCAGAAAAACACCAATCACTTAACTTAATTA 5160  
 QY 5161 CTGAAGAGACTACTCATGTTGTTATGAAGACAGATCTGAGTTGTGTGAACGACAC 5220  
 Db 5161 CTGAAGAGACTACTCATGTTGTTATGAAGACAGATCTGAGTTGTGTGAACGACAC 5220

QY 5221 TGAATATTTTCTAGGAATTTGGGGAGAGAAATGGGTAGTTAGCTATTTCTGGGTGACCC 5280  
 Db 5221 TGAATATTTTCTAGGAATTTGGGGAGAGAAATGGGTAGTTAGCTATTTCTGGGTGACCC 5280  
 QY 5281 AGCTATTTAAAGAAAGAAAAATGCTGATAGACATGATTTTGAAGTCAAGAGAGATGTGG 5340  
 Db 5281 AGCTATTTAAAGAAAGAAAAATGCTGATAGACATGATTTTGAAGTCAAGAGAGATGTGG 5340  
 QY 5341 TCAATGGAAGAAACCAACAGGTCCAAAGCGACAAAGAAATCCACAGACAGAAAGATCT 5400  
 Db 5341 TCAATGGAAGAAACCAACAGGTCCAAAGCGACAAAGAAATCCACAGACAGAAAGATCT 5400  
 QY 5401 TCAGGGGCTTAAGAAATCTGTGCTATAGGGCCCTTCAACCAATGGCCACAGATCAACTGG 5460  
 Db 5401 TCAGGGGCTTAAGAAATCTGTGCTATAGGGCCCTTCAACCAATGGCCACAGATCAACTGG 5460  
 QY 5461 AATGATGATAGCTGATGCTGTGCTTCTGTGTGAAGAGCTTTCATCATTCACCTTG 5520  
 Db 5461 AATGATGATAGCTGATGCTGTGCTTCTGTGTGAAGAGCTTTCATCATTCACCTTG 5520  
 QY 5521 GCACAGGTGTCCACCAATTTGTGTTGTGACAGATGCTGACAGAGACATGCT 5580  
 Db 5521 GCACAGGTGTCCACCAATTTGTGTTGTGACAGATGCTGACAGAGACATGCT 5580  
 QY 5581 TCCATGCAATTTGGGAGATGTGTGAGGACCTGTGTGACCCGAGAGTGGGTGGAGA 5640  
 Db 5581 TCCATGCAATTTGGGAGATGTGTGAGGACCTGTGTGACCCGAGAGTGGGTGGAGA 5640  
 QY 5641 GTGTAGCACTTACACAGTGCAGAGCTGAGACCTGATACCTGATACCCAGATCCCCACA 5700  
 Db 5641 GTGTAGCACTTACACAGTGCAGAGCTGAGACCTGATACCTGATACCCAGATCCCCACA 5700  
 QY 5701 GCCACTACTGA 5711  
 Db 5701 GCCACTACTGA 5711

RESULT 12  
 I76943  
 LOCUS I76943 5914 bp DNA linear PAT 03-APR-1998  
 DEFINITION Sequence 1 from patent US 5693473.  
 ACCESSION I76943  
 VERSION I76943.1 GI:3013097  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 5914)  
 AUTHORS Shattuck-Bidens,D.M., Simard,J., Durocher,F., Emi,M. and Nakamura,Y.  
 TITLE Linked breast and ovarian cancer susceptibility gene  
 JOURNAL Patent: US 5693473-A 1 02-DEC-1997;  
 FEATURES  
 source 1..5914  
 BASE COUNT 2006 a 1156 c 1316 g 1436 t  
 ORIGIN  
 Query Match 100.0%; Score 5709.4; DB 6; Length 5914;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 5710; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGCTGCTGAGACTTCTGAGACCCCGACACAGGCTGTGGGGTTTCTCAGATTAATGGGCC 60  
 Db 1 AGCTGCTGAGACTTCTGAGACCCCGACACAGGCTGTGGGGTTTCTCAGATTAATGGGCC 60  
 QY 61 CCTGGCTCAGAGGCTTCAACCTCTGCTGTGGTAAAGTTCATTTGAAGAGGAA 120  
 Db 61 CCTGGCTCAGAGGCTTCAACCTCTGCTGTGGTAAAGTTCATTTGAAGAGGAA 120  
 QY 121 TGGATTATCTGCTTCTGCGTGTGAAGATGAATAATGTCAATTAATGCTATGAGAAA 180  
 Db 121 TGGATTATCTGCTTCTGCGTGTGAAGATGAATAATGTCAATTAATGCTATGAGAAA 180

Db 121 TGAATTAATCTGCTCTTCCGCGTGAAGAAGTACAAATGTCAATTAATGCTATGACAGAAA 180  
Qy 181 TCTTAAGATGCCATCTGTCTGGAGTTGATCAAGAAACCTGTCCCAAGGTGACC 240  
Db 181 TCTTAAGATGCCATCTGTCTGGAGTTGATCAAGAAACCTGTGTCCCAAGGTGACC 240  
Qy 241 ACATATTTTGGAAATTTTGCATGCTGAAGCTTCTCAACAGAGAAAGGCGCTTCAAGT 300  
Db 241 ACATATTTTGGAAATTTTGCATGCTGAAGCTTCTCAACAGAGAAAGGCGCTTCAAGT 300  
Qy 301 GTCTTTATGTAAGATGATATTAACCAAAAGAGGCTTCAAGAAAGTACGAGATTTAGTC 360  
Db 301 GTCTTTATGTAAGATGATATTAACCAAAAGAGGCTTCAAGAAAGTACGAGATTTAGTC 360  
Qy 361 AACTGTGTAAGAGTATTTGAATAATTTGCTTTTCAAGTTTCAAGTTTGGAGT 420  
Db 361 AACTGTGTAAGAGTATTTGAATAATTTGCTTTTCAAGTTTCAAGTTTGGAGT 420  
Qy 421 ATGCAACAGCTATTAATTTTGCAGAAAGAAATTAATCTCTGAAACATCTAAAGATG 480  
Db 421 ATGCAACAGCTATTAATTTTGCAGAAAGAAATTAATCTCTGAAACATCTAAAGATG 480  
Qy 481 AAGTTTCTATCATCCAAAGTATGGGCTACAGAAACCGTGCCAAAGACTTCTACAGAGTG 540  
Db 481 AAGTTTCTATCATCCAAAGTATGGGCTACAGAAACCGTGCCAAAGACTTCTACAGAGTG 540  
Qy 541 AACCCGAAATCCCTCTTGAAGAAACAGTCTAGTCCAGTCTCTTAACCTTGGAA 600  
Db 541 AACCCGAAATCCCTCTTGAAGAAACAGTCTAGTCCAGTCTCTTAACCTTGGAA 600  
Qy 601 CTGTAGAACTCTGAGAGCAAAAGCAGGAGTACAACTCAAAAGAGTCTGTCTACATTTG 660  
Db 601 CTGTAGAACTCTGAGAGCAAAAGCAGGAGTACAACTCAAAAGAGTCTGTCTACATTTG 660  
Qy 661 AATTGGATCTGATTTCTTCTGAAGATACCGTTAATPAAGCACTTATGCAAGTGGAG 720  
Db 661 AATTGGATCTGATTTCTTCTGAAGATACCGTTAATPAAGCACTTATGCAAGTGGAG 720  
Qy 721 ATCAAGATGTGTTCAATCAACCCCTCAAGGAACAGGAGTAAATCAGTTGGATTCG 780  
Db 721 ATCAAGATGTGTTCAATCAACCCCTCAAGGAACAGGAGTAAATCAGTTGGATTCG 780  
Qy 781 CAAAAAGGCTGCTGTGAATTTTCTGAGACGAGTATCAAAATCTGAACATCAAC 840  
Db 781 CAAAAAGGCTGCTGTGAATTTTCTGAGACGAGTATCAAAATCTGAACATCAAC 840  
Qy 841 CCAATTAATGATTTTGAACACCTGAGAGCGTGAAGGCTGAGAGGCAATCCAGAAAGT 900  
Db 841 CCAATTAATGATTTTGAACACCTGAGAGCGTGAAGGCTGAGAGGCAATCCAGAAAGT 900  
Qy 901 ATCAGGAGTGTCTGTTCAAACTGAGAGTGGAGCAATGGGCAAAATCTCATGGCA 960  
Db 901 ATCAGGAGTGTCTGTTCAAACTGAGAGTGGAGCAATGGGCAAAATCTCATGGCA 960  
Qy 961 GCTCATTAACAGATGAGAACAGCACTTTAATCTCACTAAAGACGAATGATGAGAA 1020  
Db 961 GCTCATTAACAGATGAGAACAGCACTTTAATCTCACTAAAGACGAATGATGAGAA 1020  
Qy 1021 AGGCTGAATTTCTGTAATAAGCAACAGCTGGCTGAGCAAGGCCCAATCAAGAT 1080  
Db 1021 AGGCTGAATTTCTGTAATAAGCAACAGCTGGCTGAGCAAGGCCCAATCAAGAT 1080  
Qy 1081 GGGCTGAAGTAAAGAAACATGATAGAGCGGAGCTCCAGCACAGAAAGAAAGGTG 1140  
Db 1081 GGGCTGAAGTAAAGAAACATGATAGAGCGGAGCTCCAGCACAGAAAGAAAGGTG 1140  
Qy 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAGAAATGAGAAAGTGGCAATGCT 1200  
Db 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAGAAATGAGAAAGTGGCAATGCT 1200  
Qy 1201 CAGGAATCTGAGAGATCTGAAGATGTTCTTGTGATTAACATTAATGACAGATTCAGA 1260  
Db 1201 CAGGAATCTGAGAGATCTGAAGATGTTCTTGTGATTAACATTAATGACAGATTCAGA 1260

Qy 1261 AAGTTAATGAGTGGTTTTCCAGAGTATGAACCTGTTAGTTCATGATCAATGATG 1320  
Db 1261 AAGTTAATGAGTGGTTTTCCAGAGTATGAACCTGTTAGTTCATGATCAATGATG 1320  
Qy 1321 GGGAGTCTGAATCAAAATCCAAAGTACGTATGATTTGAAGCTTCAATGAGTATG 1380  
Db 1321 GGGAGTCTGAATCAAAATCCAAAGTACGTATGATTTGAAGCTTCAATGAGTATG 1380  
Qy 1381 AATATTCGTGTTCTTCAAGAAATTAAGCTTACGAGAGTACCTCATGAGCTTAA 1440  
Db 1381 AATATTCGTGTTCTTCAAGAAATTAAGCTTACGAGAGTACCTCATGAGCTTAA 1440  
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Qy 1501 TTGGGAAACCTATCGAAGAGGCAAGCTCCCAACTTAAGCATGTAACTGAATAATC 1560  
Db 1501 TTGGGAAACCTATCGAAGAGGCAAGCTCCCAACTTAAGCATGTAACTGAATAATC 1560  
Qy 1561 TAAATTAAGAGCATTTGTTTCTAGGACAGATTAATTAAGAGGCGCTCCCAATA 1620  
Db 1561 TAAATTAAGAGCATTTGTTTCTAGGACAGATTAATTAAGAGGCGCTCCCAATA 1620  
Qy 1621 AATTAAAGCTTAAAGAGAGCACTACATCAGGCTTCACTCTGAGATTTTATCAAGAA 1680  
Db 1621 AATTAAAGCTTAAAGAGAGCACTACATCAGGCTTCACTCTGAGATTTTATCAAGAA 1680  
Qy 1681 CAGATTTGGAGTCAAAAAGCTCTGTAATGATTAATCAAGGAACTTAACCAACGAGC 1740  
Db 1681 CAGATTTGGAGTCAAAAAGCTCTGTAATGATTAATCAAGGAACTTAACCAACGAGC 1740  
Qy 1741 AGAATGCTCAAGTATGATTAATTAATGAGTCTAATGAGTCAATGAATTAACAAAGGAT 1800  
Db 1741 AGAATGCTCAAGTATGATTAATTAATGAGTCTAATGAGTCAATGAATTAACAAAGGAT 1800  
Qy 1801 CTATTCAGAAATGAGAAATAATCTTAACCAATAGAAATCACTGAAAGAAATCTGCTTCA 1860  
Db 1801 CTATTCAGAAATGAGAAATAATCTTAACCAATAGAAATCACTGAAAGAAATCTGCTTCA 1860  
Qy 1861 AAACGAAGCTGAACCTTAATGAGAGCACTATAGCAATATGAAATCTGAATTAATTC 1920  
Db 1861 AAACGAAGCTGAACCTTAATGAGAGCACTATAGCAATATGAAATCTGAATTAATTC 1920  
Qy 1921 ACAATTCGAAAGCACTTAAGAAAGTGGCTGAGAGAGGCTTCAACGAGCATTC 1980  
Db 1921 ACAATTCGAAAGCACTTAAGAAAGTGGCTGAGAGAGGCTTCAACGAGCATTC 1980  
Qy 1981 ATGCGCTTGAAGTATGATGAGTCAAGTAAATCAACCACTAATTTGATGAATTCGAA 2040  
Db 1981 ATGCGCTTGAAGTATGATGAGTCAAGTAAATCAACCACTAATTTGATGAATTCGAA 2040  
Qy 2041 TTGATAGTGTCTTCAAGTGAAGATTAAGAAAGAAAGTACACCAATTCAGTCA 2100  
Db 2041 TTGATAGTGTCTTCAAGTGAAGATTAAGAAAGAAAGTACACCAATTCAGTCA 2100  
Qy 2101 GGCACAGAGAAACCTTAACATCAATGAGGTAAGAACTGCAACTGAGAGCCAGAGAA 2160  
Db 2101 GGCACAGAGAAACCTTAACATCAATGAGGTAAGAACTGCAACTGAGAGCCAGAGAA 2160  
Qy 2161 GTAAACAGCCAAATGAACAGACAAAGTAAAGACATGACAGGATATTTCCAGAGCTGA 2220  
Db 2161 GTAAACAGCCAAATGAACAGACAAAGTAAAGACATGACAGGATATTTCCAGAGCTGA 2220  
Qy 2221 AGTTAAACATGACACTGTGTTCTTTAATAGTTCATTAATCAAGTAAAGTAAAGAT 2280  
Db 2221 AGTTAAACATGACACTGTGTTCTTTAATAGTTCATTAATCAAGTAAAGTAAAGAT 2280  
Qy 2281 TTGTCAATCCATGCTTCCAGAGAGAAAGAAAGAAAGTAAAGTAAAGTAAAGT 2340  
Db 2281 TTGTCAATCCATGCTTCCAGAGAGAAAGAAAGAAAGTAAAGTAAAGTAAAGT 2340

|    |      |  |      |
|----|------|--|------|
| OY | 2341 | CTAATAATGCTGGAACACCCCAAGATCTCATGTTAAAGTGAGAAAGGGTTTGCAACTG       | 2400 |
| Db | 2341 | CTAAATAATGCTGGAACACCCCAAGATCTCATGTTAAAGTGAGAAAGGGTTTGCAACTG      | 2400 |
| OY | 2401 | AAAGATCTGTAGAGGTAGCAAGTATTTCAATTTGGTACCTGGAGTACGATTATGSGCACTCAGG | 2460 |
| Db | 2401 | AAAGATCTGTAGAGGTAGCAAGTATTTCAATTTGGTACCTGGAGTACGATTATGSGCACTCAGG | 2460 |
| OY | 2461 | AAAGTATCTCGTTACTGGAAGTTAGCACTCTAGGGAGGCAAAAAACAGAACCAATAAAT      | 2520 |
| Db | 2461 | AAAGTATCTCGTTACTGGAAGTTAGCACTCTAGGGAGGCAAAAAACAGAACCAATAAAT      | 2520 |
| OY | 2521 | GTGTAGTCAGTGTGCACAGCTATTGAAAAACCCCAAGGGACCTAATTCATGTTGTTCCAAAG   | 2580 |
| Db | 2521 | GTGTAGTCAGTGTGCACAGCTATTGAAAAACCCCAAGGGACCTAATTCATGTTGTTCCAAAG   | 2580 |
| OY | 2591 | ATTAATAGAAATGACACAGAAAGGCTTTAAGTATCCATTGGGACATGAAAGTTAAACACAGTC  | 2640 |
| Db | 2591 | ATTAATAGAAATGACACAGAAAGGCTTTAAGTATCCATTGGGACATGAAAGTTAAACACAGTC  | 2640 |
| OY | 2641 | GGGAAACACAGATAGAAATGGAAGAAATGCAATGATGCTCAGATTTTGCAATATCAT        | 2700 |
| Db | 2641 | GGGAAACACAGATAGAAATGGAAGAAATGCAATGATGCTCAGATTTTGCAATATCAT        | 2700 |
| OY | 2701 | TCAAAGTTTCAAAGGCCAGTCATTTGCTCTGTGTTTCAAATCCAGAAATGCAAGAAAGG      | 2760 |
| Db | 2701 | TCAAAGTTTCAAAGGCCAGTCATTTGCTCTGTGTTTCAAATCCAGAAATGCAAGAAAGG      | 2760 |
| OY | 2761 | AATGTGCAACATTCCTCTGCGCCACCTCGGGTCTTAAAGAACAAAGTCCAAAGTCACTT      | 2820 |
| Db | 2761 | AATGTGCAACATTCCTCTGCGCCACCTCGGGTCTTAAAGAACAAAGTCCAAAGTCACTT      | 2820 |
| OY | 2821 | TTGAATGTGAACAAAAGAGAAAGAAATCAAGAGAAAGATGAGTCTAATATCAAGCTGTAC     | 2880 |
| Db | 2821 | TTGAATGTGAACAAAAGAGAAAGAAATCAAGAGAAAGATGAGTCTAATATCAAGCTGTAC     | 2880 |
| OY | 2881 | AGACAGTTAATATCACTGACAGGCTTCTGTGTGTTGTCAGAGAAATATAGCCAGTTGATA     | 2940 |
| Db | 2881 | AGACAGTTAATATCACTGACAGGCTTCTGTGTGTTGTCAGAGAAATATAGCCAGTTGATA     | 2940 |
| OY | 2941 | ATGCCAATGTATGATTCAAAGAGGCTCTAGGTTTGTCTATCATCTCAGTTCAAGAGCA       | 3000 |
| Db | 2941 | ATGCCAATGTATGATTCAAAGAGGCTCTAGGTTTGTCTATCATCTCAGTTCAAGAGCA       | 3000 |
| OY | 3001 | ACGAAATCTGACCTACTTACTCCAAATAAACATGGACTTTTCAAAACCCATATGATATAC     | 3060 |
| Db | 3001 | ACGAAATCTGACCTACTTACTCCAAATAAACATGGACTTTTCAAAACCCATATGATATAC     | 3060 |
| OY | 3061 | CACCACTTTTCCATCAAGTCAATTTGTTTAAATGTAAATGTAAAGAAATCTGCTAAGG       | 3120 |
| Db | 3061 | CACCACTTTTCCATCAAGTCAATTTGTTTAAATGTAAATGTAAAGAAATCTGCTAAGG       | 3120 |
| OY | 3121 | AAAACTTTGAGAGACATTCATGTCACCTGAAGAGAAATGGAAATGAGAACATTTCCAA       | 3180 |
| Db | 3121 | AAAACTTTGAGAGACATTCATGTCACCTGAAGAGAAATGGAAATGAGAACATTTCCAA       | 3180 |
| OY | 3181 | GTAACGTAGACACATTTAGCCGTAATACTTAGAGAAATGTTTTAAAGAACCCAGCT         | 3240 |
| Db | 3181 | GTAACGTAGACACATTTAGCCGTAATACTTAGAGAAATGTTTTAAAGAACCCAGCT         | 3240 |
| OY | 3241 | CAAGCAATATTTAATGAAGTAGTTCCAGTACTAATGAAGTGGGCTCCAGTATTAATGAA      | 3300 |
| Db | 3241 | CAAGCAATATTTAATGAAGTAGTTCCAGTACTAATGAAGTGGGCTCCAGTATTAATGAA      | 3300 |
| OY | 3301 | TAGGTTCCAGTGAATGAAAAACATTCAGAGCAACTAGAGTAAACAGAGGGCCAAATTTGA     | 3360 |
| Db | 3301 | TAGGTTCCAGTGAATGAAAAACATTCAGAGCAACTAGAGTAAACAGAGGGCCAAATTTGA     | 3360 |
| OY | 3361 | ATGCTATCTTAGATTTAGGGGTTTTTGCAACTGTAGGCTTATTAACCAAGTCTTCTTGGA     | 3420 |
| Db | 3361 | ATGCTATCTTAGATTTAGGGGTTTTTGCAACTGTAGGCTTATTAACCAAGTCTTCTTGGA     | 3420 |
| OY | 3421 | GTAATTTGATGACATCTCGAATAATAAAAAGCAAGATATGAGAAAGTATGACATGTTA       | 3480 |

|    |      |  |      |
|----|------|--|------|
| Db | 3421 | GTAAATTGAACATCTCGTAAATTAAGAAAGCAAGAAATGAAAGAGTAACTTACAGCTGTTA  | 3480 |
| OY | 3481 | ATACGATTTCTCTCCATATCATGTGATTTTCAGATTAATTAGAACAGGCTATGGGAAGTATC | 3540 |
| Db | 3481 | ATACGATTTCTCTCCATATCATGTGATTTTCAGATTAATTAGAACAGGCTATGGGAAGTATC | 3540 |
| OY | 3541 | ATGCACTCAGGTTTGTTCTGAGACACCTGATGACCTGTATGATGATGATGAAATTAAG     | 3600 |
| Db | 3541 | ATGCACTCAGGTTTGTTCTGAGACACCTGATGACCTGTATGATGATGATGAAATTAAG     | 3600 |
| OY | 3601 | AAGATCTAGTTTGTCTGAAATATGACATTAAGAAAGTTGTGCTTTTGAAGAAAGCG       | 3660 |
| Db | 3601 | AAGATCTAGTTTGTCTGAAATATGACATTAAGAAAGTTGTGCTTTTGAAGAAAGCG       | 3660 |
| OY | 3661 | TCCGAAAGGAGAGCTTAGCAGAGGCTCAGGCTTACCCATACCATTTGGCTCAG          | 3720 |
| Db | 3661 | TCCGAAAGGAGAGCTTAGCAGAGGCTCAGGCTTACCCATACCATTTGGCTCAG          | 3720 |
| OY | 3721 | GTTACCGAAGAGGGGCCAAGAAATTAAGAGTCTCAGAAAGAACTTATCTAGTAGATG      | 3780 |
| Db | 3721 | GTTACCGAAGAGGGGCCAAGAAATTAAGAGTCTCAGAAAGAACTTATCTAGTAGATG      | 3780 |
| OY | 3781 | AAGAGCTTCCCTGCTTCCACACTTGTATTGTTAAAGTAAACATATACCTTCTCAGT       | 3840 |
| Db | 3781 | AAGAGCTTCCCTGCTTCCACACTTGTATTGTTAAAGTAAACATATACCTTCTCAGT       | 3840 |
| OY | 3841 | CTACTAGGCAATAGACCGGTGCTACCCGAGTCTGTCTTAAGAACACAGAGAGAAATTAAT   | 3900 |
| Db | 3841 | CTACTAGGCAATAGACCGGTGCTACCCGAGTCTGTCTTAAGAACACAGAGAGAAATTAAT   | 3900 |
| OY | 3901 | TATCATTTGAAGAAATAGCTTAATATGACTGACGTAAACACAGTAATATTGGCAAGGATCTC | 3960 |
| Db | 3901 | TATCATTTGAAGAAATAGCTTAATATGACTGACGTAAACACAGTAATATTGGCAAGGATCTC | 3960 |
| OY | 3961 | AGGAACATCACCTTAGTGAGGAAACAAATGTTCTGCTAGCTGTTTCTTACAGTGA        | 4020 |
| Db | 3961 | AGGAACATCACCTTAGTGAGGAAACAAATGTTCTGCTAGCTGTTTCTTACAGTGA        | 4020 |
| OY | 4021 | GTGAATTGGAAGACTTGAATGACAAATCAACCCAGAGATCTTTGTAATGGATCTT        | 4080 |
| Db | 4021 | GTGAATTGGAAGACTTGAATGACAAATCAACCCAGAGATCTTTGTAATGGATCTT        | 4080 |
| OY | 4081 | CCAAACAAATGAGGATCAGTCTGAAAGCCAGGAGTTGGTCTGAGTGAACAAGAAATTTG    | 4140 |
| Db | 4081 | CCAAACAAATGAGGATCAGTCTGAAAGCCAGGAGTTGGTCTGAGTGAACAAGAAATTTG    | 4140 |
| OY | 4141 | TTTCAGATGATGAAGAAAGAGAAACGGGCTTGGAAAGAAATTAATCAAGAGCAAGCA      | 4200 |
| Db | 4141 | TTTCAGATGATGAAGAAAGAGAAACGGGCTTGGAAAGAAATTAATCAAGAGCAAGCA      | 4200 |
| OY | 4201 | TGGAATTCAAATTGAGTGAAGACAGCATCTGGGTGTGAAGTGAACAAAGCTCTCTAAG     | 4260 |
| Db | 4201 | TGGAATTCAAATTGAGTGAAGACAGCATCTGGGTGTGAAGTGAACAAAGCTCTCTAAG     | 4260 |
| OY | 4261 | ACTGCTCAGGGCTATCCTCTCAGGTGACATTTTAACCATCTCAGCAAGGGATACATGC     | 4320 |
| Db | 4261 | ACTGCTCAGGGCTATCCTCTCAGGTGACATTTTAACCATCTCAGCAAGGGATACATGC     | 4320 |
| OY | 4321 | AACATTAACCTGATTAAGACTCCAGCAGGAAATGGCTGAACCTAGAAAGCTGTGTAACAGC  | 4380 |
| Db | 4321 | AACATTAACCTGATTAAGACTCCAGCAGGAAATGGCTGAACCTAGAAAGCTGTGTAACAGC  | 4380 |
| OY | 4381 | ATGGGAGCCAGGCTTCTTAACAGCTACCCCTTCATCAATAAATGACTTCTGCCCCGAGG    | 4440 |
| Db | 4381 | ATGGGAGCCAGGCTTCTTAACAGCTACCCCTTCATCAATAAATGACTTCTGCCCCGAGG    | 4440 |
| OY | 4441 | ACCTGCGAAATCCAGAACAAAGACATCAAGAAAGAGATTAATCTTCAAGAAAGTA        | 4500 |
| Db | 4441 | ACCTGCGAAATCCAGAACAAAGACATCAAGAAAGAGATTAATCTTCAAGAAAGTA        | 4500 |
| OY | 4501 | GTGAATACCCCTATAGCCAGAAATCCAGAAAGCCCTTCTGCTGACAAAGTTGAGGTGCTG   | 4560 |





Dh 541 AACCCGAAATCCCTCTTGACAGAAACAGCTCAGTGTCCAACTCTCTAACCTTGAA 600  
Qy CTGTGGAACCTCTGAGGACAAAGCAGCGATACACCTCAAAAGAGTGTGTACATTG 660  
Dh 601 CTGTGGAACCTCTGAGGACAAAGCAGCGATACACCTCAAAAGAGTGTGTACATTG 660  
Qy 661 AATTGGGATCTGATCTCTTCTGAAGATACCGTTAATAGGCACTTATGCACTGTGGAG 720  
Dh 661 AATTGGGATCTGATCTCTTCTGAAGATACCGTTAATAGGCACTTATGCACTGTGGAG 720  
Qy 721 ATCAAGATTTGTTACAAATACCCCTCAGAGAACCGGATGAAATCACTTTGGATTCTG 780  
Dh 721 ATCAAGATTTGTTACAAATACCCCTCAGAGAACCGGATGAAATCACTTTGGATTCTG 780  
Qy 781 CAAAAAGGCTGTGTTGAAATTTCTGAGCGGATGTAACAATATCTGAACATCATCAAC 840  
Dh 781 CAAAAAGGCTGTGTTGAAATTTCTGAGCGGATGTAACAATATCTGAACATCATCAAC 840  
Qy 841 CCAGTAATAATGATTTGAAACACCACTGAGAACGCTGAGAGGCAATCCAGAAAGT 900  
Dh 841 CCAGTAATAATGATTTGAAACACCACTGAGAACGCTGAGAGGCAATCCAGAAAGT 900  
Qy 901 ATAGGATGATCTGTCTTCTTCAAACTTGATGTGAGCCATGTGGCAAAATATCTCATGCCA 960  
Dh 901 ATAGGATGATCTGTCTTCTTCAAACTTGATGTGAGCCATGTGGCAAAATATCTCATGCCA 960  
Qy 961 GCTCATTAAGCATGAGAACAGCAGTTTATCTCACTAAGACAGAAATGAAATGTAGAA 1020  
Dh 961 GCTCATTAAGCATGAGAACAGCAGTTTATCTCACTAAGACAGAAATGAAATGTAGAA 1020  
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Dh 1021 AGGCTGAATTTCTGTAAATAAAGCAACAGCCTGGCTTAGCAAGAGCCAAATACAGAT 1080  
Qy 1081 GGGCTGGAAGTAAAGAAACATGTAAATGAGCGGACTCCAGACAGAAAAAAGGTAG 1140  
Dh 1081 GGGCTGGAAGTAAAGAAACATGTAAATGAGCGGACTCCAGACAGAAAAAAGGTAG 1140  
Qy 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAGATGGAATAGCAAGAAATGCCATGCT 1200  
Dh 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAGATGGAATAGCAAGAAATGCCATGCT 1200  
Qy 1201 CAGAGATCTAGAGATCTAGAGATGTTCTTGTGATTAACACTAAATAGCAGCATTCAGA 1260  
Dh 1201 CAGAGATCTAGAGATCTAGAGATGTTCTTGTGATTAACACTAAATAGCAGCATTCAGA 1260  
Qy 1261 AAGTTAATGATGTTTCCAGAAGTGAATCTGTTAGGTTCTGATGACTCATGATG 1320  
Dh 1261 AAGTTAATGATGTTTCCAGAAGTGAATCTGTTAGGTTCTGATGACTCATGATG 1320  
Qy 1321 GGGAGTCTGAATCAAAATGCCAAGTAGCTGATGTTGACGTTCTAAATGAGGTAGTG 1380  
Dh 1321 GGGAGTCTGAATCAAAATGCCAAGTAGCTGATGTTGACGTTCTAAATGAGGTAGTG 1380  
Qy 1381 AATATTCTGGTCTTCTGAGAGAAATAGACTTACTGCGCAGTGTCTCTCATGAGGCTTTAA 1440  
Dh 1381 AATATTCTGGTCTTCTGAGAGAAATAGACTTACTGCGCAGTGTCTCTCATGAGGCTTTAA 1440  
Qy 1441 TATGTAAAGTGAAGAGTCTCACTCAAAATCACTAGAGTAATATTGAACAAATAT 1500  
Dh 1441 TATGTAAAGTGAAGAGTCTCACTCAAAATCACTAGAGTAATATTGAACAAATAT 1500  
Qy 1501 TTGGGAAAACTTCTGGAGAGAGGAGGCTCCCAACTTAAGCCATGTAACCTGAATTC 1560  
Dh 1501 TTGGGAAAACTTCTGGAGAGAGGAGGCTCCCAACTTAAGCCATGTAACCTGAATTC 1560  
Qy 1561 TAAATTAAGAGCAATTTGTTACTGAGCACAAGATAATATACAGAGCGTCCCTCCACAAATA 1620  
Dh 1561 TAAATTAAGAGCAATTTGTTACTGAGCACAAGATAATATACAGAGCGTCCCTCCACAAATA 1620  
Qy 1621 AATTAAGAGTAAAGAGACCTACATCAGGCTTCTCATCTGAGATTTTATCAAGAAAG 1680  
Dh 1621 AATTAAGAGTAAAGAGACCTACATCAGGCTTCTCATCTGAGATTTTATCAAGAAAG 1680

Qy 1681 CAGATTGCGAGTTCAAAAAGCTCCCTGAATGATTAATCAGGGAACCTAACCAAGGAGC 1740  
Dh 1681 CAGATTGCGAGTTCAAAAAGCTCCCTGAATGATTAATCAGGGAACCTAACCAAGGAGC 1740  
Qy 1741 AGAATGCTCAAGTGAATTAATTAATAGTGTGATGAGATAAACAAGAGGTATT 1800  
Dh 1741 AGAATGCTCAAGTGAATTAATTAATAGTGTGATGAGATAAACAAGAGGTATT 1800  
Qy 1801 CTATTCAAGATGAGAAAAATCCTTAACCAATGAAATCACTGCAAAAAAGATCTGCTTTCA 1860  
Dh 1801 CTATTCAAGATGAGAAAAATCCTTAACCAATGAAATCACTGCAAAAAAGATCTGCTTTCA 1860  
Qy 1861 AAACGAAAGCTGAACCTATTAAGCAGAGATTAAGCAATATGGAATCGAATTAATATCC 1920  
Dh 1861 AAACGAAAGCTGAACCTATTAAGCAGAGATTAAGCAATATGGAATCGAATTAATATCC 1920  
Qy 1921 ACAATTCAAAAGCACCTTAAGAAATAGGCTGAGAGGAAAGTCTTACCAAGCATATTC 1980  
Dh 1921 ACAATTCAAAAGCACCTTAAGAAATAGGCTGAGAGGAAAGTCTTACCAAGCATATTC 1980  
Qy 1981 ATGCGCTGAATAGTATGATAGATAATCTAAGCCCACTAATTTGATCTGAATTCGAAA 2040  
Dh 1981 ATGCGCTGAATAGTATGATAGATAATCTAAGCCCACTAATTTGATCTGAATTCGAAA 2040  
Qy 2041 TTGATAGTTGTTCTAGCAGTGAAGAGATTAAGAAAAAAGTAAACCAATGCCAGTCA 2100  
Dh 2041 TTGATAGTTGTTCTAGCAGTGAAGAGATTAAGAAAAAAGTAAACCAATGCCAGTCA 2100  
Qy 2101 GGCACAGCAGAAACCTCAACTCATGGAAGGTAAAGAACTTGCAACCTGAGCCAGAGAGA 2160  
Dh 2101 GGCACAGCAGAAACCTCAACTCATGGAAGGTAAAGAACTTGCAACCTGAGCCAGAGAGA 2160  
Qy 2161 GTTAAACGCAATATGAACAGAAATGAATGAAGCATGACAGCATCTTCCAGAGCTGA 2220  
Dh 2161 GTTAAACGCAATATGAACAGAAATGAATGAAGCATGACAGCATCTTCCAGAGCTGA 2220  
Qy 2221 AGTTAAACAAATGACACTGCTGTTCTTTTAACTAAGTGTCAAAATACAGTGAATGAAT 2280  
Dh 2221 AGTTAAACAAATGACACTGCTGTTCTTTTAACTAAGTGTCAAAATACAGTGAATGAAT 2280  
Qy 2281 TTGTCAATCTGACCTTCCAGAGAGAAAGAAAGAACTAGAAACAGTTAAAGTGT 2340  
Dh 2281 TTGTCAATCTGACCTTCCAGAGAGAAAGAAAGAACTAGAAACAGTTAAAGTGT 2340  
Qy 2341 CTAAATTAATGCTAAAGACCCCAAGATCTCATGTTAAGTGAAGAGGTTTGGCAAACTG 2400  
Dh 2341 CTAAATTAATGCTAAAGACCCCAAGATCTCATGTTAAGTGAAGAGGTTTGGCAAACTG 2400  
Qy 2401 AAAGATCTGTAGAGAGTACAGTATTTTCAATGCTGCTGCTGATTAATGCACTCAGG 2460  
Dh 2401 AAAGATCTGTAGAGAGTACAGTATTTTCAATGCTGCTGCTGATTAATGCACTCAGG 2460  
Qy 2461 AAAGATCTCGTTACTGGAAGTTAGCACTTAGGGAAGGCAAAAAAGAACTAAAT 2520  
Dh 2461 AAAGATCTCGTTACTGGAAGTTAGCACTTAGGGAAGGCAAAAAAGAACTAAAT 2520  
Qy 2521 GTGTAGTCAAGTGTGACAGATTTTGAAGCCCAAGGACTAATTAATGTTTCCAAAG 2580  
Dh 2521 GTGTAGTCAAGTGTGACAGATTTTGAAGCCCAAGGACTAATTAATGTTTCCAAAG 2580  
Qy 2581 ATTAATGAAGTGAACAGAGGCTTAAGTATCCATTGGGACATGAAGTTAAACACAGTC 2640  
Dh 2581 ATTAATGAAGTGAACAGAGGCTTAAGTATCCATTGGGACATGAAGTTAAACACAGTC 2640  
Qy 2641 GGGAAAAAGCATAGAAATGGAAGAAAGTGAATCTGATGCTCAGTATTTGCAAGATACAT 2700  
Dh 2641 GGGAAAAAGCATAGAAATGGAAGAAAGTGAATCTGATGCTCAGTATTTGCAAGATACAT 2700  
Qy 2701 TCAAGCTTCAAAAGGCGCAGATCTTGTCTGTTTCAAAATCCAGGAAATGCAAGAGG 2760  
Dh 2701 TCAAGCTTCAAAAGGCGCAGATCTTGTCTGTTTCAAAATCCAGGAAATGCAAGAGG 2760

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|----|------|--|------|
| QY | 2761 | AATGTGCAACATCTCTCTGCCCACTCTGGGTCCTTTAAGAAACAAGTCCAAAAGCACTT    | 2822 |
| Db | 2761 | AATGTGCAACATCTCTCTGCCCACTCTGGGTCCTTTAAGAAACAAGTCCAAAAGCACTT    | 2820 |
| QY | 2821 | TTGAATGTGAACAAAAGAGAGAAATCAAGGAAAGATGAGCTATATCAAGCCTGTAC       | 2880 |
| Db | 2821 | TTGAATGTGAACAAAAGAGAGAAATCAAGGAAAGATGAGCTATATCAAGCCTGTAC       | 2880 |
| QY | 2881 | AGACGTTAATATCACTGCAAGCTTTCCTGTGGTTGGTCAGAAAGATAGCCAGTTGATA     | 2940 |
| Db | 2881 | AGACGTTAATATCACTGCAAGCTTTCCTGTGGTTGGTCAGAAAGATAGCCAGTTGATA     | 2940 |
| QY | 2941 | ATGCCAAATGTATATCAAAAGAGGCTTAGGTTTGTCTATCATCTCAGTTCAAGGCA       | 3000 |
| Db | 2941 | ATGCCAAATGTATATCAAAAGAGGCTTAGGTTTGTCTATCATCTCAGTTCAAGGCA       | 3000 |
| QY | 3001 | ACGAAATCTGAGCTCATCTACTCCAAATTAACATGACCTTTTACAAAACCCATATGATATAC | 3060 |
| Db | 3001 | ACGAAATCTGAGCTCATCTACTCCAAATTAACATGACCTTTTACAAAACCCATATGATATAC | 3060 |
| QY | 3061 | CACCACTTTTCCATCAAGTCACTTTGTTAAAACTAAATGTAAAGAAAAATCTGCTAGAGG   | 3120 |
| Db | 3061 | CACCACTTTTCCATCAAGTCACTTTGTTAAAACTAAATGTAAAGAAAAATCTGCTAGAGG   | 3120 |
| QY | 3121 | AAAACTTTGAGGAAACATTCATATGTCACTGAAAGGAAATGGGAAATGAGAAACATTCACAA | 3180 |
| Db | 3121 | AAAACTTTGAGGAAACATTCATATGTCACTGAAAGGAAATGGGAAATGAGAAACATTCACAA | 3180 |
| QY | 3181 | GTACAGTAGGACCAATTTAGCCGTATTAACATTAAGAGAAATGTTTTTAAAGAGGCACT    | 3240 |
| Db | 3181 | GTACAGTAGGACCAATTTAGCCGTATTAACATTAAGAGAAATGTTTTTAAAGAGGCACT    | 3240 |
| QY | 3241 | CAAGCAATATTAATGAACTAGGCTTCAGTACTAATGAAGTGGGCTCCAGTATTAATGAA    | 3300 |
| Db | 3241 | CAAGCAATATTAATGAACTAGGCTTCAGTACTAATGAAGTGGGCTCCAGTATTAATGAA    | 3300 |
| QY | 3301 | TAGGTTCCAGTATGAAAAACATTCAGAGCAACTGTGTATGAAACAGAGGGCCAAATTTGA   | 3360 |
| Db | 3301 | TAGGTTCCAGTATGAAAAACATTCAGAGCAACTGTGTATGAAACAGAGGGCCAAATTTGA   | 3360 |
| QY | 3361 | ATGCTATCTTAGATTAGGGGTTTTGCAACCTGAGGCTGTATTAACAAAGTCTTCCCTGGAA  | 3420 |
| Db | 3361 | ATGCTATCTTAGATTAGGGGTTTTGCAACCTGAGGCTGTATTAACAAAGTCTTCCCTGGAA  | 3420 |
| QY | 3421 | GTAATTGTAGCATCTCTGAAATTAAGAAAGCAAGATATGAAGAGTAAGTTCAGACTGTTA   | 3480 |
| Db | 3421 | GTAATTGTAGCATCTCTGAAATTAAGAAAGCAAGATATGAAGAGTAAGTTCAGACTGTTA   | 3480 |
| QY | 3481 | ATACAGATTTTCTCTCATATCTGATTTCAAGATACCTTGAAACAGCTTATGGGAAGTATCTC | 3540 |
| Db | 3481 | ATACAGATTTTCTCTCATATCTGATTTCAAGATACCTTGAAACAGCTTATGGGAAGTATCTC | 3540 |
| QY | 3541 | ATGCACTCAGGTTTGTCTGAGACACCTGATGACCTGTATGATATGTGTAATTAAGG       | 3600 |
| Db | 3541 | ATGCACTCAGGTTTGTCTGAGACACCTGATGACCTGTATGATATGTGTAATTAAGG       | 3600 |
| QY | 3601 | AAGATACTAGTTTGTCTGAAAAATGACATTAAGGAAAGTTGTCTGTTTTTGAACAAAACCG  | 3660 |
| Db | 3601 | AAGATACTAGTTTGTCTGAAAAATGACATTAAGGAAAGTTGTCTGTTTTTGAACAAAACCG  | 3660 |
| QY | 3661 | TCCAGAAAGAGAGCTTAGCAGAGGCTCTAGACCTTTTCAACCATACATTTGGTCTCAGG    | 3720 |
| Db | 3661 | TCCAGAAAGAGAGCTTAGCAGAGGCTCTAGACCTTTTCAACCATACATTTGGTCTCAGG    | 3720 |
| QY | 3721 | GTTACCGAAGAGGGGCCAAGAAATTAGAGTCTCTGAAGAGAACTTATCTAGTGAGATG     | 3780 |
| Db | 3721 | GTTACCGAAGAGGGGCCAAGAAATTAGAGTCTCTGAAGAGAACTTATCTAGTGAGATG     | 3780 |
| QY | 3781 | AAGAGCTTCCCTGCTTCCAAACACTTGTATTTTGTATTAAGTAAACAATATACCTTCTCAGT | 3840 |
| Db | 3781 | AAGAGCTTCCCTGCTTCCAAACACTTGTATTTTGTATTAAGTAAACAATATACCTTCTCAGT | 3840 |
| QY | 3841 | CTACTAGGCATAGCACCGGTGCTACCGAGTGTCTGTCTTAAGAACACAGAGAGAAATTTAT  | 3900 |

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|----|------|--|------|
| Db | 3841 | CTATGAGCAATGACACCGTTGCTTACCGAGTGTCTGTCTTAAGAACACAGAGAGAAATTTAT   | 3900 |
| OY | 3901 | TATCATTTGAAGATATAGCTTTAAATGACGTGACGTAAACAGTAAATATTTGGCAAGGCATCTC | 3960 |
| Db | 3901 | TATCATTTGAAGATATAGCTTTAAATGACGTGATTAACAGTAAATATTTGGCAAGGCATCTC   | 3960 |
| OY | 3961 | AGGAACATCACCTTATAGTAGAGAAACAAATGTTTGTCTAGCTGTGTTTCTTCAACAGTCA    | 4020 |
| Db | 3961 | AGGAACATCACCTTATAGTAGAGAAACAAATATTTGTCTAGCTGTGTTTCTTCAACAGTCA    | 4020 |
| OY | 4021 | GTGAATTGGAAGAATTGACTGTGCAAAATACAAACACCCAGATCTCTTCTTGAATGGTCTCT   | 4080 |
| Db | 4021 | GTGAATTGGAAGAATTGACTGTGCAAAATACAAACACCCAGATCTCTTCTTGAATGGTCTCT   | 4080 |
| OY | 4081 | CCAAACAAATGAGGCATCAGTCTGAAAGCCAGGAGTTGATCTGAGTACAAAGAAATTGG      | 4140 |
| Db | 4081 | CCAAACAAATGAGGCATCAGTCTGAAAGCCAGGAGTTGATCTGAGTACAAAGAAATTGG      | 4140 |
| OY | 4141 | TTTCAGATGATGAAAGAAAGAGAAACGGGCTTTGGAAAGAAATATATACAAAGACAAAGCA    | 4200 |
| Db | 4141 | TTTCAGATGATGAAAGAAAGAGAAACGGGCTTTGGAAAGAAATATATACAAAGACAAAGCA    | 4200 |
| OY | 4201 | TGGAATTCAACTTATAGTAGAGACAGCATTTGGGTGTGAGATGAAACAAGCGCTCTGAAG     | 4260 |
| Db | 4201 | TGGAATTCAACTTATAGTAGAGACAGCATTTGGGTGTGAGATGAAACAAGCGCTCTGAAG     | 4260 |
| OY | 4261 | ACTGCTCAGGGCTATTCCTCTGAGAGTGCATTTTAAACCCTCAGCAGAGGATACATGC       | 4320 |
| Db | 4261 | ACTGCTCAGGGCTATTCCTCTGAGAGTGCATTTTAAACCCTCAGCAGAGGATACATGC       | 4320 |
| OY | 4321 | AACATATACCTGATTAAGCTCCAGCAGAGAAATGGCTGAACTGAAGCTGTGTTAAGAACGC    | 4380 |
| Db | 4321 | AACATATACCTGATTAAGCTCCAGCAGAGAAATGGCTGAACTGAAGCTGTGTTAAGAACGC    | 4380 |
| OY | 4381 | ATGGGAGCAGGCTTCTAACAAGCTAACCTTCATCATATAGATGACCTCTCTGCGCTTGAGG    | 4440 |
| Db | 4381 | ATGGGAGCAGGCTTCTAACAAGCTAACCTTCATCATATAGATGACCTCTCTGCGCTTGAGG    | 4440 |
| OY | 4441 | ACCTGCGAAATCCAGAACAAAGCAGATCAGAAAAAGCAGTATTAACTTACAGAAAAAGTA     | 4500 |
| Db | 4441 | ACCTGCGAAATCCAGAACAAAGCAGATCAGAAAAAGCAGTATTAACTTACAGAAAAAGTA     | 4500 |
| OY | 4501 | GTGAATACCTTATAAGCCAGATTCAGAAAGCCTTTCTCTGTACAGATTGAGTGTCTG        | 4560 |
| Db | 4501 | GTGAATACCTTATAAGCCAGATTCAGAAAGCCTTTCTCTGTACAGATTGAGTGTCTG        | 4560 |
| OY | 4561 | CAGATAGTCTTACAGATTAATAAGAACAGAGATGGAAGGATCACTCCCTCTTAAT          | 4620 |
| Db | 4561 | CAGATAGTCTTACAGATTAATAAGAACAGAGATGGAAGGATCACTCCCTCTTAAT          | 4620 |
| OY | 4621 | GCCCATCTTATGATATGATAGTGTGTACATGACAGTGTGCTGTGGAGTCTTCAGAATAGAA    | 4680 |
| Db | 4621 | GCCCATCTTATGATATGATAGTGTGTACATGACAGTGTGCTGTGGAGTCTTCAGAATAGAA    | 4680 |
| OY | 4681 | ACTAACCATCTTCAAGAGAGCTCATTTAAGTTGTGATGTGAGAGCAACAGCTGGAAG        | 4740 |
| Db | 4681 | ACTAACCATCTTCAAGAGAGCTCATTTAAGTTGTGATGTGAGAGCAACAGCTGGAAG        | 4740 |
| OY | 4741 | AGTCTGGGCCACAGATTTGACGGAAACATTTACTTGGCCAAGGAAACATCTAGAGGGAA      | 4800 |
| Db | 4741 | AGTCTGGGCCACAGATTTGACGGAAACATTTACTTGGCCAAGGAAACATCTAGAGGGAA      | 4800 |
| OY | 4801 | CCCCCTTACTGGAATCTGGAAATCAGCCCTTCTCTGTATGACCTTGAATCTGATCCTTGTG    | 4860 |
| Db | 4801 | CCCCCTTACTGGAATCTGGAAATCAGCCCTTCTCTGTATGACCTTGAATCTGATCCTTGTG    | 4860 |
| OY | 4861 | AAGACAGAGCCCCAGAGTCAAGTCTGTGTTGGCAACATTCATCTTCAACCTCTGCATTTGA    | 4920 |
| Db | 4861 | AAGACAGAGCCCCAGAGTCAAGTCTGTGTTGGCAACATTCATCTTCAACCTCTGCATTTGA    | 4920 |
| OY | 4921 | AAAGTTCCCAATTGAAAGTTGCAAAATGTGCCAGAGTCCAGCTGCTCTATCTACTG         | 4980 |

| Db         | 4922   | AAAGTCCCCCAATTGAAAGTTGAGAAATCTGCCACAGTCCACACTCTCTGTCAACTACTG     | 4998                       |
|------------|--|--|----------------------------|
| QY         | 4981   | ATACTGCTGGGTATTAATGCATATGAAAGAAAGTGTGACAGGGAGAAAGCCAGATTTGACAG   | 5040                       |
| Db         | 4981   | ATACTGCTGGGTATTAATGCATATGAAAGAAAGTGTGACAGGGAGAAAGCCAGATTTGACAG   | 5040                       |
| QY         | 5041   | CTTCAACAGAAAGGGGTCAACAAAGAAATGTCATGATGTGTCTGAGCCCTGACCCAGAG      | 5100                       |
| Db         | 5041   | CTTCAACAGAAAGGGGTCAACAAAGAAATGTCATGATGTGTCTGAGCCCTGACCCAGAG      | 5100                       |
| QY         | 5101   | AATTTATGCTCGTGTACAAAGTTTGCACAGAAACACCACTCACTTAACTAATCTAATTA      | 5160                       |
| Db         | 5101   | AATTTATGCTCGTGTGTACAAAGTTTGCACAGAAACACCACTCACTTAACTAATCTAATTA    | 5160                       |
| QY         | 5161   | CTGAAGAGACTACTCATGTTGTTATGAAAAACAGATGCTGAGTTTGTGTGAACCGACAC      | 5220                       |
| Db         | 5161   | CTGAAGAGACTACTCATGTTGTTATGAAAAACAGATGCTGAGTTTGTGTGAACCGACAC      | 5220                       |
| QY         | 5221   | TGAAATATTTTCTAGGAATTTGGGGAGAGAAATGGGTAGTTAGCTAATTTCTGGGTGACCC    | 5280                       |
| Db         | 5221   | TGAAATATTTTCTAGGAATTTGGGGAGAGAAATGGGTAGTTAGCTAATTTCTGGGTGACCC    | 5280                       |
| QY         | 5281   | AGCTATTATTAAGAAAGAAATATGCTGAATGAGCATGATTTTGAATCAGAGAGATGTGG      | 5340                       |
| Db         | 5281   | AGCTATTATTAAGAAAGAAATATGCTGAATGAGCATGATTTTGAATCAGAGAGATGTGG      | 5340                       |
| QY         | 5341   | TCAATGAGAAAGAACCCAGCAAGGTCCTCAAGACGAGCAAGAGAAATCCAGAGCAGAAAGATCT | 5400                       |
| Db         | 5341   | TCAATGAGAAAGAACCCAGCAAGGTCCTCAAGACGAGCAAGAGAAATCCAGAGCAGAAAGATCT | 5400                       |
| QY         | 5401   | TCAGGGGGCTAGAAATCTGTGTCTATGAGCCCTTCAACCAATGCCCCACAGATCAACTGG     | 5460                       |
| Db         | 5401   | TCAGGGGGCTAGAAATCTGTGTCTATGAGCCCTTCAACCAATGCCCCACAGATCAACTGG     | 5460                       |
| QY         | 5461   | AATGATGTGTACAGCTGTGTGGTGCTTCTGTGTGTAAGAGCTTTCATCATTCACCCCTTG     | 5520                       |
| Db         | 5461   | AATGATGTGTACAGCTGTGTGGTGCTTCTGTGTGTAAGAGCTTTCATCATTCACCCCTTG     | 5520                       |
| QY         | 5521   | GCACAGGTGTCCACCCCAATTGTGTGTTGTGACAGCCAGATGCTGTGACAGAGACAAATGGCT  | 5580                       |
| Db         | 5521   | GCACAGGTGTCCACCCCAATTGTGTGTTGTGACAGCCAGATGCTGTGACAGAGACAAATGGCT  | 5580                       |
| QY         | 5581   | TCATATGCAATTTGGGCGAGATGTGTGAGGCCACTGTGTGACCCGAGAGTGGGTGTGGACA    | 5640                       |
| Db         | 5581   | TCATATGCAATTTGGGCGAGATGTGTGAGGCCACTGTGTGACCCGAGAGTGGGTGTGGACA    | 5640                       |
| QY         | 5641   | GTGTAGCACTCTACCAAGTGCAGAGAGCTGTGACACTTACTGTATACCCACAGATCCCCCACA  | 5700                       |
| Db         | 5641   | GTGTAGCACTCTACCAAGTGCAGAGAGCTGTGACACTTACTGTATACCCACAGATCCCCCACA  | 5700                       |
| QY         | 5701   | GCCACTACTGA 5711   |                            |
| Db         | 5701   | GCCACTACTGA 5711   |                            |
| RESULT 14  |  |  |                            |
| LOCUS      | 181034   | 5914 bp  | DNA linear PAT 10-JUN-1998 |
| DEFINITION | Sequence 1 from patent US 5710001.   |  |                            |
| ACCESSION  | 181034   |  |                            |
| VERSION    | 181034.1   | GI:3209324   |                            |
| KEYWORDS   |  |  |                            |
| SOURCE     | Unknown.   |  |                            |
| ORGANISM   | Unknown.   |  |                            |
| REFERENCE  | 1 (bases 1 to 5914)  |  |                            |
| AUTHORS    | Skolnick,M.H., Goldgar,D.E., Miki,Y., Swenson,J., Kamb,A., Hershman,K.D., Shattuck-Eidens,D.M., Tavtigian,S.V., Wiseman,R.W. and Futreal,P.Andrew. |  |                            |
| TITLE      | 17q-linked breast and ovarian cancer susceptibility gene   |  |                            |
| JOURNAL    | Patent: US 5710001-A 1 20-JAN-1998;  |  |                            |
| FEATURES   | Location/Qualifiers  |  |                            |
| source     | 1..5914  |  |                            |

| BASE COUNT            | 2006 a       | 1156 c  | 1316 g     | 1436 t      |          |
|-----------------------|--------------|---|------------|-------------|----------|
| Query Match           | 100.0%       | Score 5709.4  | DB 6       | Length 5914 |          |
| Best Local Similarity | 100.0%       | Pred. No. 0   |            |             |          |
| Matches 5710          | Conservative | 0   | Mismatches | 1           | Indels 0 |
|                       |              |   |            |             | Gaps 0   |
| QY                    | 1            | AGCTGCTGAGACCTTCTTGAGACCCCGGACACAGGCTGTGGGTTTCTCAGATTAACATGCGGC         | 60         |             |          |
| DB                    | 1            | AGCTGCTGAGACCTTCTTGAGACCCCGGACACAGGCTGTGGGTTTCTCAGATTAACATGCGGC         | 60         |             |          |
| QY                    | 61           | CCTGGCTCAGAGAGGCTTCAACCCCTGCTCGGGTAAAGTTCAATGGAAACAGAAAGAA              | 120        |             |          |
| DB                    | 61           | CCTGGCTCAGAGAGGCTTCAACCCCTGCTCGGGTAAAGTTCAATGGAAACAGAAAGAA              | 120        |             |          |
| QY                    | 121          | TGAAATTAATCTGCTCTTGGCGCTTGAGAGAGTACAAATATGATTAATCTATGACAGAAA            | 180        |             |          |
| DB                    | 121          | TGAAATTAATCTGCTCTTGGCGCTTGAGAGAGTACAAATATGATTAATCTATGACAGAAA            | 180        |             |          |
| QY                    | 181          | TCTTAGAGTGTCCCATCTGTCTGAGATTGATCAAGAAACCTGTCTCAAAAGTGTGACC              | 240        |             |          |
| DB                    | 181          | TCTTAGAGTGTCCCATCTGTCTGAGATTGATCAAGAAACCTGTCTCAAAAGTGTGACC              | 240        |             |          |
| QY                    | 241          | ACATATTTTGGAAATTTTGGCATGCTGGAACCTTTCACAGAGAAAGAGGCTTTCACAGT             | 300        |             |          |
| DB                    | 241          | ACATATTTTGGAAATTTTGGCATGCTGGAACCTTTCACAGAGAAAGAGGCTTTCACAGT             | 300        |             |          |
| QY                    | 301          | GTCCTTTATGTAGAAGATGATATAACCAAAAGAGGCTCACAGAAAGTACAGATTATGTC             | 360        |             |          |
| DB                    | 301          | GTCCTTTATGTAGAAGATGATATAACCAAAAGAGGCTCACAGAAAGTACAGATTATGTC             | 360        |             |          |
| QY                    | 361          | AACCTGTGAAGAGCTATGGAATCATTTGTGCTTTACGCTTGACAAGGTTTGGAGT                 | 420        |             |          |
| DB                    | 361          | AACCTGTGAAGAGCTATGGAATCATTTGTGCTTTACGCTTGACAAGGTTTGGAGT                 | 420        |             |          |
| QY                    | 421          | ATGCAAAAGATATATTTTGCAGAAAAAGAAAAATACTCTCCGTAACATCTAAAAAGATG             | 480        |             |          |
| DB                    | 421          | ATGCAAAAGATATATTTTGCAGAAAAAGAAAAATACTCTCCGTAACATCTAAAAAGATG             | 480        |             |          |
| QY                    | 481          | AAGTTTCTATCATCCAAAGTATGGGCTCACAGAAACCGTCCAAAGACCTTCTACAGAGTG            | 540        |             |          |
| DB                    | 481          | AAGTTTCTATCATCCAAAGTATGGGCTCACAGAAACCGTCCAAAGACCTTCTACAGAGTG            | 540        |             |          |
| QY                    | 541          | AACCCGAAAAATCCTTCTCTTGACAGAAACCACTCTCAGTGTCCAACTCTTAACCTTGGAA           | 600        |             |          |
| DB                    | 541          | AACCCGAAAAATCCTTCTCTTGACAGAAACCACTCTCAGTGTCCAACTCTTAACCTTGGAA           | 600        |             |          |
| QY                    | 601          | CTGTGAGAACCTCTGAGACCAAGACGCGGATACAACTCAAAAGACGTTCTGTCTACATG             | 660        |             |          |
| DB                    | 601          | CTGTGAGAACCTCTGAGACCAAGACGCGGATACAACTCAAAAGACGTTCTGTCTACATG             | 660        |             |          |
| QY                    | 661          | AATTGGGATCGATCTTCTGGAATTTCTGAGACGATGTAACCGTTATTAAGGCAACTATTTGCACTGTGGAG | 720        |             |          |
| DB                    | 661          | AATTGGGATCGATCTTCTGGAATTTCTGAGACGATGTAACCGTTATTAAGGCAACTATTTGCACTGTGGAG | 720        |             |          |
| QY                    | 721          | ATCAAGAAATTTGTTCAAAATCACCCCTCAAGGACCAAGGATGAATCAGTTTGGATTG              | 780        |             |          |
| DB                    | 721          | ATCAAGAAATTTGTTCAAAATCACCCCTCAAGGACCAAGGATGAATCAGTTTGGATTG              | 780        |             |          |
| QY                    | 781          | CAAAAAAGGCTGCTTGTGAATTTTCTGAGACGATGTACAAATATCTGAACATCATCAAC             | 840        |             |          |
| DB                    | 781          | CAAAAAAGGCTGCTTGTGAATTTTCTGAGACGATGTACAAATATCTGAACATCATCAAC             | 840        |             |          |
| QY                    | 841          | CCAGTATTAATGATTGATTAACCACTGAGAAAGCGTGAAGCTGAGAGGATCCAAAAAGT             | 900        |             |          |
| DB                    | 841          | CCAGTATTAATGATTGATTAACCACTGAGAAAGCGTGAAGCTGAGAGGATCCAAAAAGT             | 900        |             |          |
| QY                    | 901          | ATCAGGGATGTTCTGTTTCAAACTTGGATGTGAGCATGTGACCAAAATCTCATGCGCA              | 960        |             |          |
| DB                    | 901          | ATCAGGGATGTTCTGTTTCAAACTTGGATGTGAGCATGTGACCAAAATCTCATGCGCA              | 960        |             |          |
| QY                    | 961          | GCTCATTAACGATGAGAACGACGTTTATTAATCTCACTAAAGACAAATGATGTAGAA               | 1020       |             |          |

Db 961 GCTATTACACATGAGAACGACGATTATTACTACTAATAAGACGAATGATGAAA 1020  
Qy 1021 AGCGTGAATTTCTGTATATAAAGCAACAGCTGCTTGCAAGAGCCCACTAACAT 1080  
Db 1021 AGCGTGAATTTCTGTATATAAAGCAACAGCTGCTTGCAAGAGCCCACTAACAT 1080  
Qy 1081 GGGCTGGAGTAGGAAACATGTATAGTAGGCGGACCTCCGACACAGAAAAAGGTAG 1140  
Db 1081 GGGCTGGAGTAGGAAACATGTATAGTAGGCGGACCTCCGACACAGAAAAAGGTAG 1140  
Qy 1141 ATCTGAATGCTGATCCCTGTGTGTAGAGAAAAAGAAATGGAATAGAGAACTGCCATGCT 1200  
Db 1141 ATCTGAATGCTGATCCCTGTGTGTAGAGAAAAAGAAATGGAATAGAGAACTGCCATGCT 1200  
Qy 1201 CAGAGAACTCTAGAGATCTAGAGATGTTCTTGATTAACACTAATATAGCAGATTGACA 1260  
Db 1201 CAGAGAACTCTAGAGATCTAGAGATGTTCTTGATTAACACTAATATAGCAGATTGACA 1260  
Qy 1261 AAGTTAATGAGTGGTTTCCAGAACTGATGAATGTTGGTCTGATGATCAGATGATG 1320  
Db 1261 AAGTTAATGAGTGGTTTCCAGAACTGATGAATGTTGGTCTGATGATCAGATGATG 1320  
Qy 1321 GGGAGTCTGAATCAAAATGCCAAAGTAGCTGATGATTTGGACGTTCTAAATGAGTAGATG 1380  
Db 1321 GGGAGTCTGAATCAAAATGCCAAAGTAGCTGATGATTTGGACGTTCTAAATGAGTAGATG 1380  
Qy 1381 AATATTTCTGCTTTCTTCAAGAAATATAGACTTATGCGCCAGTATCTCATAGGCTTTAA 1440  
Db 1381 AATATTTCTGCTTTCTTCAAGAAATATAGACTTATGCGCCAGTATCTCATAGGCTTTAA 1440  
Qy 1441 TATGTAAAGTAGAAAGAGTTCCTCAATCAGTAGAGATTAATTTGAAGCAAAATAT 1500  
Db 1441 TATGTAAAGTAGAAAGAGTTCCTCAATCAGTAGAGATTAATTTGAAGCAAAATAT 1500  
Qy 1501 TTGGGAAAACTTATCGGAAGAGGAGCCTTCCCACTTAAAGCATGTAAGTGAATATC 1560  
Db 1501 TTGGGAAAACTTATCGGAAGAGGAGCCTTCCCACTTAAAGCATGTAAGTGAATATC 1560  
Qy 1561 TAAATTAATGAGAGCATTTTGTATCTGACGACAGATTAATACAGAGGCTCCCTCAAAATA 1620  
Db 1561 TAAATTAATGAGAGCATTTTGTATCTGACGACAGATTAATACAGAGGCTCCCTCAAAATA 1620  
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|    |      |   |       |
|----|------|---|-------|
| Db | 5341 | TCATATGGAAGAAACCAACCAAGCTCCAAAGCCAGCAAGAAATCCACGACAGAAAGATCT    | 54000 |
| QY | 5401 | TCAGGGGGCTAGAAAATCTGTTCCTATGAGGCCCTTCACCAACAATGCCACAGATCAACTGG  | 54600 |
| Db | 5401 | TCAGGGGGCTAGAAAATCTGTTCCTATGAGGCCCTTCACCAACAATGCCACAGATCAACTGG  | 54600 |
| QY | 5461 | AATGATGATGATCAGCTGTGTGTGTCTTCGTGTGTGTGAAGAAGCTTCATTCATCCACCTTG  | 55200 |
| Db | 5461 | AATGATGATGATCAGCTGTGTGTGTCTTCGTGTGTGTGAAGAAGCTTCATTCATTCACCTTG  | 55200 |
| QY | 5521 | GCACAGGTGTCCACCCAAATTGTGTTGTGTGCACGCAGATGCTCTGACACAGAGCAATATGCT | 55800 |
| Db | 5521 | GCACAGGTGTCCACCCAAATTGTGTTGTGTGCACGCAGATGCTCTGACACAGAGCAATATGCT | 55800 |
| QY | 5581 | TCCATGCAATTGGGGAGATGTGTGTAGGGACCTCTGTGTGTACCCGAAAGTGGGTGTGGACA  | 56400 |
| Db | 5581 | TCCATGCAATTGGGGAGATGTGTGTAGGGACCTCTGTGTGTACCCGAAAGTGGGTGTGGACA  | 56400 |
| QY | 5641 | GTGTGCACTATCACAGTGCACAGAGCTGACACCTACTCTGTATCCCCAGATATCCCCACA    | 57000 |
| Db | 5641 | GTGTGCACTATCACAGTGCACAGAGCTGACACCTACTCTGTATCCCCAGATATCCCCACA    | 57000 |
| QY | 5701 | GCCACTACTGA 5711  |       |
| Db | 5701 | GCCACTACTGA 5711  |       |

|            |                                    |         |                 |
|------------|------------------------------------|---------|-----------------|
| RESULT 15  |                                    |         |                 |
| AR048660   |                                    |         |                 |
| LOCUS      | AR048660                           | 5711 bp | DNA             |
| DEFINITION | Sequence 4 from patent US 5821328. |         | linear          |
|            |                                    |         | PAT 29-SEP-1999 |

|          |               |            |
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| VERSION  | AR048660.1    | GI:5971003 |
| KEYWORDS |               |            |
| SOURCE   | unknown.      |            |
| ORGANISM | unknown.      |            |
|          | Unclassified. |            |

|           |  |
|-----------|--|
| REFERENCE | 1 (bases 1 to 5711)  |
| AUTHORS   | King,M.-C., Friedman, L., Ostermeyer, B., Rowell, S., Lynch, E., Szabo, C. and Lee, M. |
| TITLE     | Genetic markers for breast, ovarian, and prostatic cancer                              |
| JOURNAL   | Patent: US 5821328-A 4 13-OCT-1998;  |
| FEATURES  | Location/Qualifiers  |

| source     | 1..5711                     |
|------------|-----------------------------|
| BASE COUNT | 1956 a 1099 c 1275 g 1381 t |
| ORIGIN     |                             |

|                            |        |              |      |                   |
|----------------------------|--------|--------------|------|-------------------|
| Query Match                | 99.9%  | Score 5707.8 | DB 6 | Length 5711       |
| Best Local Similarity      | 100.0% | Pred. No. 0  |      |                   |
| Matches 5709; Conservative | 0      | Mismatches   | 2    | Indels 0; Gaps 0; |

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|||||

Db 1 AGCTGCTGAGACTTCTCTGGACCCGCGACCAAGCTGTGAGGTTTCTCAGATPACTGGGCC 60  
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121 TGGATTTATCTGCTCTTCGCGTTGAAGAATACAAATGTCATTAACTATGCAGAAA 180

121 TGGATTTATCTGCTCTTCGCGTTGAAGAATACAAATGTCATTAACTATGCAGAAA 180

Qy 181 TCTTAGAGTGTCCCATCTGTCMGAGTTGATCAAGAACTGTCTCCACAAGTGACC 240  
db 181 TCTTGAAGCTCTCTCTCTCGACTGATAAAGCAACCTCTCTCCACAAAGTGACC 240

[illegible]

**Z**

|    |      |  |      |
|----|------|--|------|
| QY | 301  | ATCCCTTATGTAAAGATATTAACCAAAAGACGCTACAAAGAAAGTACGAGATTTAGTC     | 360  |
| Db | 301  | GTCCCTTATGTAAAGATATTAACCAAAAGAGCTACAAAGAAAGTACGAGATTTAGTC      | 360  |
| QY | 361  | AACTTGTTGAAGAGCTATTTGAAAAATCAATTTGTCTTTTCAGCTTGACAAGGTTTGAGT   | 420  |
| Db | 361  | AACTTGTTGAAGAGCTATTTGAAAAATCAATTTGTCTTTTCAGCTTGACAAGGTTTGAGT   | 420  |
| QY | 421  | ATGCAAAAGCTATTAATTTTGCAAAAAAGAAAAATTAATCTCCCTGAACATCTAAAGATG   | 480  |
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| QY | 481  | AAAGTTTCATATCCAAAGTATGGGCTTACAGAAAACCGTGCCMAAAGACTTTCAGAGTGTG  | 540  |
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| QY | 541  | AAACCGAAAAATCCCTCTCTTGCAAGAAACCACTCTCAGTGTCCAACTCTCTAACCTTGAAA | 600  |
| Db | 541  | AAACCGAAAAATCCCTCTCTTGCAAGAAACCACTCTCAGTGTCCAACTCTCTAACCTTGAAA | 600  |
| QY | 601  | CTGTGAGAACTCTGTAGGACAAAGACGGGATACAACTCAAAAGACGTCGTACAAATG      | 660  |
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| QY | 661  | AATTGGATCTGATTTCTTGAAAGATACCGTTAATAAGGCACTTAATTCAGTGTGGAG      | 720  |
| Db | 661  | AATTGGATCTGATTTCTTGAAAGATACCGTTAATAAGGCACTTAATTCAGTGTGGAG      | 720  |
| QY | 721  | ATCAAGAAATTTCTTCAAAATCAACCCCTCAAGGAACCAAGGAATGAATCATGTTGATCTG  | 780  |
| Db | 721  | ATCAAGAAATTTCTTCAAAATCAACCCCTCAAGGAACCAAGGAATGAATCATGTTGATCTG  | 780  |
| QY | 781  | CAAAAAAGGCTGCTTGATGAAATTTTCTGAGACGAGTGTACAAATATCTGAACATCATCAAC | 840  |
| Db | 781  | CAAAAAAGGCTGCTTGATGAAATTTTCTGAGACGAGTGTACAAATATCTGAACATCATCAAC | 840  |
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| Db | 841  | CCAGTAAATATGATTTGAAACCACTGAGAAAGCGTGCAGCTGAGAGGCTATCAGAAAAAGT  | 900  |
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| Db | 901  | ATCAGGGAGATCTGTTTCAAACTGTGCAATGAGCAATGTGGGACAAATATCTCATGCCA    | 960  |
| QY | 961  | GCTCATTAACAGCATGAGAAACAGCAATTATTACTCACTAAAGACAGAAATGATGTAGAAA  | 1020 |
| Db | 961  | GCTCATTAACAGCATGAGAAACAGCAATTATTACTCACTAAAGACAGAAATGATGTAGAAA  | 1020 |
| QY | 1021 | AGGCTGAATTCGTATTAATAAGCAAAACAGCCTGGCTTAGCAAGAGGCCAATPAACAGAT   | 1080 |
| Db | 1021 | AGGCTGAATTCGTATTAATAAGCAAAACAGCCTGGCTTAGCAAGAGGCCAATPAACAGAT   | 1080 |
| QY | 1081 | GGGCTGGAAGTAAAGAAACATGTAATGATAGCGGCACTCCAGACAAGAAAAAAGGTAG     | 1140 |
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| QY | 1141 | ATCTGAATGCTGATCCCTGTGTGTAGAGAAAAAGATGGAATTAACCAAAAATGCGCATGCT  | 1200 |
| Db | 1141 | ATCTGAATGCTGATCCCTGTGTGTAGAGAAAAAGATGGAATTAACCAAAAATGCGCATGCT  | 1200 |
| QY | 1201 | CAGAGAAATCCTAGAGATACTGAAGATGTTCTTGATGAATACCTPAATATAGCAGATTGAGA | 1260 |
| Db | 1201 | CAGAGAAATCCTAGAGATACTGAAGATGTTCTTGATGAATACCTPAATATAGCAGATTGAGA | 1260 |
| QY | 1261 | AAAGTTAATGAGTGGTTTCCAGAAAGATGATGAACGTGTAGGTTCTGATGACTCAATGATG  | 1320 |
| Db | 1261 | AAAGTTAATGAGTGGTTTCCAGAAAGATGATGAACGTGTAGGTTCTGATGACTCAATGATG  | 1320 |
| QY | 1321 | GGGAGTCTGAATCAAAATCCAAATATGATGATGAAAGCTTCAAAATAGGATAGT         | 1380 |
| Db | 1321 | GGGAGTCTGAATCAAAATCCAAATATGATGATGAAAGCTTCAAAATAGGATAGT         | 1380 |
| QY | 1381 | AATATTTCTGTTCTTCAGAGAAAAATAGACTTAATCAGGCGAGTATCCTCATAGGCTTTAA  | 1440 |
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Mon Jun 16 08:11:53 2003

Search completed: June 13, 2003, 08:24:59  
Job time : 14055 secs

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PI Allen AC, Alvares CP, Critz BS, Murphy PD, Olson SJ;  
PI Schelker DB, Zeng B;  
DR WPI; 1998-296774/26.  
DR P-PSDB; AAM76099.  
XX BRCA1 omi gene coding sequences - useful for distinguishing between  
PT polymorphisms and mutation(s) in the screening for disposition to  
PT breast or ovarian cancer  
PS Claim 2d; Column 41-46; 54pp; English.  
XX  
CC This sequence encodes the human BRCA1 (breast and ovarian cancer  
CC predisposing gene) omi2 gene. This sequence and polymorphic variations of  
CC this sequence are useful for the identification of an individual who may  
CC or may not have an increased susceptibility to breast or ovarian cancer.  
CC The sequences used identify gene changes which are due to polymorphisms,  
CC rather than cancer causing mutations. BRCA1 is an anti-oncogene (tumour  
CC suppressor) which is involved in genetic inheritance of cancers,  
CC especially breast and ovarian cancer. It is found at human chromosome 17q  
CC which is known to be linked to cancer susceptibility, especially breast  
CC cancer. Cells containing a mutation in this gene lose the wild-type  
CC function of BRCA1 and are more susceptible to cancers.  
XX  
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Best Local Similarity 100.0%; Pred. No. 0;  
Matches 5711; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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 QY 2941 ATGCCAAATGTAGTATCAAGAGAGCTAGGTTTGTCTATCATCTCAGTTGAGAGCA 3000  
 DB 2941 ATGCCAAATGTAGTATCAAGAGAGCTAGGTTTGTCTATCATCTCAGTTGAGAGCA 3000  
 QY 3001 AGCAAACTGACTCAATTAATCTCAAAATTAATGAGCACTTTTACAAACCAATATGATAC 3060  
 DB 3001 AGCAAACTGACTCAATTAATCTCAAAATTAATGAGCACTTTTACAAACCAATATGATAC 3060  
 QY 3061 CACCACTTTTCCCACTCAAGTCAATTTGTTAAATCTAAGTGAAGAAATCTGCTAGAG 3120  
 DB 3061 CACCACTTTTCCCACTCAAGTCAATTTGTTAAATCTAAGTGAAGAAATCTGCTAGAG 3120  
 QY 3121 AAAACTTTGAGGAAATTCATGATGCTGAGAGAGAAATGAGAAATGAGAAATTCATCA 3180  
 DB 3121 AAAACTTTGAGGAAATTCATGATGCTGAGAGAGAAATGAGAAATGAGAAATTCATCA 3180  
 QY 3181 GTACAGTGAACAATTAATGAGAGAGCTGATTAATGAGAAATGTTTAAAGAAAGCAGCT 3240  
 DB 3181 GTACAGTGAACAATTAATGAGAGAGCTGATTAATGAGAAATGTTTAAAGAAAGCAGCT 3240  
 QY 3241 CAAAGCAATTTAATGAGAGAGTTCAGATCTAATGAAGTGGCTCAATTAATGA 3300  
 DB 3241 CAAAGCAATTTAATGAGAGAGTTCAGATCTAATGAAGTGGCTCAATTAATGA 3300  
 QY 3301 TAGGTTCCAGTGAATGAACATTCAGAGAGAACTAGTGAAGAAAGAGAGGCCAAATTTGA 3360  
 DB 3301 TAGGTTCCAGTGAATGAACATTCAGAGAGAACTAGTGAAGAAAGAGAGGCCAAATTTGA 3360  
 QY 3361 ATGCTATGCTTGAATGAGAGGTTTTCGAACTGAGGCTATTAACAAAGTCTTCTGGA 3420  
 DB 3361 ATGCTATGCTTGAATGAGAGGTTTTCGAACTGAGGCTATTAACAAAGTCTTCTGGA 3420  
 QY 3421 GTTATTTGAAGCATCTGTAATTAAGAAAGCAAGAAATTAAGAAAGTTCAGACTGTA 3480  
 DB 3421 GTTATTTGAAGCATCTGTAATTAAGAAAGCAAGAAATTAAGAAAGTTCAGACTGTA 3480  
 QY 3481 ATACAGATTTCTCTCATATCTGATTTAGATTAATGAGAAAGCTTATGAGAAATTAAG 3540  
 DB 3481 ATACAGATTTCTCTCATATCTGATTTAGATTAATGAGAAAGCTTATGAGAAATTAAG 3540  
 QY 3541 ATGCAATCTGAGTTTGTCTGAGACACTGATGACCTGTTAATGATGAGAAATTAAG 3600  
 DB 3541 ATGCAATCTGAGTTTGTCTGAGACACTGATGACCTGTTAATGATGAGAAATTAAG 3600  
 QY 3601 AAGATTAATGTTTGTCTGAAATTAAGCAATTAAGAAAGTCTGCTTTTGAAGAAAGG 3660  
 DB 3601 AAGATTAATGTTTGTCTGAAATTAAGCAATTAAGAAAGTCTGCTTTTGAAGAAAGG 3660  
 QY 3661 TCCAGAAAGAGAGCTTACAGAGAGCTAGGCTTTCACCAATACACTTTGGGCTCAG 3720  
 DB 3661 TCCAGAAAGAGAGCTTACAGAGAGCTAGGCTTTCACCAATACACTTTGGGCTCAG 3720  
 QY 3721 GTTACCGAAGAGAGGCGCAAGAAATTAAGATCTCTCAGAGAGAAATTAATGAGATG 3780  
 DB 3721 GTTACCGAAGAGAGGCGCAAGAAATTAAGATCTCTCAGAGAGAAATTAATGAGATG 3780  
 QY 3781 AAGAGCTTCCCTGCTTCCAACTGTTATTTGTTGAAGTAAAGTAAATTAATCTCTCAG 3840  
 DB 3781 AAGAGCTTCCCTGCTTCCAACTGTTATTTGTTGAAGTAAAGTAAATTAATCTCTCAG 3840  
 QY 3841 CTACTAGGATGACACCGTGTCTACAGAGTGTCTGTTAAGAAACAGAGGAGAAATTTAT 3900  
 DB 3841 CTACTAGGATGACACCGTGTCTACAGAGTGTCTGTTAAGAAACAGAGGAGAAATTTAT 3900  
 QY 3901 TATCATTTGAAGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3960

Db 3901 TATCATTTGAAGATAGCTTTAATGACTGACATACAGGTATATTTGCAAAAGGACATCTC 3960  
 QY AGGAACATCATCTTATGTAAGGAAACAAAATGTTCTGCTAGCTTTGTTTCTTCAACAGTGA 4020  
 Db 3961 AGGAACATCATCTTATGTAAGGAAACAAAATGTTCTGCTAGCTTTGTTTCTTCAACAGTGA 4020  
 QY 4021 GTGATTTGGAAGACTGACTGCAATATCAAAACACCAGGATCTTTCTGATTTGGTTCTT 4080  
 Db 4021 GTGATTTGGAAGACTGACTGCAATATCAAAACACCAGGATCTTTCTGATTTGGTTCTT 4080  
 QY 4081 CCAAAACAATGAGGATCAGTCTGAAAGCCAGGAGTTGGTCTGAGTGAACAAGATTGG 4140  
 Db 4081 CCAAAACAATGAGGATCAGTCTGAAAGCCAGGAGTTGGTCTGAGTGAACAAGATTGG 4140  
 QY 4141 TTTTCAGATGATGAAGAAAGAGAACGGGTTGGAAAGAAATATCAAGAAAGCAAGAGA 4200  
 Db 4141 TTTTCAGATGATGAAGAAAGAGAACGGGTTGGAAAGAAATATCAAGAAAGCAAGAGA 4200  
 QY 4201 TGGATTTCAACTTAGTGAGAGCAGATCTGGGTGTGAGAGTGAACCAAGCCTCTCTGAG 4260  
 Db 4201 TGGATTTCAACTTAGTGAGAGCAGATCTGGGTGTGAGAGTGAACCAAGCCTCTCTGAG 4260  
 QY 4261 ACTGCTCAGGGCTATCTCTCAGAGTGAACATTTTAACTCAGCAGAGGAGATACCATGC 4320  
 Db 4261 ACTGCTCAGGGCTATCTCTCAGAGTGAACATTTTAACTCAGCAGAGGAGATACCATGC 4320  
 QY 4321 AACATTAACCTGATTAAGCTTCCAGCAGAAATGGCTGAATAGAGTGTGTTAGAACAGC 4380  
 Db 4321 AACATTAACCTGATTAAGCTTCCAGCAGAAATGGCTGAATAGAGTGTGTTAGAACAGC 4380  
 QY 4381 ATGGAGAGCAGGCTTCTAACAGCTACCCCTTCATCATAGTACTCTTCTGCTTGAAG 4440  
 Db 4381 ATGGAGAGCAGGCTTCTAACAGCTACCCCTTCATCATAGTACTCTTCTGCTTGAAG 4440  
 QY 4441 ACTGCGAAATCCAGAACCAACCATCATGAAAAACGATTTAACTTCAAGAAAAGTA 4500  
 Db 4441 ACTGCGAAATCCAGAACCAACCATCATGAAAAACGATTTAACTTCAAGAAAAGTA 4500  
 QY 4501 GTGATTAACCTTAAGCCAGATCCAGAGGCTTCTGCTGACAAAGTTTGAGGTCTG 4560  
 Db 4501 GTGATTAACCTTAAGCCAGATCCAGAGGCTTCTGCTGACAAAGTTTGAGGTCTG 4560  
 QY 4561 CAGATAGTTCTTACAGTAATAATAAAGAACAGAGTGAAGATCCCTCTTAAAT 4620  
 Db 4561 CAGATAGTTCTTACAGTAATAATAAAGAACAGAGTGAAGATCCCTCTTAAAT 4620  
 QY 4621 GCCCATCATTTAGATAGTGGTGTATCATGCAAGATTGCTCTGGAGTCTTCAAGATGAA 4680  
 Db 4621 GCCCATCATTTAGATAGTGGTGTATCATGCAAGATTGCTCTGGAGTCTTCAAGATGAA 4680  
 QY 4681 ACTAACCCATCTCAAGAGAGCTCAATTAAGTTGTGATGTGAGAGCAACAGCTGGAAG 4740  
 Db 4681 ACTAACCCATCTCAAGAGAGCTCAATTAAGTTGTGATGTGAGAGCAACAGCTGGAAG 4740  
 QY 4741 AGCTGGGCGCACACGATTTGACGAAACATCTTACTTGCAGAGCAAGATCTAGAGGAA 4800  
 Db 4741 AGCTGGGCGCACACGATTTGACGAAACATCTTACTTGCAGAGCAAGATCTAGAGGAA 4800  
 QY 4801 CCCCTTACCTGGAATCTGGAATCAGCCTCTCTGATGACCTGGAATCTGATCCCTCTG 4860  
 Db 4801 CCCCTTACCTGGAATCTGGAATCAGCCTCTCTGATGACCTGGAATCTGATCCCTCTG 4860  
 QY 4861 AAGAAGAGCCCGCAGAGTACGCTGCTGTGGCAACATTCATCTTAACTCTGCAATGA 4920  
 Db 4861 AAGAAGAGCCCGCAGAGTACGCTGCTGTGGCAACATTCATCTTAACTCTGCAATGA 4920  
 QY 4921 AAGTTCGCCAATTGAAAGTTGCAATCTGCCAGAGTCCAGCTGCTCATACTACTG 4980  
 Db 4921 AAGTTCGCCAATTGAAAGTTGCAATCTGCCAGAGTCCAGCTGCTCATACTACTG 4980  
 QY 4981 ATACTGCTGGGTATATGCAATGGAAGAAAGTGTGACAGAGGAGAACCAAGATTGACAG 5040  
 Db 4981 ATACTGCTGGGTATATGCAATGGAAGAAAGTGTGACAGAGGAGAACCAAGATTGACAG 5040

QY 5041 CTTCAACAGAAAGGCTCAACAAAGAAATGTCATGCTGTGTCTGCGCTGACCCAGAG 5100  
 Db 5041 CTTCAACAGAAAGGCTCAACAAAGAAATGTCATGCTGTGTCTGCGCTGACCCAGAG 5100  
 QY 5101 AATTATGCTGTGTAAGAGTTTGCAGAAAACCAACATCACTTAATTAATTAATTA 5160  
 Db 5101 AATTATGCTGTGTAAGAGTTTGCAGAAAACCAACATCACTTAATTAATTAATTA 5160  
 QY 5161 CTGAAGAGACTACATCTTGTATGAAAACAGATGCTGAGTTGTGTGAAAGCAGAC 5220  
 Db 5161 CTGAAGAGACTACATCTTGTATGAAAACAGATGCTGAGTTGTGTGAAAGCAGAC 5220  
 QY 5221 TGAATATTTTCTAGAAATTCGGGAGAGAAAATGGTAGTTAGCTATTTCTGGGTGACC 5280  
 Db 5221 TGAATATTTTCTAGAAATTCGGGAGAGAAAATGGTAGTTAGCTATTTCTGGGTGACC 5280  
 QY 5281 AGCTATTATTAAGAAAGAAATGCTGAATGACATGATTTTGAAGTCAAGAGAGATGTG 5340  
 Db 5281 AGCTATTATTAAGAAAGAAATGCTGAATGACATGATTTTGAAGTCAAGAGAGATGTG 5340  
 QY 5341 TCAATGGAAGAAACCAACAGTCCAAAGCAGAGAAAGATCCAGAGCAAGAAAGTCT 5400  
 Db 5341 TCAATGGAAGAAACCAACAGTCCAAAGCAGAGAAAGATCCAGAGCAAGAAAGTCT 5400  
 QY 5401 TCAGGGGGCTAGAAATCTGTTGCTATGAGGACCTTCAACCAATGCCCCAGATCACTGG 5460  
 Db 5401 TCAGGGGGCTAGAAATCTGTTGCTATGAGGACCTTCAACCAATGCCCCAGATCACTGG 5460  
 QY 5461 AATGATGATGACAGCTGTGTGTCTTCTGTGTGTAAGAGCTTTCATCACTCCCTG 5520  
 Db 5461 AATGATGATGACAGCTGTGTGTCTTCTGTGTGTAAGAGCTTTCATCACTCCCTG 5520  
 QY 5521 GCACAGGTGTCCACCAATTTGTGTGTGACAGCAATGCTGTGACAGAGAGCAATGGCT 5580  
 Db 5521 GCACAGGTGTCCACCAATTTGTGTGTGACAGCAATGCTGTGACAGAGAGCAATGGCT 5580  
 QY 5581 TCCATGCAATTTGGGAGATGTGTGAGGACCTGTGTGTGACCCGAGATGGGTGTTGACA 5640  
 Db 5581 TCCATGCAATTTGGGAGATGTGTGAGGACCTGTGTGTGACCCGAGATGGGTGTTGACA 5640  
 QY 5641 GTGTGACACTTACCAAGTCCAGAGAGCTGACACCTTACCTGATACCCAGATCCCCACA 5700  
 Db 5641 GTGTGACACTTACCAAGTCCAGAGAGCTGACACCTTACCTGATACCCAGATCCCCACA 5700  
 QY 5701 GCCACTACTGA 5711  
 Db 5701 GCCACTACTGA 5711  
 RESULT 2  
 AAC60795  
 ID AAC60795 standard; cDNA; 5711 BP.  
 XX AAC60795;  
 DT 07-FEB-2001 (first entry)  
 DE Human BRCA1 (om13) nucleotide sequence SEQ ID NO:5.  
 XX  
 DE Human; BRCA1; chromosome 17; 17q21; breast cancer; ovarian cancer;  
 KW gene therapy; diagnosis; cytostatic; genetic susceptibility; mutation;  
 KW polymorphism; identification; ss.  
 OS Homo sapiens.  
 XX  
 OS  
 PN US6130322-A.  
 XX  
 PD 10-OCT-2000.  
 XX  
 PF 06-MAY-1998; 98US-0074476.  
 XX  
 PR 12-FEB-1996; 96US-0598591.

PR 12-DEC-1997; 97US-0798691.  
XX (GENE-) GENE LOGIC INC.  
XX  
PI Zeng B, Thurber D, Olson SJ, Alvares CP, Allen ACP, Murphy PD,  
PI Ciliz BS;  
XX  
DR WPI: 2000-646756/62.  
DR P-PSDB; AAB24219.  
XX  
PT New coding sequence of the human BRCA1 gene, i.e. BRCA1 (om12), useful  
PT in gene therapy, especially for preventing or treating breast or  
PT ovarian cancer, as well as for diagnosing or monitoring breast or  
PT ovarian cancer -  
XX  
XX  
PS Example 4; Column 59-66; 56pp; English.  
XX  
CC AAC60793 to AAC60795 encode the human BRCA1 (om1-3) proteins given in  
CC AAB24217 to AAB24219 respectively. BRCA1 is found on chromosome 17  
CC mapping to position 17q21. The BRCA1 (om12) coding sequence is  
CC specifically claimed in the present invention. The BRCA1 (om12) coding  
CC sequence is useful in gene therapy, especially for preventing or treating  
CC breast or ovarian cancer. It is also useful for diagnosing or monitoring  
CC breast or ovarian cancer. Furthermore, the BRCA1 (om12) coding sequence  
CC is useful for: (a) identifying individuals having BRCA1 gene mutations  
CC and having an increased genetic susceptibility to breast or ovarian  
CC cancer, or identifying a mutation that increases the genetic  
CC susceptibility to breast or ovarian cancer; (b) avoiding  
CC misinterpretation of polymorphisms found in the BRCA1 gene; (c)  
CC determining the presence of a previously unknown mutation in the BRCA1  
CC gene; (d) probing a human sample of the BRCA1 gene by allele to determine  
CC the presence of either polymorphic alleles or mutations; and (e)  
CC performing diagnosis with a reagent derived from the BRCA1 (om1) cDNA  
CC sequence. AAC60796 to AAC60861 represent PCR primers for the BRCA1 gene,  
CC which are used in an example from the present invention.  
XX  
SQ Sequence 5711 BP; 1956 A; 1098 C; 1274 G; 1383 T; 0 other;  
XX  
Query Match 100.0%; Score 5711; DB 21; Length 5711;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 5711; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AGCTCGGTGAGACTTCTCTGAGACCCGCGACGAGGTGGGTTCTCAGATACTGGGC 60  
DB 1 AGCTCGGTGAGACTTCTCTGAGACCCGCGACGAGGTGGGTTCTCAGATACTGGGC 60  
QY 61 CTTGCGCTGAGAGGCTTCACTCTGCTCTGGGTAAAGTTCAATGGAAACAGAAAGAA 120  
DB 61 CTTGCGCTGAGAGGCTTCACTCTGCTCTGGGTAAAGTTCAATGGAAACAGAAAGAA 120  
QY 121 TGAATTTATCTGCTCTGCGGTTGGAAGAAATGATCAATAATGCTATGTCAGAAAA 180  
DB 121 TGAATTTATCTGCTCTGCGGTTGGAAGAAATGATCAATAATGCTATGTCAGAAAA 180  
QY 181 TCTTGAAGTGTCCATCTGCTCTGAGAGTTGATCAAGAACTCTCCCAAAAGTGGACC 240  
DB 181 TCTTGAAGTGTCCATCTGCTCTGAGAGTTGATCAAGAACTCTCCCAAAAGTGGACC 240  
QY 241 ACATATTTTGCAGAAATTTTGGATCTGTAACCTTCTCAACGAAAGAAAGGCTTCAAGT 300  
DB 241 ACATATTTTGCAGAAATTTTGGATCTGTAACCTTCTCAACGAAAGAAAGGCTTCAAGT 300  
QY 301 GTCTTTATGTAAGATGATATTAACCAAGAGGCTTCAAGAAAGTATGATGTC 360  
DB 301 GTCTTTATGTAAGATGATATTAACCAAGAGGCTTCAAGAAAGTATGATGTC 360  
QY 361 AACTTGTGAAGAGCTATGTAAGAAATCAATTTGCTTTTCACTTGAACAGGTTTGAAGT 420  
DB 361 AACTTGTGAAGAGCTATGTAAGAAATCAATTTGCTTTTCACTTGAACAGGTTTGAAGT 420  
QY 421 ATGCAAAACAGCTTAATTTTGGCAAAAAGAAATTAATCTTCTGTAACATTAAGATG 480  
DB 421 ATGCAAAACAGCTTAATTTTGGCAAAAAGAAATTAATCTTCTGTAACATTAAGATG 480

QY 481 AAGTTTCTATCATCCAAAGATGGGCTACAGAAACCGTGCCAAAAGACTTCTACAGAGTG 540  
DB 481 AAGTTTCTATCATCCAAAGATGGGCTACAGAAACCGTGCCAAAAGACTTCTACAGAGTG 540  
QY 541 AACCCGAAAATCCTTCTCTGAGAGAAACGAGTCTAGTGTCAACTCTCTAACCTTGA 600  
DB 541 AACCCGAAAATCCTTCTCTGAGAGAAACGAGTCTAGTGTCAACTCTCTAACCTTGA 600  
QY 601 CTGTGAAACTCTGAGAGCAAGACGCGATACAACTCAAAAAGAGTCTGTCTAATG 660  
DB 601 CTGTGAAACTCTGAGAGCAAGACGCGATACAACTCAAAAAGAGTCTGTCTAATG 660  
QY 661 AATTGGATCTGATCTTCTGAAAGATACCGTTAATAGGCACTTATGACGTGGAG 720  
DB 661 AATTGGATCTGATCTTCTGAAAGATACCGTTAATAGGCACTTATGACGTGGAG 720  
QY 721 ATCAAGAAATGTTTAAATCAACCCCTCAAGAAACGAGGATGAATCAGTTTGGATCTG 780  
DB 721 ATCAAGAAATGTTTAAATCAACCCCTCAAGAAACGAGGATGAATCAGTTTGGATCTG 780  
QY 781 CAAAAAAGGCTGTTGTGAATTTTCTGAGACGATGTAACTGAACATCATCAAC 840  
DB 781 CAAAAAAGGCTGTTGTGAATTTTCTGAGACGATGTAACTGAACATCATCAAC 840  
QY 841 CCAGTAATATGATTTGAAACACCACTGAGAGGCTGAGAGCATCCAGAAAGT 900  
DB 841 CCAGTAATATGATTTGAAACACCACTGAGAGGCTGAGAGCATCCAGAAAGT 900  
QY 901 ATCAGGATGTTCTGTTTCAAACTTGATGAGGATGAGGATGAGCAAAATCTCATGCCA 960  
DB 901 ATCAGGATGTTCTGTTTCAAACTTGATGAGGATGAGGATGAGCAAAATCTCATGCCA 960  
QY 961 GCTCATTAAGCATGAGAAACAGAGTTTATCTACTCTAAGACAGATGATGTGAAA 1020  
DB 961 GCTCATTAAGCATGAGAAACAGAGTTTATCTACTCTAAGACAGATGATGTGAAA 1020  
QY 1021 AGGCTGAATTCGTATTAATAAGCAACAGCTGGCTTACAGAGGACCAATTAAGAT 1080  
DB 1021 AGGCTGAATTCGTATTAATAAGCAACAGCTGGCTTACAGAGGACCAATTAAGAT 1080  
QY 1081 GGGCTGGAAGTAAGAAACATGATGATAGGCGGACTCCAGACAGAAAAAAGGTAG 1140  
DB 1081 GGGCTGGAAGTAAGAAACATGATGATAGGCGGACTCCAGACAGAAAAAAGGTAG 1140  
QY 1141 ATCTGAATCTGATCCCTGTGTGAGAGAAAGAAATGAAATAGCAGAAACCTGCATGCT 1200  
DB 1141 ATCTGAATCTGATCCCTGTGTGAGAGAAAGAAATGAAATAGCAGAAACCTGCATGCT 1200  
QY 1201 CAGAGAACTCTGAGATGATGAAATGCTCTGATTAACATTAATACAGATTCAGA 1260  
DB 1201 CAGAGAACTCTGAGATGATGAAATGCTCTGATTAACATTAATACAGATTCAGA 1260  
QY 1261 AAGTTAATGAGTGTCTTCCAGAAAGTGAATGTTAGTCTGATGATGATGATG 1320  
DB 1261 AAGTTAATGAGTGTCTTCCAGAAAGTGAATGTTAGTCTGATGATGATGATGATG 1320  
QY 1321 GGGAGTCTGAATCAAAATGCTGAATGATGATGATGATGATGATGATGATGATG 1380  
DB 1321 GGGAGTCTGAATCAAAATGCTGAATGATGATGATGATGATGATGATGATGATGATG 1380  
QY 1381 AATATTTCTGCTTCTCAGAGAAATAGATTAATGAGGCTGATGATGATGATGATG 1440  
DB 1381 AATATTTCTGCTTCTCAGAGAAATAGATTAATGAGGCTGATGATGATGATGATGATG 1440  
QY 1441 TATGTAAGAGTGAAGATTCATCCAAATCAGTGAAGATTAATGTAAGACAAATAT 1500  
DB 1441 TATGTAAGAGTGAAGATTCATCCAAATCAGTGAAGATTAATGTAAGACAAATAT 1500  
QY 1501 TTGGGAAAACCTATGGAAGAGGCAAGCTCCCACTTAAGCAATGTAATCTGAAATC 1560  
DB 1501 TTGGGAAAACCTATGGAAGAGGCAAGCTCCCACTTAAGCAATGTAATCTGAAATC 1560

|    |      |   |      |
|----|------|---|------|
| QY | 1561 | TAATTAATGAGACATTTGTTACTGAGCCACAGATPATACAGAGCGTCCCTCCCAATA     | 1620 |
| Db | 1561 | TAATTAATGAGACATTTGTTACTGAGCCACAGATPATACAGAGCGTCCCTCCCAATA     | 1620 |
| QY | 1691 | AAATTAACCGTAAAGAGACCTACATCAGGCGTTCACTCGAGGATTTTATCAAGAAG      | 1680 |
| Db | 1691 | AAATTAACCGTAAAGAGACCTACATCAGGCGTTCACTCGAGGATTTTATCAAGAAG      | 1680 |
| QY | 1691 | CAGATTTGGCAGTTCCAAAAGACTCCTGAAATGATTAATCAGGGACTAACCAA         | 1740 |
| Db | 1691 | CAGATTTGGCAGTTCCAAAAGACTCCTGAAATGATTAATCAGGGACTAACCAA         | 1740 |
| QY | 1741 | AGATGCTCAAGTGTGAATATTACTAATTAAGTGTGATGAGATTAACAAAGCTGATT      | 1800 |
| Db | 1741 | AGATGCTCAAGTGTGAATATTACTAATTAAGTGTGATGAGATTAACAAAGCTGATT      | 1800 |
| QY | 1801 | CTATTCAAGATGAGAAAAATCCTAACCAATAGAAATCCTGAAAAAGAAATCTGCTTTCA   | 1860 |
| Db | 1801 | CTATTCAAGATGAGAAAAATCCTAACCAATAGAAATCCTGAAAAAGAAATCTGCTTTCA   | 1860 |
| QY | 1861 | AAACGAAAGCTGAACTTAATAAGCAGCATATAGCAATATGAAACTCGAATTAATAATCC   | 1920 |
| Db | 1861 | AAACGAAAGCTGAACTTAATAAGCAGCATATAGCAATATGAAACTCGAATTAATAATCC   | 1920 |
| QY | 1921 | ACAATTCAAAAGCCTTAATAAGATAGCGCTGAGAGGAAGTCTTCTACAGCAATATTC     | 1980 |
| Db | 1921 | ACAATTCAAAAGCCTTAATAAGATAGCGCTGAGAGGAAGTCTTCTACAGCAATATTC     | 1980 |
| QY | 1991 | ATGCGCTTGAACCTAGTACTAGTGAATCTTAAGCCCACTTAATTGTACTGAATTTGCAA   | 2040 |
| Db | 1991 | ATGCGCTTGAACCTAGTACTAGTGAATCTTAAGCCCACTTAATTGTACTGAATTTGCAA   | 2040 |
| QY | 2041 | TTGATAGTGTCTCTAGCAGTGAAGATTAAGAAAAAAAGATACCAACCAATGCGCAGTCA   | 2100 |
| Db | 2041 | TTGATAGTGTCTCTAGCAGTGAAGATTAAGAAAAAAAGATACCAACCAATGCGCAGTCA   | 2100 |
| QY | 2101 | GGCACAGCAGAAACCTTACAACTCATGGAAGTTAAAGAACTTGCAACTGAGCCCAAGAA   | 2160 |
| Db | 2101 | GGCACAGCAGAAACCTTACAACTCATGGAAGTTAAAGAACTTGCAACTGAGCCCAAGAA   | 2160 |
| QY | 2161 | GTAACCAACCCAAATGAACAGACAGTAATAACATGAGAGATCTTTCCCAAGCTGA       | 2220 |
| Db | 2161 | GTAACCAACCCAAATGAACAGACAGTAATAACATGAGAGATCTTTCCCAAGCTGA       | 2220 |
| QY | 2221 | AGTTTACCAATGACCTGCTTTCTTTTACTAAGTGTTCAAATACAGAGTAACTTAAAGAT   | 2280 |
| Db | 2221 | AGTTTACCAATGACCTGCTTTCTTTTACTAAGTGTTCAAATACAGAGTAACTTAAAGAT   | 2280 |
| QY | 2281 | TTGTCAATCTTACGCTTCCAAAGAGAAAAAGAAAGAGAAATCTAGAAACAGTTAAAGTGT  | 2340 |
| Db | 2281 | TTGTCAATCTTACGCTTCCAAAGAGAAAAAGAAAGAGAAATCTAGAAACAGTTAAAGTGT  | 2340 |
| QY | 2341 | CTAATTAATGCTTGAAGACCCCAAAAGTCTCACTGTTAAGTGGAGAAAGGTTTGGCAACTG | 2400 |
| Db | 2341 | CTAATTAATGCTTGAAGACCCCAAAAGTCTCACTGTTAAGTGGAGAAAGGTTTGGCAACTG | 2400 |
| QY | 2401 | AAAAGTCTGTAGAGAGTGAAGAGTATTTCAATTTGGTACCTGTATAGTAATGACACTCAGG | 2460 |
| Db | 2401 | AAAAGTCTGTAGAGAGTGAAGAGTATTTCAATTTGGTACCTGTATAGTAATGACACTCAGG | 2460 |
| QY | 2461 | AAAGTATCTGTTACTGGAAGTTAGCACTTAGGGAGGCAAAAAAGAAACCAATTAAT      | 2520 |
| Db | 2461 | AAAGTATCTGTTACTGGAAGTTAGCACTTAGGGAGGCAAAAAAGAAACCAATTAAT      | 2520 |
| QY | 2521 | GTTGTAGTCAAGTGTGACGATTTGAAAAACCCCAAGGACCTAATTCATGTTGTTCCAAAG  | 2580 |
| Db | 2521 | GTTGTAGTCAAGTGTGACGATTTGAAAAACCCCAAGGACCTAATTCATGTTGTTCCAAAG  | 2580 |
| QY | 2581 | ATAATAGAAATGACACAGAGGCTTAAAGTATCAATTTGGGACATGAAATTAACAACAGTCT | 2640 |
| Db | 2581 | ATAATAGAAATGACACAGAGGCTTAAAGTATCAATTTGGGACATGAAATTAACAACAGTCT | 2640 |
| QY | 2641 | GGGAAACAGCATAGAAATGGAAGAAATGAACTGATGCTCAGTATTTGCAGAATCAT      | 2700 |

|    |      |   |      |
|----|------|---|------|
| Db | 2641 | GGGAAAACACATGAAATGGAAGGAAAGTGAACCTTGATGCTCAGTATTTGCAATACAT    | 2700 |
| Oy | 2701 | TCAGGTTTTCAAAGCCGCCAGTCATTTGCTCTGTTTTCAAATCCAGAAATGACAGAGG    | 2760 |
| Db | 2701 | TCAGGTTTTCAAAGCCGCCAGTCATTTGCTCTGTTTTCAAATCCAGAAATGACAGAGG    | 2760 |
| Oy | 2761 | AATGTCACATCTCTCTGCCCACTCTGGGTCTTAAAGAACAAAGTCCAAAGTCATT       | 2820 |
| Db | 2761 | AATGTCACATCTCTCTGCCCACTCTGGGTCTTAAAGAACAAAGTCCAAAGTCACTT      | 2820 |
| Oy | 2821 | TTGAAATGTGAACAAAAGGAAGAAATCAAGSAAACAAATGAGCTCAATCAAGCTGTAC    | 2880 |
| Db | 2821 | TTGAAATGTGAACAAAAGGAAGAAATCAAGSAAACAAATGAGCTCAATCAAGCTGTAC    | 2880 |
| Oy | 2881 | AGACAGTTAATATACCTGACAGGCTTTCCTGTGTTGTCAGAAAGATPAGCCAGTTGATA   | 2940 |
| Db | 2881 | AGACAGTTAATATACCTGACAGGCTTTCCTGTGTTGTCAGAAAGATPAGCCAGTTGATA   | 2940 |
| Oy | 2941 | ATGCGAAATGATGATCAAGAGGCTCTAGGTTTGTCTATCATCTCAGTTCAGAGCA       | 3000 |
| Db | 2941 | ATGCGAAATGATGATCAAGAGGCTCTAGGTTTGTCTATCATCTCAGTTCAGAGCA       | 3000 |
| Oy | 3001 | ACGAAATGTGACATCTTACCTCCAAATPAAACATGAGCTTTTCAAAACCCATATGTATAC  | 3060 |
| Db | 3001 | ACGAAATGTGACATCTTACCTCCAAATPAAACATGAGCTTTTCAAAACCCATATGTATAC  | 3060 |
| Oy | 3061 | CACACATTTTTCCCATCAAGTCATTTGTTTAAACATAAATGTAAGAAATATGCTGTAAGG  | 3120 |
| Db | 3061 | CACACATTTTTCCCATCAAGTCATTTGTTTAAACATAAATGTAAGAAATATGCTGTAAGG  | 3120 |
| Oy | 3121 | AAAACTTTGAGGAACATTCATGTGCACTGAAAGGAATGGGAATGAGAACATTCGAA      | 3180 |
| Db | 3121 | AAAACTTTGAGGAACATTCATGTGCACTGAAAGGAATGGGAATGAGAACATTCGAA      | 3180 |
| Oy | 3181 | GTACAGTGAACCAATTAAGCCGTAATACATTAGAGAAATGTTTTTAAAGAACCCAGCT    | 3240 |
| Db | 3181 | GTACAGTGAACCAATTAAGCCGTAATACATTAGAGAAATGTTTTTAAAGAACCCAGCT    | 3240 |
| Oy | 3241 | CAAGCAATTTAATGAAAGTAGTCCAGACTAAATGAAGTGGGCTCCAGTATTAAATGAA    | 3300 |
| Db | 3241 | CAAGCAATTTAATGAAAGTAGTCCAGACTAAATGAAGTGGGCTCCAGTATTAAATGAA    | 3300 |
| Oy | 3301 | TAGGTTCCAGTGTGAAAAATTCAAGCAGAACTAGTAGAAGAACAGAGGCCAAATATGA    | 3360 |
| Db | 3301 | TAGGTTCCAGTGTGAAAAATTCAAGCAGAACTAGTAGAAGAACAGAGGCCAAATATGA    | 3360 |
| Oy | 3361 | ATGCTATGCTTAAGATTAGGGGTTTGGCACTGAGAGCTTATTAACAAAGTCTTCTGGAA   | 3420 |
| Db | 3361 | ATGCTATGCTTAAGATTAGGGGTTTGGCACTGAGAGCTTATTAACAAAGTCTTCTGGAA   | 3420 |
| Oy | 3421 | GTAAATTTAAGCATCTCGAAATPAAAAACAAAGATATGAAGAGTAGTCCAGACTGTA     | 3480 |
| Db | 3421 | GTAAATTTAAGCATCTCGAAATPAAAAACAAAGATATGAAGAGTAGTCCAGACTGTA     | 3480 |
| Oy | 3481 | ATACAGATTTCTCTGCATATCTGATTTTCAGATACCTTAAGAACAGGCTATGGAAGTAGTC | 3540 |
| Db | 3481 | ATACAGATTTCTCTGCATATCTGATTTTCAGATACCTTAAGAACAGGCTATGGAAGTAGTC | 3540 |
| Oy | 3541 | ATGCAATCTAGGTTTGTTCAGACACTGATGACCTGTTAGATGATGCTGAATTAAGG      | 3600 |
| Db | 3541 | ATGCAATCTAGGTTTGTTCAGACACTGATGACCTGTTAGATGATGCTGAATTAAGG      | 3600 |
| Oy | 3601 | AAGATTAATCTTTTGTCTGAAATGACATTAAGSAAAGTCTGCTGTTTTTATGCAAAAGCG  | 3660 |
| Db | 3601 | AAGATTAATCTTTTGTCTGAAATGACATTAAGSAAAGTCTGCTGTTTTTATGCAAAAGCG  | 3660 |
| Oy | 3661 | TCCAGAAAGAGAGCTTTAGCAGAGTCTAGCCCTTACACCATACACATTTGGCTAGG      | 3720 |
| Db | 3661 | TCCAGAAAGAGAGCTTTAGCAGAGTCTAGCCCTTACACCATACACATTTGGCTAGG      | 3720 |
| Oy | 3721 | GTATCCGAGAGAGGGCCAAAGAAATTAAGACTCTCAGAGAGAACTTATCTAGTAGAGATG  | 3780 |
| Db | 3721 | GTATCCGAGAGAGGGCCAAAGAAATTAAGACTCTCAGAGAGAACTTATCTAGTAGAGATG  | 3780 |

Db 3721 GTTACCGAAGAGGGGCCAAGAAATTAGATCTCAGAGAGAACTTATCTAGAGATG 3780  
QY 3781 AAGAGCTTCCCTGCTCCAAACCTTGTATTTGGTAAAGTAACAATATACCTTCCAGT 3840  
Db 3781 AAGAGCTTCCCTGCTCCAAACCTTGTATTTGGTAAAGTAACAATATACCTTCCAGT 3840  
QY 3841 CTACTAGCATTAGCACCCTGTCTACCGAGTGTCTGTCTAAGAACACAGAGAGATTTAT 3900  
Db 3841 CTACTAGCATTAGCACCCTGTCTACCGAGTGTCTGTCTAAGAACACAGAGAGATTTAT 3900  
QY 3901 TATCATTTGAAGATAGCTTAAATGATCTGCAATACCAAGTAATTTGGCAAGGCATCTC 3960  
Db 3901 TATCATTTGAAGATAGCTTAAATGATCTGCAATACCAAGTAATTTGGCAAGGCATCTC 3960  
QY 3961 AGGAACATCACTTATGAGAGAAACAAATGTTCTGTAGCTTGTCTTCCACAGTCA 4020  
Db 3961 AGGAACATCACTTATGAGAGAAACAAATGTTCTGTAGCTTGTCTTCCACAGTCA 4020  
QY 4021 GTGATTTGGAAGAATTGACTGCAAAATACAAACCCAGATCCCTTCTTGAATTTGTTCTT 4080  
Db 4021 GTGATTTGGAAGAATTGACTGCAAAATACAAACCCAGATCCCTTCTTGAATTTGTTCTT 4080  
QY 4081 CCAAAACAATGAGGCATCACTGTGAAAGCCAGAGATTTGGTCTGAGTCAAGAGATTTGG 4140  
Db 4081 CCAAAACAATGAGGCATCACTGTGAAAGCCAGAGATTTGGTCTGAGTCAAGAGATTTGG 4140  
QY 4141 TTTTCAGATGATGAAGAAAGAGAAACGGGCTTGGAGAAATATATCAAGAGAGCAAGCA 4200  
Db 4141 TTTTCAGATGATGAAGAAAGAGAAACGGGCTTGGAGAAATATATCAAGAGAGCAAGCA 4200  
QY 4201 TGGATTTCAAACTTATGATGAGAGCAGCATCTGGGTGTGAGTGAACAAGAGCTCTGAG 4260  
Db 4201 TGGATTTCAAACTTATGATGAGAGCAGCATCTGGGTGTGAGTGAACAAGAGCTCTGAG 4260  
QY 4261 ACTGCTCAGGGCTATCTCTCAGATGACATTTTAACTCAGCAGAGAGATTAACAATGC 4320  
Db 4261 ACTGCTCAGGGCTATCTCTCAGATGACATTTTAACTCAGCAGAGAGATTAACAATGC 4320  
QY 4321 AACATTAACCTGATTAAGAGCTCAGAGAGAAATGGCTGAACCTAGAAAGCTGTTGAACAGC 4380  
Db 4321 AACATTAACCTGATTAAGAGCTCAGAGAGAAATGGCTGAACCTAGAAAGCTGTTGAACAGC 4380  
QY 4381 ATGGAGCCAGCCTTCTTAACAGTCACTCCATCAATATGATCTCTTCTGCCCTTGAGG 4440  
Db 4381 ATGGAGCCAGCCTTCTTAACAGTCACTCCATCAATATGATCTCTTCTGCCCTTGAGG 4440  
QY 4441 ACCCTGCGAAATCCAGAAACAAAGCACAATCAGAAAAAGCAGATTTTCAACAGAAAAATG 4500  
Db 4441 ACCCTGCGAAATCCAGAAACAAAGCACAATCAGAAAAAGCAGATTTTCAACAGAAAAATG 4500  
QY 4501 GTGATTAACCTTATTAAGCCAAATCCAGAAAGCCTTCTGTGCAAGTTTGAAGTGTG 4560  
Db 4501 GTGATTAACCTTATTAAGCCAAATCCAGAAAGCCTTCTGTGCAAGTTTGAAGTGTG 4560  
QY 4561 CAGATAGTTCTACACAGTAAATAAAGAACAGAGAGTGAAGATCCCTTCTTAAT 4620  
Db 4561 CAGATAGTTCTACACAGTAAATAAAGAACAGAGAGTGAAGATCCCTTCTTAAT 4620  
QY 4621 GCCCATCATTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4680  
Db 4621 GCCCATCATTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4680  
QY 4681 ACTTACCATCTCAAGAGAGAGCTCAATTAAGTGTGATGATGATGATGATGATGATGATG 4740  
Db 4681 ACTTACCATCTCAAGAGAGAGCTCAATTAAGTGTGATGATGATGATGATGATGATGATG 4740  
QY 4741 AGTCTGGGCCACAGATTTGACGAAACATCTTACTTGCAGAGCAAGATCTAGAGGAA 4800  
Db 4741 AGTCTGGGCCACAGATTTGACGAAACATCTTACTTGCAGAGCAAGATCTAGAGGAA 4800  
QY 4801 CCCCTTACTGGAATCTGGAATCAGCCTTCTCTGATGACCTGTAATCTGATCTTCTG 4860  
Db 4801 CCCCTTACTGGAATCTGGAATCAGCCTTCTCTGATGACCTGTAATCTGATCTTCTG 4860

QY 4861 AAGACAGAGCCCGAGAGTCACTGCTGTGTGGCAACAATACCATCTCAACCTCTGATTA 4920  
Db 4861 AAGACAGAGCCCGAGAGTCACTGCTGTGTGGCAACAATACCATCTCAACCTCTGATTA 4920  
QY 4921 AAGTCCCAATTTGAAGTTGACGAATCTGCCAGAGTCCAGCTGTCTCATTAATCTG 4980  
Db 4921 AAGTCCCAATTTGAAGTTGACGAATCTGCCAGAGTCCAGCTGTCTCATTAATCTG 4980  
QY 4981 ATATCTGTGGGTATTAATGCAATGGAAGAAAGTGTGACAGAGGAAAGCCAGATTTGAC 5040  
Db 4981 ATATCTGTGGGTATTAATGCAATGGAAGAAAGTGTGACAGAGGAAAGCCAGATTTGAC 5040  
QY 5041 CTTCAACAGAAAGGTCACAAAGATGTCATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5100  
Db 5041 CTTCAACAGAAAGGTCACAAAGATGTCATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5100  
QY 5101 AATTTATGCTCGTGAACAAGTTTGCAGAAACACCAATCACTTTAATCTTAATTA 5160  
Db 5101 AATTTATGCTCGTGAACAAGTTTGCAGAAACACCAATCACTTTAATCTTAATTA 5160  
QY 5161 CTGAAAGACTACTCATGTGTGTATGAAACAGATCTGAGTTGTGTGTGTGTGTGTGTGTGT 5220  
Db 5161 CTGAAAGACTACTCATGTGTGTATGAAACAGATCTGAGTTGTGTGTGTGTGTGTGTGTGT 5220  
QY 5221 TGAATATTTTCTAGGAATTTGCGGAGAGAAATGGGTAGTGTATTTCTGGGTGACC 5280  
Db 5221 TGAATATTTTCTAGGAATTTGCGGAGAGAAATGGGTAGTGTATTTCTGGGTGACC 5280  
QY 5281 AGTCTATTAAGAGAAAGAAATGCTGAATAGAGCATTTTGAAGTCAGAGAGATGTG 5340  
Db 5281 AGTCTATTAAGAGAAAGAAATGCTGAATAGAGCATTTTGAAGTCAGAGAGATGTG 5340  
QY 5341 TCAATGGAAGAAACCAAGGTCCAAAGCAGCAAGAGATTCACGACAGAAAGATCT 5400  
Db 5341 TCAATGGAAGAAACCAAGGTCCAAAGCAGCAAGAGATTCACGACAGAAAGATCT 5400  
QY 5401 TCAGGGGGCTAGAAATCTGT 5460  
Db 5401 TCAGGGGGCTAGAAATCTGT 5460  
QY 5461 AATGATGATGACAGCTGT 5520  
Db 5461 AATGATGATGACAGCTGT 5520  
QY 5521 GCAAGGTGTCCACCAATTTGT 5580  
Db 5521 GCAAGGTGTCCACCAATTTGT 5580  
QY 5581 TCCATGCAATTTGGGCGAGT 5640  
Db 5581 TCCATGCAATTTGGGCGAGT 5640  
QY 5641 GTGTAGCACTTACAGAGTCCAGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5700  
Db 5641 GTGTAGCACTTACAGAGTCCAGAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5700  
QY 5701 GCCACTACTGA 5711  
Db 5701 GCCACTACTGA 5711  
RESULT 3  
AAT17493 standard; cDNA; 5914 BP.  
ID AAT17493  
XX AAT17493;  
AC AAT17493;  
DT 02-OCT-1996 (first entry)  
XX Mutated BRCA1 coding sequence from PM06.  
XX Cancer therapy; breast and ovarian cancer predisposing gene; immunogen;  
KW

KM antibody production; germine alteration; probe; lesion neoplasia; human;  
KW gene therapy; protein replacement therapy; protein mimetic; BRCA1; ds.  
XX Homo sapiens.  
XX Location/Qualifiers  
FH Key 120..5711  
FT CDS /\*tag= a  
FT /\*product= BRCA1 mutant  
FT mutation 2731  
FT /\*tag= b  
FT /\*note= "C to T mutation"  
XX  
XX MO9605306-A2.  
XX  
XX 22-FEB-1996.  
XX  
XX 11-AUG-1995; 95WO-US10202.  
XX  
XX 07-JUN-1995; 95US-0481553.  
XX 12-AUG-1994; 94US-0288221.  
XX 02-SEP-1994; 94US-0300266.  
XX 16-SEP-1994; 94US-0308104.  
XX 29-NOV-1994; 94US-0348824.  
XX 24-MAR-1995; 95US-0409305.  
XX 07-JUN-1995; 95US-0480784.  
XX  
XX (MYRI-) MYRIAD GENETICS INC.  
XX (CMC-) CANCER INST.  
XX (RECH-) CENT RECH DU CHUL.  
XX  
XX Durocher F, Emi M, Nakamura Y, Simard J, Shattuck-Bidens DM;  
XX  
XX WPI; 1996-139702/14.  
XX P-PSDB; AAR81535.  
XX  
XX New nucleic acid and polypeptide for mutant or polymorphic BRCA1  
XX PT gene - for diagnosis and therapy of human breast and ovarian cancer  
XX PT and for diagnosing pre-disposition to these cancers  
XX  
XX Claim 1; ; 218bp; English.  
XX  
XX AAT17439-T17453 and AAT17455-T17529 represent mutations of the human  
XX CC breast and ovarian cancer predisposing gene (BRCA1) (for wild type see  
XX CC AAT17438). Proteins encoded by these mutations (see AAR81483-R81497 and  
XX CC AAR81499-R81566) can be used as immunogens for antibody production.  
XX CC These mutant BRCA1 genes have at least 1 mutation or polymorphism in  
XX CC comparison to the wild type sequence. By detecting a germine alteration  
XX CC in the wild type BRCA1 gene, a predisposition for breast and ovarian  
XX CC cancer can be diagnosed. In one method, BRCA1 mRNA isolated from a tissue  
XX CC sample from a subject has a probe, corresponding to a fragment of the  
XX CC wild type sequence (or an allele-specific probe for one of these  
XX CC mutations), added to it. The conditions allow for hybridisation of the  
XX CC probe to the mRNA, and any hybridisation which occurs is detected.  
XX CC Alternatively the BRCA1 gene in the tissue sample is isolated, and a  
XX CC shift in electrophoretic mobility of single stranded DNA from the sample  
XX CC on a non-denaturing polyacrylamide gel indicates a mutation. These  
XX CC methods of detection can also diagnose a lesion neoplasia associated with  
XX CC the BRCA1 locus. The methods may be used in gene therapy, protein  
XX CC replacement therapy and protein mimetics, and may be used to screen for  
XX CC drugs in cancer therapy.  
XX  
XX Sequence 5914 BP; 2006 A; 1155 C; 1316 G; 1437 T; 0 other;  
SQ  
Query Match 100.0%; Score 5711; DB 17; Length 5914;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 5711; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGCTGAGAGCTTCCGAGACCCCGCAGGCTGTGGGTTTCCAGATAAATGAGGC 60  
DB 1 AGCTGCTGAGAGCTTCCGAGACCCCGCAGGCTGTGGGTTTCCAGATAAATGAGGC 60  
QY 61 CTGCGCTCAGAGAGCTTCCGAGACCCCGCAGGCTGTGGGTTTCCAGATAAATGAGGC 120

DB 61 CTGCGCTCAGAGAGCTTCCGAGACCCCGCAGGCTGTGGGTTTCCAGATAAATGAGGC 120  
QY 121 TGGATTATATCTGCTCTTGGCGTTGAAGAAGTACAAAATGTCTAATATGCTATGCAAGAAA 180  
DB 121 TGGATTATATCTGCTCTTGGCGTTGAAGAAGTACAAAATGTCTAATATGCTATGCAAGAAA 180  
QY 181 TCTTAGAGTGTCCCATCTGCTGGAGTGTGATCAAGAACTGTCTCCCAAAAGTGTGACC 240  
DB 181 TCTTAGAGTGTCCCATCTGCTGGAGTGTGATCAAGAACTGTCTCCCAAAAGTGTGACC 240  
QY 241 ACATATTTTGCATAATTTTGCATGCTGAATCTTCAACAGAGAAAAGGGCTTACAGT 300  
DB 241 ACATATTTTGCATAATTTTGCATGCTGAATCTTCAACAGAGAAAAGGGCTTACAGT 300  
QY 301 GTCTCTTATATGTAAGTATTAATTAACCAAAAGAGCTTCAAGAAAGTATGAGATTTAGTC 360  
DB 301 GTCTCTTATATGTAAGTATTAATTAACCAAAAGAGCTTCAAGAAAGTATGAGATTTAGTC 360  
QY 361 AACTGTGTAAGAGCTATTTGAATAATCATTTGTGCTTTCACTTGACACAGGTTTGGAGT 420  
DB 361 AACTGTGTAAGAGCTATTTGAATAATCATTTGTGCTTTCACTTGACACAGGTTTGGAGT 420  
QY 421 ATGCAACAGCTATTAATTTTGCATAATTTTGCATAATTTTGCATAATTTTGCATAATTTT 480  
DB 421 ATGCAACAGCTATTAATTTTGCATAATTTTGCATAATTTTGCATAATTTTGCATAATTTT 480  
QY 481 AAGTTTCTATCATCCAAAGTATGGGCTACAAAACCGGCCAAAGCTTCAAGAGT 540  
DB 481 AAGTTTCTATCATCCAAAGTATGGGCTACAAAACCGGCCAAAGCTTCAAGAGT 540  
QY 541 AACCAGAAATCTCTCTTGCAGAGAAACAGCTCAAGTCAACTCTTAACCTTGGAA 600  
DB 541 AACCAGAAATCTCTCTTGCAGAGAAACAGCTCAAGTCAACTCTTAACCTTGGAA 600  
QY 601 CTGTGAGAACTCTGAGACCAAGACGCGGATTAACCTCAAAAGAGCTTCTTCAATG 660  
DB 601 CTGTGAGAACTCTGAGACCAAGACGCGGATTAACCTCAAAAGAGCTTCTTCAATG 660  
QY 661 AATTGGGATCTGATTTCTTCTGAAGATACCGTTAATAGGCAACTTATTCGAGTGTGGAG 720  
DB 661 AATTGGGATCTGATTTCTTCTGAAGATACCGTTAATAGGCAACTTATTCGAGTGTGGAG 720  
QY 721 ATCAAGATTTGTAACCAATCAACCTCAAGAACGAGGATGAATCAATGATTTGATCTG 780  
DB 721 ATCAAGATTTGTAACCAATCAACCTCAAGAACGAGGATGAATCAATGATTTGATCTG 780  
QY 781 CAAAAGAGCTGCTTGTGAATTTTCTGAGAGGATTAACAAATTAATCAATCATCAAC 840  
DB 781 CAAAAGAGCTGCTTGTGAATTTTCTGAGAGGATTAACAAATTAATCAATCATCAAC 840  
QY 841 CAGATTAATTAATTAATTAACCAACCTCAAGAACGAGGATGAATCAATGATTTGATCTG 900  
DB 841 CAGATTAATTAATTAATTAACCAACCTCAAGAACGAGGATGAATCAATGATTTGATCTG 900  
QY 901 ATCAGAGTATTTCTTCAAACTGATGAGACCTGAGCAATGAGCAAAATCTCATGCA 960  
DB 901 ATCAGAGTATTTCTTCAAACTGATGAGACCTGAGCAATGAGCAAAATCTCATGCA 960  
QY 961 GCTCATTAACAGATGAGAACAGAGCTTATTAATCACTAAGAGAGATGATATAGAAA 1020  
DB 961 GCTCATTAACAGATGAGAACAGAGCTTATTAATCACTAAGAGAGATGATATAGAAA 1020  
QY 1021 AGGCTGAATTTCTGTAATTAAGCAACGCTGCTTGAAGAGCAATCAATCAATCAAT 1080  
DB 1021 AGGCTGAATTTCTGTAATTAAGCAACGCTGCTTGAAGAGCAATCAATCAATCAATCAAT 1080  
QY 1081 GGGCTGAAGTGAAGAAACATGTAATGATAGGCGGATCTCCAGACAGAAAAAAGGTAG 1140  
DB 1081 GGGCTGAAGTGAAGAAACATGTAATGATAGGCGGATCTCCAGACAGAAAAAAGGTAG 1140  
QY 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAAAGATGATTAAGCAATGCTGCT 1200  
DB 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAAAGATGATTAAGCAATGCTGCTGCT 1200



Db 1141 ATCTGAATGCTGATCCCCGTGTGAGAGAAAAAGATGAAATAGCAGAAAATGCCATGCT 1200  
Qy 1201 CAGAGAACTCTAGAGATAGTAAGATGTTCTTGATTAACACTAAATAGCAGATTGAGA 1260  
Db 1201 CAGAGAACTCTAGAGATAGTAAGATGTTCTTGATTAACACTAAATAGCAGATTGAGA 1260  
Qy 1261 AAGTTAATGAGTGTGTTTCCAGAAAGTGAATCTGTTAGTTCGTGATGACTCAATGATG 1320  
Db 1261 AAGTTAATGAGTGTGTTTCCAGAAAGTGAATCTGTTAGTTCGTGATGACTCAATGATG 1320  
Qy 1321 GGGAGTCTGAAATCAAAATGCCAAAGTACTGATGATTTGGACGTTCTTAATAGAGTATG 1380  
Db 1321 GGGAGTCTGAAATCAAAATGCCAAAGTACTGATGATTTGGACGTTCTTAATAGAGTATG 1380  
Qy 1381 AATATTCGTGTTCTTCAGAGAAAATAGACTTACTGGCCAGTGAATCCCATGAGGCTTTAA 1440  
Db 1381 AATATTCGTGTTCTTCAGAGAAAATAGACTTACTGGCCAGTGAATCCCATGAGGCTTTAA 1440  
Qy 1441 TATGTAAAGTGAAGAAGTTCACCTCCAAATCAGTAGAGATTAATTTGAAGACAAAATAT 1500  
Db 1441 TATGTAAAGTGAAGAAGTTCACCTCCAAATCAGTAGAGATTAATTTGAAGACAAAATAT 1500  
Qy 1501 TTGGGAAAACCTATCGGAAAGAGCAGCCTCCCACTTAAGCATGTAACTGAAATATC 1560  
Db 1501 TTGGGAAAACCTATCGGAAAGAGCAGCCTCCCACTTAAGCATGTAACTGAAATATC 1560  
Qy 1561 TAAATTAAGAGCATTTGTTACTGAGCCAGATTAATACAAAGAGCCCTCCCAATAA 1620  
Db 1561 TAAATTAAGAGCATTTGTTACTGAGCCAGATTAATACAAAGAGCCCTCCCAATAA 1620  
Qy 1621 AATTAAGAGCATTTGTTACTGAGCCAGATTAATACAAAGAGCCCTCCCAATAA 1680  
Db 1621 AATTAAGAGCATTTGTTACTGAGCCAGATTAATACAAAGAGCCCTCCCAATAA 1680  
Qy 1681 CAAATTTGGAGATTCACAAAACCTCTGAATGATTAATCGGGAATCAACAAAGAGC 1740  
Db 1681 CAAATTTGGAGATTCACAAAACCTCTGAATGATTAATCGGGAATCAACAAAGAGC 1740  
Qy 1741 AGAATGGTCAAGTGAATTAATTAATGATGATGATGATGATGATGATGATGATGATG 1800  
Db 1741 AGAATGGTCAAGTGAATTAATTAATGATGATGATGATGATGATGATGATGATGATG 1800  
Qy 1801 CTATTCAGATGAGAAAAATCTTAACCAATAGATCACTGAAAAAGATTCGCTTTCA 1860  
Db 1801 CTATTCAGATGAGAAAAATCTTAACCAATAGATCACTGAAAAAGATTCGCTTTCA 1860  
Qy 1861 AAACGAAAGCTGAACCTATTAAGCAGATTAAGCAATATGGAATCGAATTAATATCC 1920  
Db 1861 AAACGAAAGCTGAACCTATTAAGCAGATTAAGCAATATGGAATCGAATTAATATCC 1920  
Qy 1921 ACAATTCAAAAGACCTTAAGAAATAGCTGAGAGGAAATCTTCTACAGGCAATATTC 1980  
Db 1921 ACAATTCAAAAGACCTTAAGAAATAGCTGAGAGGAAATCTTCTACAGGCAATATTC 1980  
Qy 1981 ATGCGCTTGAATAGTCAAGTGAATTAAGCCCACTTAATGATGATGATGATGATGATG 2040  
Db 1981 ATGCGCTTGAATAGTCAAGTGAATTAAGCCCACTTAATGATGATGATGATGATGATG 2040  
Qy 2041 TTGATAGTGTGTTTACGAGTGAAGATTAAGAAAAAAAGTAAAGCAAAATGCGAGTCA 2100  
Db 2041 TTGATAGTGTGTTTACGAGTGAAGATTAAGAAAAAAAGTAAAGCAAAATGCGAGTCA 2100  
Qy 2101 GGCACAGCAGAAACCTTAACATGAGAGTAAAGACCTGCACTGAGGCAAGAAAGA 2160  
Db 2101 GGCACAGCAGAAACCTTAACATGAGAGTAAAGACCTGCACTGAGGCAAGAAAGA 2160  
Qy 2161 GTAAACAGCCAAATGAACAGACAAATGAAGACATGACAGCATCTTTCCAGAGCTGA 2220  
Db 2161 GTAAACAGCCAAATGAACAGACAAATGAAGACATGACAGCATCTTTCCAGAGCTGA 2220  
Qy 2221 AGTTAACAATGACCTGCTTTCTTTTAATTAAGTTCAAATACAGTGAATTAAGAAAT 2280  
Db 2221 AGTTAACAATGACCTGCTTTCTTTTAATTAAGTTCAAATACAGTGAATTAAGAAAT 2280

Qy 2281 TTGTCAATCCTAGCCTTCCAGAGAGAAAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 2340  
Db 2281 TTGTCAATCCTAGCCTTCCAGAGAGAAAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 2340  
Qy 2341 CTAAATATGCTGAAGACCCCAAGATCTCATGTTAAATGAGAGAGGTTTCCAAATG 2400  
Db 2341 CTAAATATGCTGAAGACCCCAAGATCTCATGTTAAATGAGAGAGGTTTCCAAATG 2400  
Qy 2401 AAAGATCTGAGAGATGACAGATTTCAATGTTACTGCTGATCTGATTAATGAGACAGG 2460  
Db 2401 AAAGATCTGAGAGATGACAGATTTCAATGTTACTGCTGATCTGATTAATGAGACAGG 2460  
Qy 2461 AAAGATCTGAGAGATGAGAGATTTAGACCTCTAGGAGGCAAAAAAGAAAGAAAGAAAG 2520  
Db 2461 AAAGATCTGAGAGATGAGAGATTTAGACCTCTAGGAGGCAAAAAAGAAAGAAAGAAAG 2520  
Qy 2521 GTGTGAGTCAAGTGTGAGCATTGAAACCCCAAGGAGCTAATTCATGTTGTTCCAAAG 2580  
Db 2521 GTGTGAGTCAAGTGTGAGCATTGAAACCCCAAGGAGCTAATTCATGTTGTTCCAAAG 2580  
Qy 2581 ATAAATGAATGACACAGAAAGCTTTAATGATTCATTTGGACATGAAGTTAACCAAGTC 2640  
Db 2581 ATAAATGAATGACACAGAAAGCTTTAATGATTCATTTGGACATGAAGTTAACCAAGTC 2640  
Qy 2641 GGGAAACAGCATAGAAATGGAAGAAAGTGAACCTGATGCTGATTTGCAAGATATCAT 2700  
Db 2641 GGGAAACAGCATAGAAATGGAAGAAAGTGAACCTGATGCTGATTTGCAAGATATCAT 2700  
Qy 2701 TCAAGGTTTCAAGGCGCAGTATTTGCTGTTTCAATCCAGGAAATGCAAGAGAG 2760  
Db 2701 TCAAGGTTTCAAGGCGCAGTATTTGCTGTTTCAATCCAGGAAATGCAAGAGAG 2760  
Qy 2761 AATGTGCAATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2820  
Db 2761 AATGTGCAATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2820  
Qy 2821 TTGAATGTGAACAAAGAAAGAAATCAAGAAAGAAATGAGTCTAATCAAGCCCTGATC 2880  
Db 2821 TTGAATGTGAACAAAGAAAGAAATCAAGAAAGAAATGAGTCTAATCAAGCCCTGATC 2880  
Qy 2881 AGACAGTTAATATCACTGAGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2940  
Db 2881 AGACAGTTAATATCACTGAGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2940  
Qy 2941 ATGCCAAATGTATCAAGAGAGCTCTAGGTTTGTCTATCATCTCAGTTCAGAGGCA 3000  
Db 2941 ATGCCAAATGTATCAAGAGAGCTCTAGGTTTGTCTATCATCTCAGTTCAGAGGCA 3000  
Qy 3001 AGGAAACGAGCTCAATTACTCCAAATTAACATGAGCCTTTTACAAACCCATATCGATAC 3060  
Db 3001 AGGAAACGAGCTCAATTACTCCAAATTAACATGAGCCTTTTACAAACCCATATCGATAC 3060  
Qy 3061 CACCACTTTTCCATCAAGATGTTGTTAAATTAATGTAAGAAAAATCTGCTAGAGG 3120  
Db 3061 CACCACTTTTCCATCAAGATGTTGTTAAATTAATGTAAGAAAAATCTGCTAGAGG 3120  
Qy 3121 AAAAATTGAGGAAACATTCATATGCTCACTGAAAGAGAAATGGAATGGAACATTTCCA 3180  
Db 3121 AAAAATTGAGGAAACATTCATATGCTCACTGAAAGAGAAATGGAATGGAACATTTCCA 3180  
Qy 3181 GTACAGTGAACATTTAGCCGTTAATTAATTAATTAAGAGAAATGTTTAAAGAGCAGCT 3240  
Db 3181 GTACAGTGAACATTTAGCCGTTAATTAATTAATTAAGAGAAATGTTTAAAGAGCAGCT 3240  
Qy 3241 CAAGCAATTAATTAAGAGTATGCTCAGTAAATGAAGTGGCTCAGATTAATTAATGAAG 3300  
Db 3241 CAAGCAATTAATTAAGAGTATGCTCAGTAAATGAAGTGGCTCAGATTAATTAATGAAG 3300  
Qy 3301 TAGGTTCCAGTATGAAACATTTCAAGCAGAACTAGTGAAGAAACAGAGGCGCAAAATGGA 3360  
Db 3301 TAGGTTCCAGTATGAAACATTTCAAGCAGAACTAGTGAAGAAACAGAGGCGCAAAATGGA 3360

|    |      |   |      |
|----|------|---|------|
| QY | 3361 | ATGCTATGCTTATAGATTAGGGGTTTTCGCAACTGAGGCTCTATTAACAAGTCTTCTGGA  | 3420 |
| Dp | 3361 | ATGCTATGCTTATAGATTAGGGGTTTTCGCAACTGAGGCTCTATTAACAAGTCTTCTGGA  | 3420 |
| QY | 3421 | GTAATTGTAGACATCTGCTGAAATTAATAAAGCAAGATATGAAGAACTAGTGCAGCTGTTA | 3480 |
| Dp | 3421 | GTAATTGTAGACATCTGCTGAAATTAATAAAGCAAGATATGAAGAACTAGTGCAGCTGTTA | 3480 |
| QY | 3481 | ATACAGATTTCTCTCATAATCTGATTTGACATTAACCTTAGAAACGCTTAGGGAAGTATC  | 3540 |
| Dp | 3481 | ATACAGATTTCTCTCATAATCTGATTTGACATTAACCTTAGAAACGCTTAGGGAAGTATC  | 3540 |
| QY | 3541 | ATGCACTTCAGAGTTGTCTGAGACACCTGAGACCTGTATGATATGATGTGAAATTAAGG   | 3600 |
| Dp | 3541 | ATGCACTTCAGAGTTGTCTGAGACACCTGAGACCTGTATGATATGATGTGAAATTAAGG   | 3600 |
| QY | 3601 | AAGATACTAGTTTGTGCTGAAAATGACATTAAGGAAGTTGTGCTGTTTGTGCAAAACG    | 3660 |
| Dp | 3601 | AAGATACTAGTTTGTGCTGAAAATGACATTAAGGAAGTTGTGCTGTTTGTGCAAAACG    | 3660 |
| QY | 3661 | TCCAGAAAGAGAGGCTTAGACAGAGATCTGAGCCCTTTACACCATACATTTGGCTCAG    | 3720 |
| Dp | 3661 | TCCAGAAAGAGAGGCTTAGACAGAGATCTGAGCCCTTTACACCATACATTTGGCTCAG    | 3720 |
| QY | 3721 | GTTACCGAAGAGGGGCGCAAGAAATTAAGAGTCTCGAAGAGACCTTATCTAGTAGATG    | 3780 |
| Dp | 3721 | GTTACCGAAGAGGGGCGCAAGAAATTAAGAGTCTCGAAGAGACCTTATCTAGTAGATG    | 3780 |
| QY | 3781 | AAGAGCTTCCCGCTTCCACAACCTGTATTTGGTAAGTAACAATACCTTCTCAGT        | 3840 |
| Dp | 3781 | AAGAGCTTCCCGCTTCCACAACCTGTATTTGGTAAGTAACAATACCTTCTCAGT        | 3840 |
| QY | 3841 | CTACTAGGCAATAGCAACCGTTGCTACCGAGTGTCTGTAGAACACAGAGAGAAATTAAT   | 3900 |
| Dp | 3841 | CTACTAGGCAATAGCAACCGTTGCTACCGAGTGTCTGTAGAACACAGAGAGAAATTAAT   | 3900 |
| QY | 3901 | TATCATTTAGAGATAGCTTAAATGACTGCAATACCAAGTAATATGGCAAAAGCATTC     | 3960 |
| Dp | 3901 | TATCATTTAGAGATAGCTTAAATGACTGCAATACCAAGTAATATGGCAAAAGCATTC     | 3960 |
| QY | 3961 | AGGAACATCACCTTGTAGAGGAAACAAATGTCTGTAAGCTGTTTCTTCAACGTCA       | 4020 |
| Dp | 3961 | AGGAACATCACCTTGTAGAGGAAACAAATGTCTGTAAGCTGTTTCTTCAACGTCA       | 4020 |
| QY | 4021 | GTTGAATTGGAAGACTTGACCTGCAATACAAACCCACAGATCCTTCTTGATTGGTCTT    | 4080 |
| Dp | 4021 | GTTGAATTGGAAGACTTGACCTGCAATACAAACCCACAGATCCTTCTTGATTGGTCTT    | 4080 |
| QY | 4081 | CCAAACAAATGAGCATCATGTCGAAAGCCAGGGAGTTGTCTGAGTACAAAGAAATTGG    | 4140 |
| Dp | 4081 | CCAAACAAATGAGCATCATGTCGAAAGCCAGGGAGTTGTCTGAGTACAAAGAAATTGG    | 4140 |
| QY | 4141 | TTTCAGATGATCAAAAGAGGAAGGGGCTTGGAAGAAATTAATCAAGAGCAAAACA       | 4200 |
| Dp | 4141 | TTTCAGATGATCAAAAGAGGAAGGGGCTTGGAAGAAATTAATCAAGAGCAAAACA       | 4200 |
| QY | 4201 | TGGATTTCAAACCTTAGGTAGAGAGCATCTGGGTGTGAGAGTGAACCAAGCCTCTAG     | 4260 |
| Dp | 4201 | TGGATTTCAAACCTTAGGTAGAGAGCATCTGGGTGTGAGAGTGAACCAAGCCTCTAG     | 4260 |
| QY | 4261 | ACTGCTCAGGCTATCTCTCAGATGACATTTTAACACTCAGCAGAGGGATACATGC       | 4320 |
| Dp | 4261 | ACTGCTCAGGCTATCTCTCAGATGACATTTTAACACTCAGCAGAGGGATACATGC       | 4320 |
| QY | 4321 | AACATTAACCTGATTAAGCTCCGACGAGAAATGGCTGAACCTGATTAACACGC         | 4380 |
| Dp | 4321 | AACATTAACCTGATTAAGCTCCGACGAGAAATGGCTGAACCTGATTAACACGC         | 4380 |
| QY | 4381 | ATGGAGCGAGCCTTCTTAACAGACTACCTTCATATAAGTAGACTCTTCTGCGCTTAGG    | 4440 |
| Dp | 4381 | ATGGAGCGAGCCTTCTTAACAGACTACCTTCATATAAGTAGACTCTTCTGCGCTTAGG    | 4440 |
| QY | 4441 | ACCTGCGAAATTCAGAACCAACACATCAGAAAAAGCAGTATTAATTCCAGAAAAAGTA    | 4500 |

|   |   |  |      |   |      |
|---|---|--|------|---|------|
| D | b |  | 4441 | ACCTGCGAAATCCGAACAAAGCACTACGAAAAAGCATTTTACTTCACAGAAAAGTA          | 4500 |
| O | y |  | 4501 | GTGAATAACCCATATAAGCCAGAAATCCAAAGGCCCTTTCTGCTGACAAAGTTTGAGGTCTCTG  | 4560 |
| D | b |  | 4501 | GTGAATACCCATATAAGCCAGAAATCCAGAGGCCCTTTCTGCTGACAAAGTTTGAGGTCTCTG   | 4560 |
| O | y |  | 4561 | CAGATAGTTCTTACACGATTAATAATAAGAACCCAGAGTGGAAAGTCAATCCCTTTCTTAAT    | 4620 |
| D | b |  | 4561 | CAGATAGTTCTTACACGATTAATAATAAGAACCCAGAGTGGAAAGTCAATCCCTTTCTTAAT    | 4620 |
| O | y |  | 4621 | GCCCATCATTTAGATGATGATGGTACATGCAAGATTGCTCTGGAGAGCTTCAGAAATGAA      | 4680 |
| D | b |  | 4621 | GCCCATCATTTAGATGATGATGGTACATGCAAGATTGCTCTGGAGAGCTTCAGAAATGAA      | 4680 |
| O | y |  | 4681 | ACTAACCCATCTCAAGAGAGGCTCAATTAAGTTGTTGATGTGGAGACCAACAGCTGAG        | 4740 |
| D | b |  | 4681 | ACTAACCCATCTCAAGAGAGGCTCAATTAAGTTGTTGATGTGGAGACCAACAGCTGAG        | 4740 |
| O | y |  | 4741 | AGTCTGGGCGCACACGAAATTGACGGAAACATCTTACTTCCAAAGCAAGATCTAGAGGAA      | 4800 |
| D | b |  | 4741 | AGTCTGGGCGCACACGAAATTGACGGAAACATCTTACTTCCAAAGCAAGATCTAGAGGAA      | 4800 |
| O | y |  | 4801 | CCCCCTTACCTGGAAATCTGGAAATCAGCCTCTTCTGTGATGACCCCTGAATCTGAATCTCTCTG | 4860 |
| D | b |  | 4801 | CCCCCTTACCTGGAAATCTGGAAATCAGCCTCTTCTGTGATGACCCCTGAATCTGAATCTCTCTG | 4860 |
| O | y |  | 4861 | AAGACAGAGCCCCAGAGAGCTGCTGTTGGCAACATACATCTTCAACCTCTGCATTGA         | 4920 |
| D | b |  | 4861 | AAGACAGAGCCCCAGAGAGCTGCTGTTGGCAACATACATCTTCAACCTCTGCATTGA         | 4920 |
| O | y |  | 4921 | AAGTTCCCGCAATTGAAAGTTGACAGATCTGCCAGATCCAGCTGCTGCTCATTACTA         | 4980 |
| D | b |  | 4921 | AAGTTCCCGCAATTGAAAGTTGACAGATCTGCCAGATCCAGCTGCTGCTCATTACTA         | 4980 |
| O | y |  | 4981 | ATACTGCTGGGTATAATGCAATGGAAGAAGTGTGACAGAGGAAAGCCAGAAATTGACAG       | 5040 |
| D | b |  | 4981 | ATACTGCTGGGTATAATGCAATGGAAGAAGTGTGACAGAGGAAAGCCAGAAATTGACAG       | 5040 |
| O | y |  | 5041 | CTTCAACAGAAAGGCTCAACAAAAGATGTCATGATGTGTGCTGAGCCTGACCCCAAG         | 5100 |
| D | b |  | 5041 | CTTCAACAGAAAGGCTCAACAAAAGATGTCATGATGTGTGCTGAGCCTGACCCCAAG         | 5100 |
| O | y |  | 5101 | AATTTATGCTGTGTACAGATTGTCAGAAAACACACATCACTTAATTAATTAATTA           | 5160 |
| D | b |  | 5101 | AATTTATGCTGTGTACAGATTGTCAGAAAACACACATCACTTAATTAATTAATTA           | 5160 |
| O | y |  | 5161 | CTGAAGAGACTACATCATGTTGTTATGAAAACAGATGCTGAGTTGTGTGGAACGGAC         | 5220 |
| D | b |  | 5161 | CTGAAGAGACTACATCATGTTGTTATGAAAACAGATGCTGAGTTGTGTGGAACGGAC         | 5220 |
| O | y |  | 5221 | TGAATATATTTCTGGAATTCGGGAGAGAAATGGGATGTAGCTATTTCTGGGTGACC          | 5280 |
| D | b |  | 5221 | TGAATATATTTCTGGAATTCGGGAGAGAAATGGGATGTAGCTATTTCTGGGTGACC          | 5280 |
| O | y |  | 5281 | AGTCTATTTAAGAAAGAAAAATGCTGTAATGACATGATTTTGAAGTCAAGAGAGATGTGG      | 5340 |
| D | b |  | 5281 | AGTCTATTTAAGAAAGAAAAATGCTGTAATGACATGATTTTGAAGTCAAGAGAGATGTGG      | 5340 |
| O | y |  | 5341 | TCAATGGAAGAAACCAACCAAGGTCCTCAAGGAGACAGAGAAATCCACAGAGAGAAATCT      | 5400 |
| D | b |  | 5341 | TCAATGGAAGAAACCAACCAAGGTCCTCAAGGAGACAGAGAAATCCACAGAGAGAAATCT      | 5400 |
| O | y |  | 5401 | TCAGAGGGGCTTGAAGATCTGTTGCTATGAGGCCCTTACCAACATATGCCACGATCAATCG     | 5460 |
| D | b |  | 5401 | TCAGAGGGGCTTGAAGATCTGTTGCTATGAGGCCCTTACCAACATATGCCACGATCAATCG     | 5460 |
| O | y |  | 5461 | AATGATATGTAACAGCTGTGTGTCTCTGTGTGTAAGAGAGCTTCAATTCACCTCTG          | 5520 |
| D | b |  | 5461 | AATGATATGTAACAGCTGTGTGTCTCTGTGTGTAAGAGAGCTTCAATTCACCTCTG          | 5520 |
| O | y |  | 5521 | GCAACAGGTGTCACATTCATTTGTGTGTGACCGACAGATGCTTGACAGAGAGCAATGCT       | 5580 |
| D | b |  | 5521 | GCAACAGGTGTCACATTCATTTGTGTGTGACCGACAGATGCTTGACAGAGAGCAATGCT       | 5580 |

Db 5521 GCACAGGTGTCCACCAATTGTGTGTGACGCCAGATGCTTGACAGACGACATGGCT 5580  
Qy 5581 TCCATGCAATTTGGGACAGATGTGTGAGGACCTGTGTGAGACCCGAGAGTGGGTGTGAGCA 5640  
Db 5581 TCCATGCAATTTGGGACAGATGTGTGAGGACCTGTGTGAGACCCGAGAGTGGGTGTGAGCA 5640  
Qy 5641 GTGTAGCACTCTACCACTGCGCAGAGAGCTTGACACCTGATATACCCAGATCCGCCACA 5700  
Db 5641 GTGTAGCACTCTACCACTGCGCAGAGAGCTTGACACCTGATATACCCAGATCCGCCACA 5700  
Qy 5701 GCCACTACTGA 5711  
Db 5701 GCCACTACTGA 5711

RESULT 4  
AAV46463  
ID AAV46463 standard, cDNA; 5711 BP.

XX AAV46463;

DT 18-NOV-1998 (first entry)

XX Human BRCA1 omi2 polymorphism #6 cDNA.

XX BRCA1; omi2; human; breast and ovarian cancer predisposing gene;  
KM polymorphism; susceptibility; anti-oncogene; tumour suppressor;  
XX chromosome 17q; ss.

OS Homo sapiens.

XX Key Location/Qualifiers

FT CDS 120..5711

FT /\*tag= a

FT /\*product= "BRCA1 omi2 protein"

FT /\*tag= b

FT /note= "This polymorphic variation can be a T or C  
nucleotide"

XX US5750400-A.

XX 12-MAY-1998.

XX 12-FEB-1997; 97US-0798691.

XX 12-FEB-1996; 96US-0598591.

XX 12-FEB-1997; 97US-0798691.

XX (ONCO-) ONCOMED INC.

XX Allen AC, Alvares CP, Critz BS, Murphy PD, Olson SJ;  
PI Schelter DB, Zeng B;

XX WPI; 1998-296774/26.

PT BRCA1 omi2 gene coding sequences - useful for distinguishing between  
PT polymorphisms and mutation(s) in the screening for disposition to  
PT breast or ovarian cancer

XX Claim 2e; Page -; 54bp; English.

XX This sequence encodes a human BRCA1 (breast and ovarian cancer  
CC predisposing gene) omi2 gene in which a polymorphic variation occurs at  
CC nucleotide 4427. This sequence and other polymorphic variations of this  
CC sequence are useful for the identification of an individual who may or  
CC may not have an increased susceptibility to breast or ovarian cancer.  
CC The sequences used identify gene changes which are due to polymorphisms,  
CC rather than cancer causing mutations. BRCA1 is an anti-oncogene (tumour  
CC suppressor) which is involved in genetic inheritance of cancers,  
CC especially breast and ovarian cancer. It is found at human chromosome  
CC 17q which is known to be linked to cancer susceptibility, especially  
CC breast cancer. Cells containing a mutation in this gene lose the

CC wild-type function of BRCA1 and are more susceptible to cancers.  
CC NOTE: This sequence does not appear in the specification but has been  
CC created from the wild type BRCA1 omi2 gene represented in AAV46449.  
XX  
SQ Sequence 5711 BP; 1956 A; 1098 C; 1274 G; 1382 T; 1 other;

Query Match 100.0%; Score 5710.6; DB 19; Length 5711;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 5710; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGCTGCTGAGACTTCTGAGACCCGACACAGGCTGTGAGGTTTCTCAATTAATCGGCC 60  
Db 1 AGCTGCTGAGACTTCTGAGACCCGACACAGGCTGTGAGGTTTCTCAATTAATCGGCC 60  
Qy 61 CCGGCGCTGAGAGGCGCTTACCCCTGTGCTGTGAGTAAAGTTTATGGAACAGAAAGAA 120  
Db 61 CCGGCGCTGAGAGGCGCTTACCCCTGTGCTGTGAGTAAAGTTTATGGAACAGAAAGAA 120  
Qy 121 TGGATTATCTGCTCTTCCGCTTGAAGAAGTACAAATGTCATTAATGCTATGCAAGAAA 180  
Db 121 TGGATTATCTGCTCTTCCGCTTGAAGAAGTACAAATGTCATTAATGCTATGCAAGAAA 180  
Qy 181 TCTTAGAGTGTCCCATCTGTCTGAGTGTATCAAGAACCTGTCTCAAAAGTGTGACC 240  
Db 181 TCTTAGAGTGTCCCATCTGTCTGAGTGTATCAAGAACCTGTCTCAAAAGTGTGACC 240  
Qy 241 ACATATTTGGCAAAATTTTCATGCTGAACCTTCTCAACAGAAAGAGGCGCTTCACAGT 300  
Db 241 ACATATTTGGCAAAATTTTCATGCTGAACCTTCTCAACAGAAAGAGGCGCTTCACAGT 300  
Qy 301 GTCTTTATGTAAAGATGATATACCAAAAGAGCCTTACAAAGATGAGATTATAGTC 360  
Db 301 GTCTTTATGTAAAGATGATATACCAAAAGAGCCTTACAAAGATGAGATTATAGTC 360  
Qy 361 AACTGTTGAAGAGCTATTGAATAATCATTTTGCTTTTCACTTGCACAGGTTTGAGT 420  
Db 361 AACTGTTGAAGAGCTATTGAATAATCATTTTGCTTTTCACTTGCACAGGTTTGAGT 420  
Qy 421 ATGCAAACAGCTATATTTTGGCAAAAAGAAATTAACCTCTGTAACATCTAAAGAGT 480  
Db 421 ATGCAAACAGCTATATTTTGGCAAAAAGAAATTAACCTCTGTAACATCTAAAGAGT 480  
Qy 481 AAGTTTCTATCAATCCAAAGTATGAGCTACAGAAACCGTCCAAAGACTTCTACAGAGT 540  
Db 481 AAGTTTCTATCAATCCAAAGTATGAGCTACAGAAACCGTCCAAAGACTTCTACAGAGT 540  
Qy 541 AACCCGAAATCTTCTCTTGGAGAAACCAAGTCAAGTCTCAACTCTTAACTTTGAA 600  
Db 541 AACCCGAAATCTTCTCTTGGAGAAACCAAGTCAAGTCTCAACTCTTAACTTTGAA 600  
Qy 601 CTGTAGAACTCTGAGGACAAAGCAGCGGATCAACCTCAAAAGAGCTGTCTACATTG 660  
Db 601 CTGTAGAACTCTGAGGACAAAGCAGCGGATCAACCTCAAAAGAGCTGTCTACATTG 660  
Qy 661 AATTGGATCTGATCTTCTGAAGATACCGTAAATAGGCACTTATTCAGTGTGGAG 720  
Db 661 AATTGGATCTGATCTTCTGAAGATACCGTAAATAGGCACTTATTCAGTGTGGAG 720  
Qy 721 ATCAAGAAATTTTCAAAATCACCCCTCAAGGAACAGGGATGAATCAATTGATTCG 780  
Db 721 ATCAAGAAATTTTCAAAATCACCCCTCAAGGAACAGGGATGAATCAATTGATTCG 780  
Qy 781 CAAAAAAGGCTCTGTGAATTTTCTGAGACGAGATGAACAAATCTGAACATCTCAAC 840  
Db 781 CAAAAAAGGCTCTGTGAATTTTCTGAGACGAGATGAACAAATCTGAACATCTCAAC 840  
Qy 841 CCAATTAATATATTTGAACACCACTGAGAACCTGTGAGGAGCTTCAGAAAGT 900  
Db 841 CCAATTAATATATTTGAACACCACTGAGAACCTGTGAGGAGCTTCAGAAAGT 900  
Qy 901 ATCAGGGTATGTTCTGTTTCAAACTTGATGTGAGGACCATGTGGCAAAATACTCATGCCA 960  
Db 901 ATCAGGGTATGTTCTGTTTCAAACTTGATGTGAGGACCATGTGGCAAAATACTCATGCCA 960

QY 961 GCTATTACAGCATGAGAACAGACGTTTATTACTGACTAAGACAGAAATGATGANA 1020  
Db 961 GCTATTACAGCATGAGAACAGACGTTTATTACTGACTAAGACAGAAATGATGANA 1020  
QY 1021 AGGCTGAATTCGTATATAAAGCAAAACAGCTGGCTTAGCAAGAGCCAACTAACAGAT 1080  
Db 1021 AGGCTGAATTCGTATATAAAGCAAAACAGCTGGCTTAGCAAGAGCCAACTAACAGAT 1080  
QY 1081 GGGCTGGAAGTAAAGAAACATGTAATGATAGCGGACTCCGACACAGAAAAAAGGTG 1140  
Db 1081 GGGCTGGAAGTAAAGAAACATGTAATGATAGCGGACTCCGACACAGAAAAAAGGTG 1140  
QY 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAAAATGGAATAGCAGAACTGCCATGCT 1200  
Db 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAAAATGGAATAGCAGAACTGCCATGCT 1200  
QY 1201 CAGAGAAATCTAGAGATACGTAAGATGTTCTTGGATTAACATAATAGCAGCATTCAGA 1260  
Db 1201 CAGAGAAATCTAGAGATACGTAAGATGTTCTTGGATTAACATAATAGCAGCATTCAGA 1260  
QY 1261 AAGTTAATGAGTGGTTTCCAGAGATGATGAATGTTAGTTCTGATGACTCAATGATG 1320  
Db 1261 AAGTTAATGAGTGGTTTCCAGAGATGATGAATGTTAGTTCTGATGACTCAATGATG 1320  
QY 1321 GGGAGTCTGAATCAAAATGCGCAAGTAGATGTAATGGACGTTCTAAATGAGGTAGATG 1380  
Db 1321 GGGAGTCTGAATCAAAATGCGCAAGTAGATGTAATGGACGTTCTAAATGAGGTAGATG 1380  
QY 1381 AATATTCGTGTTCTTCAGAGAAATAGACTTACGCGCAGTATCCTCATGAGGCTTTAA 1440  
Db 1381 AATATTCGTGTTCTTCAGAGAAATAGACTTACGCGCAGTATCCTCATGAGGCTTTAA 1440  
QY 1441 TATGTAAAGTGAAGAGATTCCTCCAATCAGTAGAGATTAATTTGAAGCAAAATAT 1500  
Db 1441 TATGTAAAGTGAAGAGATTCCTCCAATCAGTAGAGATTAATTTGAAGCAAAATAT 1500  
QY 1501 TTGGGAAAACCTATGGAAGAGGCAAGCTCCCACTTAAGCCATGTAAGTGAATATC 1560  
Db 1501 TTGGGAAAACCTATGGAAGAGGCAAGCTCCCACTTAAGCCATGTAAGTGAATATC 1560  
QY 1561 TAAATTATGAGACATTTGTTACTGAGCCAAGATTAATACAGAGCGTCCCTCACAAATA 1620  
Db 1561 TAAATTATGAGACATTTGTTACTGAGCCAAGATTAATACAGAGCGTCCCTCACAAATA 1620  
QY 1621 AATTAAACCTTAAAGAGACCTACATCAGGCTTCATCTGAGGATTTTATCAAGAAAG 1680  
Db 1621 AATTAAACCTTAAAGAGACCTACATCAGGCTTCATCTGAGGATTTTATCAAGAAAG 1680  
QY 1681 CAGATTTGSCAGTTCAAAAAGACTCCTGAAATGATTAATCAGGGAATTAACCAAGAGC 1740  
Db 1681 CAGATTTGSCAGTTCAAAAAGACTCCTGAAATGATTAATCAGGGAATTAACCAAGAGC 1740  
QY 1741 AGAATGTCAGAGTGAATATTAATGATGTCATGAGAAATTAACAAAAAGGTGAT 1800  
Db 1741 AGAATGTCAGAGTGAATATTAATGATGTCATGAGAAATTAACAAAAAGGTGAT 1800  
QY 1801 CTAATTCAGAAATGAAAAATCCTAACCCCAATAGAACTCGAAAAAAGAAATGCTTTGA 1860  
Db 1801 CTAATTCAGAAATGAAAAATCCTAACCCCAATAGAACTCGAAAAAAGAAATGCTTTGA 1860  
QY 1861 AAAAGAAAGCTGAACCTTAATAGCAGATTAAGCAATTAAGCAATTAAGCAATTAATCC 1920  
Db 1861 AAAAGAAAGCTGAACCTTAATAGCAGATTAAGCAATTAAGCAATTAAGCAATTAATCC 1920  
QY 1921 ACAATTTCAAAAGCACTTAATAAGAAATAGGCTGAGGAGAAAGTCTTACCAAGCAATATC 1980  
Db 1921 ACAATTTCAAAAGCACTTAATAAGAAATAGGCTGAGGAGAAAGTCTTACCAAGCAATATC 1980  
QY 1981 ATGCGCTTGAATAGTACAGTAGAAATCTAAAGCCACTTAATGTACTGAATTTGCAAA 2040  
Db 1981 ATGCGCTTGAATAGTACAGTAGAAATCTAAAGCCACTTAATGTACTGAATTTGCAAA 2040

QY 2041 TTGATAGTTGTTCTAGCAGTAGAAGATTAAGAAAAAAGTAAACAACCAATGCGACTCA 2100  
Db 2041 TTGATAGTTGTTCTAGCAGTAGAAGATTAAGAAAAAAGTAAACAACCAATGCGACTCA 2100  
QY 2101 GGCACAGAGAAACCTCAACTCATGAGAGTAAAGAACCTGCAATGAGCCAGAGAA 2160  
Db 2101 GGCACAGAGAAACCTCAACTCATGAGAGTAAAGAACCTGCAATGAGCCAGAGAA 2160  
QY 2161 GTAAACAACCAATGAACAGCAAGTAAAGACATGACAGGATCTTCCAGAGCTGA 2220  
Db 2161 GTAAACAACCAATGAACAGCAAGTAAAGACATGACAGGATCTTCCAGAGCTGA 2220  
QY 2221 AGTTAAACAATGACACTGCTTCTTTAATAAGTTCATAATCCAGTAACTTAAGAAAT 2280  
Db 2221 AGTTAAACAATGACACTGCTTCTTTAATAAGTTCATAATCCAGTAACTTAAGAAAT 2280  
QY 2281 TTGTCAATCTAGACCTTCGAGAGAGAAAAAGAGAAACCTAGAAACGTTAAAGTGT 2340  
Db 2281 TTGTCAATCTAGACCTTCGAGAGAGAAAAAGAGAAACCTAGAAACGTTAAAGTGT 2340  
QY 2341 CTAATAATGCTGAAGACCCCAAGATCTCATGTTAGTGAAGAAAGGTTTTCGAAACTG 2400  
Db 2341 CTAATAATGCTGAAGACCCCAAGATCTCATGTTAGTGAAGAAAGGTTTTCGAAACTG 2400  
QY 2401 AAAGATCTGTAGAGAGTAGCAGTATTTCAATTGTAACCTGTGATGATGAGCACTCAG 2460  
Db 2401 AAAGATCTGTAGAGAGTAGCAGTATTTCAATTGTAACCTGTGATGATGAGCACTCAG 2460  
QY 2461 AAAGTATCTGTTACTGGAAGTTAGCACTTAGGAAAGGCAAAACCAATTAAT 2520  
Db 2461 AAAGTATCTGTTACTGGAAGTTAGCACTTAGGAAAGGCAAAACCAATTAAT 2520  
QY 2521 GTGTAGTCAAGTGGCAGCACTTGAAGAAACCCCAAGGAACTAATCATGTTGTTCCAAAG 2580  
Db 2521 GTGTAGTCAAGTGGCAGCACTTGAAGAAACCCCAAGGAACTAATCATGTTGTTCCAAAG 2580  
QY 2581 ATATATGAAATGACACAGAAAGCTTTAAGTATCCATTGGGACATGAATTAACCAAGTC 2640  
Db 2581 ATATATGAAATGACACAGAAAGCTTTAAGTATCCATTGGGACATGAATTAACCAAGTC 2640  
QY 2641 GGGAAAACAGCATGAAATGGAAGAAAGTGAATGCTCAGTATTTTCAGAAATCAT 2700  
Db 2641 GGGAAAACAGCATGAAATGGAAGAAAGTGAATGCTCAGTATTTTCAGAAATCAT 2700  
QY 2701 TCAAGCTTCAAGAGGCGCAGTATTTGCTGTTTCAAAATCCAGAAATGCAAGAGG 2760  
Db 2701 TCAAGCTTCAAGAGGCGCAGTATTTGCTGTTTCAAAATCCAGAAATGCAAGAGG 2760  
QY 2761 AATGTGCAACATTCCTGCCCCACTCTGGGCTCTTAAGAAACCAAAAGTCACTT 2820  
Db 2761 AATGTGCAACATTCCTGCCCCACTCTGGGCTCTTAAGAAACCAAAAGTCACTT 2820  
QY 2821 TTGAATGGAACAAAAAGAGAAATGAGTATGAGTCTTAATATCAAGCTGTAC 2880  
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QY 2881 AGACAGTTAATATCACTGACAGCTTCTGTTGTTGTCAGAAAGATPAACAGTTGATA 2940  
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QY 3001 ACGAAATCTGAACATACTCAATTAACATGAGCTTTTAAACAAACCCATATCTGTATAC 3060  
Db 3001 ACGAAATCTGAACATACTCAATTAACATGAGCTTTTAAACAAACCCATATCTGTATAC 3060  
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Db 3061 CACCACTTTTCCCATCAAGTCAATGTTTAAATGTAATGTAAGAAATCTGTGAGAG 3120  
QY 3121 AAACTTTGAGGAACATTCAATGTCACTGAAAGAGAAATGAGAAATGAGAAATTC 3180

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Db 3121 AAAACCTTGAGAAACATTCATGTCACCTGAAAGAAATGGGAAATGAGAACTTCCTCAA 3180
Qy 3181 GTACAGGAGACACAATTAGCCGTAAATACTTAGAGAAATGTTTTTAAAGAACCCAGCT 3240
Db 3181 GTACAGGAGACACAATTAGCCGTAAATACTTAGAGAAATGTTTTTAAAGAACCCAGCT 3240
Qy 3241 CAAGCAATATTAATGAAGTAGTCCAGTACTAATGAGTGGGCTCCAGATTATTAAGAA 3300
Db 3241 CAAGCAATATTAATGAAGTAGTCCAGTACTAATGAGTGGGCTCCAGATTATTAAGAA 3300
Qy 3301 TAGGTTCCAGTGATGAAACATTCACAGCAAGTAAAGAAACAGAGGCCCAAAATGTA 3360
Db 3301 TAGGTTCCAGTGATGAAACATTCACAGCAAGTAAAGAAACAGAGGCCCAAAATGTA 3360
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Db 3361 ATGCTATGCTTAGATTGGGGTTTTGCACTGAGGCTCTAATAACAAAGCTTCCTGGAA 3420
Qy 3421 GTAATTGTAAAGCATCCTGAATATAAAAGCAAGAAATGAAGAGTTCAGACTGTTA 3480
Db 3421 GTAATTGTAAAGCATCCTGAATATAAAAGCAAGAAATGAAGAGTTCAGACTGTTA 3480
Qy 3481 ATACAGATTTCTCTCCATATCTGATTTCAATTAACCTTAGAACAGCCTATGGGAAAGTGC 3540
Db 3481 ATACAGATTTCTCTCCATATCTGATTTCAATTAACCTTAGAACAGCCTATGGGAAAGTGC 3540
Qy 3541 ATGCTATCAGGTTTGTCTGAGACACCTGATGACCTGTTAGATGATGGGAAATTAAG 3600
Db 3541 ATGCTATCAGGTTTGTCTGAGACACCTGATGACCTGTTAGATGATGGGAAATTAAG 3600
Qy 3601 AAGATACTAGTTTGTGTAATAATGACATTAAGAAATTTCTGCTGTTTTAGCAAAAGC 3660
Db 3601 AAGATACTAGTTTGTGTAATAATGACATTAAGAAATTTCTGCTGTTTTAGCAAAAGC 3660
Qy 3661 TCCAGAAAGAGAGCTTAGCAGAGAGTCTAGCCCTTTACCCATACATTTGGCTCAGG 3720
Db 3661 TCCAGAAAGAGAGCTTAGCAGAGAGTCTAGCCCTTTACCCATACATTTGGCTCAGG 3720
Qy 3721 GTTACCGAAGAGGGGCCAAGAAATTAAGATCTCAGAGAGAACTTATCTAGAGAGATG 3780
Db 3721 GTTACCGAAGAGGGGCCAAGAAATTAAGATCTCAGAGAGAACTTATCTAGAGAGATG 3780
Qy 3781 AAGAGCTTCCCTGCTTCCACACACTTGTATTGTTGTAAGTAAGCAATATACCTTCAGT 3840
Db 3781 AAGAGCTTCCCTGCTTCCACACACTTGTATTGTTGTAAGTAAGCAATATACCTTCAGT 3840
Qy 3841 CTACTAGCATTAGCACCGTTGCTACCGAGTGTCTGTCTAGAAACAGAGAGAAATTTAT 3900
Db 3841 CTACTAGCATTAGCACCGTTGCTACCGAGTGTCTGTCTAGAAACAGAGAGAAATTTAT 3900
Qy 3901 TATCATTTGAAGATAGCTTAAATGACGTGCAATACCCAGGTAAATTTGGCAAGCATCTC 3960
Db 3901 TATCATTTGAAGATAGCTTAAATGACGTGCAATACCCAGGTAAATTTGGCAAGCATCTC 3960
Qy 3961 AGGAACATCACCCTTAGTGAGGAAACAAATGTTCTGCTAGCTTGTCTTCACAGTGA 4020
Db 3961 AGGAACATCACCCTTAGTGAGGAAACAAATGTTCTGCTAGCTTGTCTTCACAGTGA 4020
Qy 4021 GTGAATTGGAAGACTTGACTGCAAAATACAAACCCAGATCCTTTCTTGATTTGTTCTT 4080
Db 4021 GTGAATTGGAAGACTTGACTGCAAAATACAAACCCAGATCCTTTCTTGATTTGTTCTT 4080
Qy 4081 CCAAAACAAATGAGCATCACTTGAAAGCCAGGAGTGTGTCTGAGTGAAGAGATTTGG 4140
Db 4081 CCAAAACAAATGAGCATCACTTGAAAGCCAGGAGTGTGTCTGAGTGAAGAGATTTGG 4140
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Db 4141 TTTTCAGATGATGAAGAAAGAGAAACGGGCTTGAAGAAATTAATCAAGAAAGCAAGCA 4200
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Db 4201 TGAATTCAAACTTAGGTGAAGCAGCATCTGGGTGTGAGAGTGAACAAAGCTCTGGAAG 4260

Db 4201 TGAATTCAAACTTAGGTGAAGCAGCATCTGGGTGTGAGAGTGAACAAAGCTCTGGAAG 4260
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Db 4261 ACTGCTCAGGGCTATCTCTCAGAGTGAACATTTTAAACCTGACAGAGGGATACCATGC 4320
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Db 4321 AACATTAACCTGATTAAGGCTCCAGCAGAAATGGCTGAAGTGAAGCTGTGTGAACAGC 4380
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Db 4381 ATGGAGCCAGCCTTTTAAACAGTACCTTCATCATTAAGTGACTTTCTGCTTGAAG 4440
Qy 4441 ACCTGGAATCCAGAACAAAGACATCGAAGAAACAGATTAATCTTACAGAAAGTA 4500
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Db 4501 GTGAATACCCCTATTAACCCAGAAATCCAGAAAGCCTTTCTGCTGCAAGTTGAGTGTCTG 4560
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Db 4561 CAGATAGTTCTACAGATTAATAAAGAACAGAGAGTGAAGAGTCACTCCCTTCTAAAT 4620
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Db 4621 GCCCATCATTAATGATGATAGTGGTATGATGACAGTTCCTGGAGATCTTCAGAAATGA 4680
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Db 5281 AGTCTATTAAGAAAGAAATGCTGAATGACATGATTTTGAAGTCAAGAGAGATGTGG 5340
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PS 5341 TCAATGGAGAAACCAACAGGTCGAAAGCGAGCAAGAGATCCAGAGAGAGATCT 5400
XX |||||||
QY 5401 TCAGGGGGCTGAAATCTGTTGCTATGGGCCCTTCACCAATGCCCCAGATCAACTGG 5460
XX |||||||
Db 5401 TCAGGGGGCTGAAATCTGTTGCTATGGGCCCTTCACCAATGCCCCAGATCAACTGG 5460
QY 5461 AATGATGTCACAGTGTGTGCTTCTGTGTGTGAAGAGCTTTTCATTCACCCCTTG 5520
XX |||||||
Db 5461 AATGATGTCACAGTGTGTGCTTCTGTGTGTGAAGAGCTTTTCATTCACCCCTTG 5520
QY 5521 GCACAGGTGTCCACCAATTGCTGTGTGTGACAGAGTCTGACAGAGCAATGAGCT 5580
XX |||||||
Db 5521 GCACAGGTGTCCACCAATTGCTGTGTGTGACAGAGTCTGACAGAGCAATGAGCT 5580
QY 5581 TCCATGCAATTGGGCGAGATGTGTGAAGCAGCTGTGTGTGACCCGAGAGTGTGTGACA 5640
XX |||||||
Db 5581 TCCATGCAATTGGGCGAGATGTGTGAAGCAGCTGTGTGTGACCCGAGAGTGTGTGACA 5640
QY 5641 GTGAGCCTCTTACCAAGTCCGAGAGCTGAGACACTTGTATCCCCAGATCCCCCACA 5700
XX |||||||
Db 5641 GTGAGCCTCTTACCAAGTCCGAGAGCTGAGACACTTGTATCCCCAGATCCCCCACA 5700
QY 5701 GCCACTACTGA 5711
XX |||||||
Db 5701 GCCACTACTGA 5711

RESULT 5
AAV46464
ID AAV46464 standard; cDNA; 5711 BP.
XX
XX AAV46464;
XX
XX 18-NOV-1998 (first entry)
XX
DE Human BRCA1 omi2 polymorphism #7 cDNA.
XX
XX BRCA1; omi1; human; breast and ovarian cancer predisposing gene;
XX polymorphism; susceptibility; anti-oncogene; tumour suppressor;
XX chromosome 17q; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 120..5711
FT /*tag= a
FT /product= "BRCA1 omi2 protein"
FT variation 4956
FT /*tag= b
FT /note= "This polymorphic variation can be an A or G
nucleotide"
XX
XX US5750400-A.
XX
XX 12-MAY-1998.
XX
XX 12-FEB-1997; 97US-0798691.
XX
XX 12-FEB-1996; 96US-0598591.
XX
XX 12-FEB-1997; 97US-0798691.
XX
XX (ONCO-) ONCOMED INC.
XX
XX Allen AC, Alvares CP, Ciliz BS, Murphy PD, Olson SJ;
XX Schelter DB, Zeng B;
XX
XX WPI; 1998-296774/26.
XX
XX BRCA1 omi gene coding sequences - useful for distinguishing between
XX polymorphisms and mutation(s) in the screening for disposition to
```

```
PT breast or ovarian cancer
XX
XX Claim 2e; Page -: 54pp; English.
XX
XX This sequence encodes a human BRCA1 (breast and ovarian cancer
CC predisposing gene) omi2 gene in which a polymorphic variation occurs at
CC nucleotide 4956. This sequence and other polymorphic variations of this
CC sequence are useful for the identification of an individual who may or
CC may not have an increased susceptibility to breast or ovarian cancer.
CC The sequences used identify gene changes which are due to polymorphisms,
CC rather than cancer causing mutations. BRCA1 is an anti-oncogene (tumour
CC suppressor) which is involved in genetic inheritance of cancers,
CC especially breast and ovarian cancer. It is found at human chromosome
CC 17q which is known to be linked to cancer susceptibility, especially
CC breast cancer. Cells containing a mutation in this gene lose the
CC wild-type function of BRCA1 and are more susceptible to cancers.
CC NOTE: This sequence does not appear in the specification but has been
CC created from the wild type BRCA1 omi2 gene represented in AAV46449.
XX
SQ Sequence 5711 BP; 1955 A; 1098 C; 1274 G; 1383 T; 1 other;
```

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Query Match 100.0%; Score 5710.6; DB 19; Length 5711;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5710; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY 1 AGCTGCTGAGACTCTCTGACCCCGACACAGGCTGTGGGTTCTCAGATTAAGTGGGCC 60
Db 1 AGCTGCTGAGACTCTCTGACCCCGACACAGGCTGTGGGTTCTCAGATTAAGTGGGCC 60
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Db 61 CCTGGCTCAGAGAGGCTTCAACCTCTGCTGTGGTAAAGTTCAATGGAACAGAAAGAA 120
QY 121 TGGATTTATCGCTCTTGGCGGTGAAGAGTAAATGTCATTAATGCTATGCAGAAA 180
Db 121 TGGATTTATCGCTCTTGGCGGTGAAGAGTAAATGTCATTAATGCTATGCAGAAA 180
QY 181 TCTTAGAGTGTCCCATCTGTCTGAGAGTGTATCAAGAACTGTCTCCACAAAGTGTACC 240
Db 181 TCTTAGAGTGTCCCATCTGTCTGAGAGTGTATCAAGAACTGTCTCCACAAAGTGTACC 240
QY 241 ACATATTTTGCATAATTTTGCATGCTGAACCTTCTCAACAGAAAGAGGCGCTTCAAGT 300
Db 241 ACATATTTTGCATAATTTTGCATGCTGAACCTTCTCAACAGAAAGAGGCGCTTCAAGT 300
QY 301 GTCCCTTTATGTAAGATATATATTAACCAAAAGAGGCTTCAAGAAAGTATGAGTTAGTC 360
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QY 361 AACTGTGTAAGAGCTATTTGAAATCAATTTGTCTTTTCAAGCTTGACACAGGTTGGAGT 420
Db 361 AACTGTGTAAGAGCTATTTGAAATCAATTTGTCTTTTCAAGCTTGACACAGGTTGGAGT 420
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Db 541 AACCGAAATATCTTCTCTGACGAAACAGTCTCAGTGTCAACTCTTAACCTTGGAA 600
QY 601 CTGTGAGAACTCTGAGCAAAAGAGGAGATACAACTCAAAAGAGCTGTGTACTGTTG 660
Db 601 CTGTGAGAACTCTGAGCAAAAGAGGAGATACAACTCAAAAGAGCTGTGTACTGTTG 660
QY 661 AATTGGGATCTGATTTCTTGAAGATACCGTTAATAGGCACTTATTTGAGTGGAG 720
Db 661 AATTGGGATCTGATTTCTTGAAGATACCGTTAATAGGCACTTATTTGAGTGGAG 720
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QY 781 CAAAAAGGCTGCTTGGAATTTTCTGAGACGATGTAACAATACCTGAAATCATCTAC 840  
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Db 901 ATCAGGGTAGTCTGTTTCAAACTTGATGAGGACATGTGGACAAATATCTCATGCCA 960  
QY 961 GCTCATTTACGACATGAGAACACGATTTATTACTCATTAAGACAGATGATGTGAAA 1020  
Db 961 GCTCATTTACGACATGAGAACACGATTTATTACTCATTAAGACAGATGATGTGAAA 1020  
QY 1021 AGGCTGAATCTGTAATTAAGCAACAGCGCTGAGCAAGGACCAATACAGAT 1080  
Db 1021 AGGCTGAATCTGTAATTAAGCAACAGCGCTGAGCAAGGACCAATACAGAT 1080  
QY 1081 GGGCTGGAAGTAAAGAAACATGTAATGATAGCGGACTCCAGACAAGAAAAAGGTAG 1140  
Db 1081 GGGCTGGAAGTAAAGAAACATGTAATGATAGCGGACTCCAGACAAGAAAAAGGTAG 1140  
QY 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAAAGATGAAATAGCAGAACTCCATGCT 1200  
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QY 1201 CAGAGATCCTAGAGATCTAGAGATGTTCTTGATTAACCTAAATAGCAGATTCAGA 1260  
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QY 1741 AGAATGCTCAAGTGAATATTAATTAATGATGATGATGATGATGATGATGATGATG 1800  
Db 1741 AGAATGCTCAAGTGAATATTAATTAATGATGATGATGATGATGATGATGATGATG 1800  
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 DB 5161 CTGAAGAGACTACTCATGTTGTTATGAAAAAGATGCTGAGTTGTGTGAACGAGAC 5220  
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 DB 5701 GCCACTACTGA 5711

RESULT 6  
 AAV46458  
 ID AAV46458 standard; cDNA; 5711 BP.  
 AC AAV46458;  
 XX  
 DT 18-NOV-1998 (first entry)  
 XX  
 DE Human BRCA1 omi2 polymorphism #1 cDNA.  
 XX  
 KM BRCA1; omi2; human; breast and ovarian cancer predisposing gene;  
 XX polymorphism; susceptibility; anti-oncogene; tumour suppressor;  
 XX chromosome 17q; ss.  
 XX  
 OS Homo sapiens.  
 XX  
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 FT variation 2201  
 FT /\*tag= b  
 FT /note= "This polymorphic variation can be a C or T  
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 XX  
 PN US5750400-A.  
 XX  
 PD 12-MAY-1998.

XX  
 PF 12-FEB-1997; 97US-0798691.  
 XX  
 PR 12-FEB-1996; 96US-0598591.  
 PR 12-FEB-1997; 97US-0798691.  
 XX  
 PA (ONCO-) ONCORMED INC.  
 XX  
 PI Allen AC, Alvaras CP, Critz BS, Murphy PD, Olson SJ;  
 PI Schelter DB, Zeng B;  
 XX  
 DR MPI; 1998-296774/26.  
 XX  
 PT BRCA1 omi2 gene coding sequences - useful for distinguishing between  
 PT polymorphisms and mutation(s) in the screening for disposition to  
 PT breast or ovarian cancer  
 XX  
 PS Claim 2e; Page -; 54pp; English.  
 XX  
 CC This sequence encodes a human BRCA1 (breast and ovarian cancer  
 CC predisposing gene) omi2 gene in which a polymorphic variation occurs at  
 CC nucleotide 2201. This sequence and other polymorphic variations of this  
 CC sequence are useful for the identification of an individual who may or  
 CC may not have an increased susceptibility to breast or ovarian cancer.  
 CC The sequences used identify gene changes which are due to polymorphisms,  
 CC rather than cancer causing mutations. BRCA1 is an anti-oncogene (tumour  
 CC suppressor) which is involved in genetic inheritance of cancers,  
 CC especially breast and ovarian cancer. It is found at human chromosome  
 CC 17q which is known to be linked to cancer susceptibility, especially  
 CC breast cancer. Cells containing a mutation in this gene lose the  
 CC wild-type function of BRCA1 and are more susceptible to cancers.  
 CC NOTE: This sequence does not appear in the specification but has been  
 CC created from the wild type BRCA1 omi2 gene represented in AAV46449.  
 XX  
 SQ Sequence 5711 BP; 1956 A; 1098 C; 1274 G; 1382 T; 1 other;

Query Match 100.0%; Score 5710.6; DB 19; Length 5711;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 5710; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACCTGCGTGAGACTTCTGAGACCCGACAGGCTGTGGGTTTCTAGATTAATGGGCC 60  
 DB 1 ACCTGCGTGAGACTTCTGAGACCCGACAGGCTGTGGGTTTCTAGATTAATGGGCC 60  
 QY 61 CCTGGCGTACAGAGGCTTCAACCTTCTGCTGTGGGTAAGTTCATTTGAGCAAGAGAA 120  
 DB 61 CCTGGCGTACAGAGGCTTCAACCTTCTGCTGTGGGTAAGTTCATTTGAGCAAGAGAA 120  
 QY 121 TGGATTATCTCTCTCTGCGGTTGAAGAGATGCAAAATGCTAATGCTATGACAGAAA 180  
 DB 121 TGGATTATCTCTCTCTGCGGTTGAAGAGATGCAAAATGCTAATGCTATGACAGAAA 180  
 QY 181 TCTTAGAGTGTCCATCTGTGTGAGATTGATCAAGAACCTGTCTCCACAAAGTGTACC 240  
 DB 181 TCTTAGAGTGTCCATCTGTGTGAGATTGATCAAGAACCTGTCTCCACAAAGTGTACC 240  
 QY 241 AATATATTTTGCAAATTTTGCATGCTGAACCTTCTCAACCAAGAAAGAGGCTTTCACAGT 300  
 DB 241 AATATATTTTGCAAATTTTGCATGCTGAACCTTCTCAACCAAGAAAGAGGCTTTCACAGT 300  
 QY 241 ACATATTTTGGCAAAATTTTGCATGCTGAACCTTCTCAACCAAGAAAGAGGCTTTCACAGT 300  
 DB 241 ACATATTTTGGCAAAATTTTGCATGCTGAACCTTCTCAACCAAGAAAGAGGCTTTCACAGT 300  
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 DB 361 AACTGTTGAGAGCTATTGAAATCATTTGTGCTTTTCAAGCTTGACACAGGTTTGGAGT 420  
 QY 421 ATGCAACAGCTATATTTTGAAGAAAGAAATTAATCTCTCTGTAACCTTAAGAGATG 480  
 DB 421 ATGCAACAGCTATATTTTGAAGAAAGAAATTAATCTCTCTGTAACCTTAAGAGATG 480  
 QY 481 AAGTTTCTATCATCAAGATATGGGCTACAGAAACCGTGCAGAAAGACTTCTACAGAGTG 540

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Db 481 AAGTTTCATCATCCAAAGTATGGGTACAGAAACCGTCCAAAGACCTTCAACAGAGTG 540
Qy 541 AACCAGAAATCTCTTCCTTGCGAGAAACAGTCTCACTGTCCAACTCTTAACCTTGAA 600
Db 541 AACCAGAAATCTCTTCCTTGCGAGAAACAGTCTCACTGTCCAACTCTTAACCTTGAA 600
Qy 601 CTGTGAGAACTCTGAGAACCAAGCAGCGATCAACCTCAAAAGAGCTGTCTACATTTG 660
Db 601 CTGTGAGAACTCTGAGAACCAAGCAGCGATCAACCTCAAAAGAGCTGTCTACATTTG 660
Qy 661 AATTGGGATCTGATTTCTTCTGAAGATACCGTTAATTAAGGCAATTATTCAGTGTGGAG 720
Db 661 AATTGGGATCTGATTTCTTCTGAAGATACCGTTAATTAAGGCAATTATTCAGTGTGGAG 720
Qy 721 ATCAAGATTTGTTACAAATCACCCCTCAAGAAACCGAGATGAATCACTTTGGATTCTG 780
Db 721 ATCAAGATTTGTTACAAATCACCCCTCAAGAAACCGAGATGAATCACTTTGGATTCTG 780
Qy 781 CAAAAAAGGCTGCTGTGAAATTTTCTGAGACGAGATTAACAATACTGAACATCATCAAC 840
Db 781 CAAAAAAGGCTGCTGTGAAATTTTCTGAGACGAGATTAACAATACTGAACATCATCAAC 840
Qy 841 CCAGTAATTAATGATTTGAAACACCACTGAGAAACGCTGACCTGAGAGGCATCCAGAAAGT 900
Db 841 CCAGTAATTAATGATTTGAAACACCACTGAGAAACGCTGACCTGAGAGGCATCCAGAAAGT 900
Qy 901 ATCAGGGATGTTCTGTTTCAAACTTGCAATGTGAGCCATGTGGCCAAATACTCATGCCA 960
Db 901 ATCAGGGATGTTCTGTTTCAAACTTGCAATGTGAGCCATGTGGCCAAATACTCATGCCA 960
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Db 961 GCTCATTAACAGATGAGAAACAGACAGTTTATCTACTAAAGACAGATGAATGTGAAA 1020
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Db 1021 AGGCTGAATTTCTGTAATAAAGCAAAACAGCTTGCTTACCAAGAGCCAACTAACAGAT 1080
Qy 1081 GGGCTGGAAGTAAAGAAACATGTAATGATGAGCGGACCTCCAGCAGCAAGAAAAAGTG 1140
Db 1081 GGGCTGGAAGTAAAGAAACATGTAATGATGAGCGGACCTCCAGCAGCAAGAAAAAGTG 1140
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Db 1141 ATCTGAATGCTGATCCCTGCTGTGAGAGAAAGAAATGAATGAAGCAAGAACTGCCATGCT 1200
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Db 1261 AAGTTAATGAGGTGTTTCCAGAGATGAAGCTGTAGATTTCTGATGATCACTACATGAG 1320
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Db 1321 GGGAGTCTGAATCAATGCAAGATGATGATGATGATGATGATGATGATGATGATGATG 1380
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Db 1381 AATATTTCTGTTCTTCAGAGAAATAGACTTACTGCGCAGATCTCTCATGAGGCTTTAA 1440
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Db 1861 AAGGAAAGCTGAACCTTAATTAAGCAGCAGTATTAAGCAATATGAACTGAAATTAATTC 1920
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Db 2101 GGCACAGAGAAACCTTAACATCTCATGAGAAAGTAAAGAACTGCACTGAGCCAAAGAA 2160
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Db 2221 AGTTAAACAAATGACCTGTTCTTTTACTAAGTTCCTAAATACAGTGAATTTAAGAAAT 2280
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Db 2521 GTGTAGTCAAGTGCAGCACTTTGAAACCCCAAGGAGCTAATTCATGTTGTTCCAAAG 2580
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Db 2581 AATATGAAATGACACAGAGGCTTTAAGTATTCATTGGAATGGAATTAACCAAGTC 2640
Qy 2641 GGGAAAACAGATGGAATGGAAGAAAGTGAATGATGATGATGATGATGATGATGATGAT 2700
Db 2641 GGGAAAACAGATGGAATGGAAGAAAGTGAATGATGATGATGATGATGATGATGATGAT 2700
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QY 2701 TCAAGTTTCAAGCGCCAGTCATTTGCTGTGTTTCAATCCAGGAAATGACAGAGG 2760  
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QY 2761 AATGTGCAACATTTCTGCGCACTGTGGTCTTTAAAGAAACAAAGTCCAAAGTCACTT 2820  
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DB 3421 GTAAATTGTAAGCATCTGAAATTAAGCAAGAAATGAGAAAGTATGAGTCTGGA 3480  
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DB 3481 ATACAGATTTCTCTCATATCTGATTTCAATTAAGTAAAGCAAGCTATGAGAAATGATC 3540  
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DB 3901 TATCATTTAAGAAATGCTTAAATGACCTGAGTAAACAGGTAATATTTGGCAAGGCAATC 3960  
QY 3961 AGGAACATCACTTATGAGGAAACAAATGTTCTGCTAGCTTGTCTTCACTGAG 4020  
DB 3961 AGGAACATCACTTATGAGGAAACAAATGTTCTGCTAGCTTGTCTTCACTGAG 4020  
QY 4021 GTGAATTGGAAGACTTGAATCAACCAACCAAGATCTTTGTTGATTTGTTCTT 4080  
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DB 4081 CCAACCAATGAGGATCACTGAAAGCAGAGGAGTGTCTGAGTGAACAGGAATTTGG 4140  
QY 4141 TTTCAATGATGAAGAAAGAGAGAGCGGCTTGAAGAAATATATCAAGAGAGCAAGCA 4200  
DB 4141 TTTCAATGATGAAGAAAGAGAGAGCGGCTTGAAGAAATATATCAAGAGAGCAAGCA 4200  
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DB 4621 GCCCATCAATTAAGTATGAGTGTGATCAGTCAAGTGTGCTGAGAGTCTTCAAGTAA 4680  
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Db      4921  AAGTTCCTCCCAATTGAAGTTGCAGAAATCTGCCAGAGTCCAGCTGCTCTACTACTG 4980
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Db      4981  ATACTGCTGGGTATTAATGCAATGGAAGAAAGTGTGAGCAGGAGAGCAGAAATTGAC 5040
Qy      5041  CTTCAACAGAAAGGGTCAACAAAGAAATGTCATGATGCTGCTGCTGACCCAGAG 5100
Db      5041  CTTCAACAGAAAGGGTCAACAAAGAAATGTCATGATGCTGCTGCTGACCCAGAG 5100
Qy      5101  AATTATGCTGCTGTAACAAGTTGGCAGAAAACACCACTACTTTAACTTAATTA 5160
Db      5101  AATTATGCTGCTGTAACAAGTTGGCAGAAAACACCACTACTTTAACTTAATTA 5160
Qy      5161  CTGAAGAGACTACTGATGTTGTTATGAAAACAGATGCTGATGTTGTTGTAACGAC 5220
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Qy      5221  TGAATATATTTTCTAGAAATGCGGAGAGAAATGGGTAGTTAGCTAATTTCTGGT 5280
Db      5221  TGAATATATTTTCTAGAAATGCGGAGAGAAATGGGTAGTTAGCTAATTTCTGGT 5280
Qy      5281  AGTCTATTTAAAGAAAGAAAATGCTGAATGAGCATGATTTTGAAGTCAGAGAGAT 5340
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Db      5401  TCAGGGGGCTAGAAATCTGTTGCTATGAGCCCTTCAACCAATGCCCCAGATCA 5460
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Qy      5521  GCACAGGTGTCACACCAATGTTGTTGTCACAGATGCTGACAGAGAGCAATGCT 5580
Db      5521  GCACAGGTGTCACACCAATGTTGTTGTCACAGATGCTGACAGAGAGCAATGCT 5580
Qy      5581  TCCATGCAATTGGGAGATGTTGTAAGCACTGTGTGTAACCCGAGAGTGGTGTG 5640
Db      5581  TCCATGCAATTGGGAGATGTTGTAAGCACTGTGTGTAACCCGAGAGTGGTGTG 5640
Qy      5641  GTGTAGCACTCTACCAAGTCCGAGAGCTGAGACACTACTGATATCCCGAGATCC 5700
Db      5641  GTGTAGCACTCTACCAAGTCCGAGAGCTGAGACACTACTGATATCCCGAGATCC 5700
Qy      5701  GCCACTACTGA 5711
Db      5701  GCCACTACTGA 5711

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RESULT 7  
AAV46459  
ID AAV46459 standard; cDNA; 5711 BP.

AC AAV46459;  
XX  
XX 18-NOV-1998 (first entry)  
XX  
XX Human BRCA1 omi2 polymorphism #2 cDNA.  
DE  
XX BRCA1; omi2; human; breast and ovarian cancer predisposing gene;  
KM polymorphism; susceptibility; anti-oncogene; tumour suppressor;  
KW chromosome 17q; ss.

```

XX OS Homo sapiens.
XX FH Key
XX FT CDS
XX FT variation
XX FT /tag= b
XX FT /note= "This polymorphic variation can be a T or C
XX FT nucleotide"
XX PN US5750400-A.
XX PD 12-MAY-1998.
XX PF 12-FEB-1997; 97US-0798691.
XX PR 12-FEB-1996; 96US-0538591.
XX PR 12-FEB-1997; 97US-0798691.
XX PA (ONCO-) ONCORMED INC.
XX PI Allen AC, Alvares CP, Critz BS, Murphy PD, Olson SJ;
XX PI Schelter DB, Zeng B;
XX DR WPI; 1998-296774/26.
XX PT BRCA1 omi gene coding sequences - useful for distinguishing between
XX PT polymorphisms and mutation(s) in the screening for disposition to
XX PT breast or ovarian cancer
XX PS Claim 2e; Page -: 54pp; English.
XX CC This sequence encodes a human BRCA1 (breast and ovarian cancer
XX CC predisposing gene) omi2 gene in which a polymorphic variation occurs at
XX CC nucleotide 2430. This sequence and other polymorphic variations of this
XX CC sequence are useful for the identification of an individual who may or
XX CC may not have an increased susceptibility to breast or ovarian cancer.
XX CC The sequences used identify gene changes which are due to polymorphisms,
XX CC rather than cancer causing mutations. BRCA1 is an anti-oncogene (tumour
XX CC suppressor) which is involved in genetic inheritance of cancers,
XX CC especially breast and ovarian cancer. It is found at human chromosome
XX CC 17q which is known to be linked to cancer susceptibility, especially
XX CC breast cancer. Cells containing a mutation in this gene lose the
XX CC wild-type function of BRCA1 and are more susceptible to cancers.
XX CC NOTE: This sequence does not appear in the specification but has been
XX CC created from the wild type BRCA1 omi2 gene represented in AAV46449.
XX CC
XX SQ Sequence 5711 BP; 1956 A; 1098 C; 1274 G; 1382 T; 1 other;

Query Match 100.0%; Score 5710.6; DB 19; Length 5711;
Best Local Similarity 100.0%; Pired. No. 0;
Matches 5710; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGCTGCTGAGAGCTTCTGAGACCCCGACAGCGGTGTGGGTTCTCAGATACTGGGCC 60
Db 1 AGCTGCTGAGAGCTTCTGAGACCCCGACAGCGGTGTGGGTTCTCAGATACTGGGCC 60
Qy 61 CTTGGCTCAGAGAGCCCTTCACTCTGCTGTGGGTAAAGTTCAATTGAAACAGAAAGAA 120
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Db 121 TGGATTTATCTGCTCTTGGCTTGAAGAGTAAAGTCAATTAATGATCAAGAAA 180
Qy 181 TCTTAGAGTGCCTCATCTGTGAGATTGATCAAGAACTGCTCCACAAAGTGTGACC 240
Db 181 TCTTAGAGTGCCTCATCTGTGAGATTGATCAAGAACTGCTCCACAAAGTGTGACC 240
Qy 241 ACATATTTTGGCAATTTTGGCATGCTGAACTTCAACAGAAAGGGCTTTCACAGT 300

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QY 361 AACTTGTGAAGAGCTATTTGCAAAATCAATTTGCTTTTTCAGCTTGAACAGAGTTTGAAGT 420  
Db 361 AACTTGTGAAGAGCTATTTGCAAAATCAATTTGCTTTTTCAGCTTGAACAGAGTTTGAAGT 420  
QY 421 ATGCAAAACAGCTATATTTTGCACAAAAGAAATTAATCTCTGTAACATCTTAAAGATG 480  
Db 421 ATGCAAAACAGCTATATTTTGCACAAAAGAAATTAATCTCTGTAACATCTTAAAGATG 480  
QY 481 AAGTTCTATCATCCAAAGATGAGGCTACAGAAACCGTCCAAAGAGCTTCTACAGAGT 540  
Db 481 AAGTTCTATCATCCAAAGATGAGGCTACAGAAACCGTCCAAAGAGCTTCTACAGAGT 540  
QY 541 AACCCGAAAATCCTTCCCTTGCAGAGAAACAGTCTCAGGTGTCACACTCTTAACTTGA 600  
Db 541 AACCCGAAAATCCTTCCCTTGCAGAGAAACAGTCTCAGGTGTCACACTCTTAACTTGA 600  
QY 601 CTGTGGAAGCTCTGAGAGCAAAAGCAGGAGTACAACTTCAAAAGAGCTCTGTACATG 660  
Db 601 CTGTGGAAGCTCTGAGAGCAAAAGCAGGAGTACAACTTCAAAAGAGCTCTGTGTACATG 660  
QY 661 AATTGGAGTCTGATTTCTTCTGAAGATACCGTTAATAAGGCACTTATTGCAAGTGGAG 720  
Db 661 AATTGGAGTCTGATTTCTTCTGAAGATACCGTTAATAAGGCACTTATTGCAAGTGGAG 720  
QY 721 ATCAAGATTTGTATCAAAATCACCCCTCAAGAAACAGAGATGAATCAGTTTGGATTCTG 780  
Db 721 ATCAAGATTTGTATCAAAATCACCCCTCAAGAAACAGAGATGAATCAGTTTGGATTCTG 780  
QY 781 CAAAAAAGCGTCTGTGGAATTTTCTGAGACGAGATGTAACTTGAACATCATCAAC 840  
Db 781 CAAAAAAGCGTCTGTGGAATTTTCTGAGACGAGATGTAACTTGAACATCATCAAC 840  
QY 841 CCAGTATATATGATTTGAACACCACTGAGAAAGCGTCACTGAGAGGATCCAGAAAGT 900  
Db 841 CCAGTATATATGATTTGAACACCACTGAGAAAGCGTCACTGAGAGGATCCAGAAAGT 900  
QY 901 ATCAGGATGTTCTGTTTCAAACTTGCATGTGAGGCACTGAGCAAAATCACTCATGCA 960  
Db 901 ATCAGGATGTTCTGTTTCAAACTTGCATGTGAGGCACTGAGCAAAATCACTCATGCA 960  
QY 961 GCTCATTAACAGCTGAGAGCAAGATTTTACTCTCAATAAGACAGAAATGATGAGAA 1020  
Db 961 GCTCATTAACAGCTGAGAGCAAGATTTTACTCTCAATAAGACAGAAATGATGAGAA 1020  
QY 961 GCTCATTAACAGCTGAGAGCAAGATTTTACTCTCAATAAGACAGAAATGATGAGAA 1020  
Db 961 GCTCATTAACAGCTGAGAGCAAGATTTTACTCTCAATAAGACAGAAATGATGAGAA 1020  
QY 1021 AGGCTGAATTTCTGTATTAAGCAAAAGCGCTGTAGCAAGGAGCCAAATTAACAGAT 1080  
Db 1021 AGGCTGAATTTCTGTATTAAGCAAAAGCGCTGTAGCAAGGAGCCAAATTAACAGAT 1080  
QY 1081 GGGCTGGAAGTAAAGAAACATGTATAGAGCGGATCCCAAGCAAGAAAAAAGGTAG 1140  
Db 1081 GGGCTGGAAGTAAAGAAACATGTATAGAGCGGATCCCAAGCAAGAAAAAAGGTAG 1140  
QY 1141 ATCTGAATGCTGATCCCCCTGTGTGAGAGAAAGATGAATTAAGCAAACTGCCATGCT 1200  
Db 1141 ATCTGAATGCTGATCCCCCTGTGTGAGAGAAAGATGAATTAAGCAAACTGCCATGCT 1200  
QY 1201 CAGAGATCTAGAGATGATGAGATGTTCTTGAATTAACACTAAATTAAGAGATTCACA 1260  
Db 1201 CAGAGATCTAGAGATGATGAGATGTTCTTGAATTAACACTAAATTAAGAGATTCACA 1260  
QY 1261 AAGTTAATAGAGTGTTCAGAAAGTGAACCTGTTAGGTTCTGATGACTCAATGATG 1320  
Db 1261 AAGTTAATAGAGTGTTCAGAAAGTGAACCTGTTAGGTTCTGATGACTCAATGATG 1320  
QY 1321 GGGAGTCTGAATCAAAATGCAAAAGTGAAGTATTTGAGCGTTCTTAAATGAGGTAGT 1380  
Db 1321 GGGAGTCTGAATCAAAATGCAAAAGTGAAGTATTTGAGCGTTCTTAAATGAGGTAGT 1380

QY 1381 AATATTTCTGTTCTTTCAGAGAAATAGACTTACTGCGCAGTATCCTCATGAGGCTTAA 1440  
Db 1381 AATATTTCTGTTCTTTCAGAGAAATAGACTTACTGCGCAGTATCCTCATGAGGCTTAA 1440  
QY 1441 TATGTAAAGTGAAGAGTTCATCCCAATCAGTGAAGATATATTTGAAGCAAAATAT 1500  
Db 1441 TATGTAAAGTGAAGAGTTCATCCCAATCAGTGAAGATATATTTGAAGCAAAATAT 1500  
QY 1501 TTGGGAAAACTTATGGAAGAGGAGGCTTCCCACTTAAGCCATGTAACGAAATC 1560  
Db 1501 TTGGGAAAACTTATGGAAGAGGAGGCTTCCCACTTAAGCCATGTAACGAAATC 1560  
QY 1561 TAAATATAGAGCATTTGTTTACTGAGCCACAGATATATACAGAGGCTCCCTCAAAATA 1620  
Db 1561 TAAATATAGAGCATTTGTTTACTGAGCCACAGATATATACAGAGGCTCCCTCAAAATA 1620  
QY 1621 AATTAAGCGTAAAGAGAGAGCTTACATCAGGCTTATCTGAGATTTTATCAAGAAAG 1680  
Db 1621 AATTAAGCGTAAAGAGAGAGCTTACATCAGGCTTATCTGAGATTTTATCAAGAAAG 1680  
QY 1681 CAGATTTGCAATTCAAAAGAGCTTCTGAAATGATTAATCAGGAACTAACCAAGGAGC 1740  
Db 1681 CAGATTTGCAATTCAAAAGAGCTTCTGAAATGATTAATCAGGAACTAACCAAGGAGC 1740  
QY 1741 AAGATGCTAAGTGAATATTTACTTAATAGTGTCAATGAGATTAACCAAAAGGTATT 1800  
Db 1741 AAGATGCTAAGTGAATATTTACTTAATAGTGTCAATGAGATTAACCAAAAGGTATT 1800  
QY 1801 CTATTCAGATGAGAAAAATCCTTAACCAATGAATCACTCGAAAAAGATCTGCTTCA 1860  
Db 1801 CTATTCAGATGAGAAAAATCCTTAACCAATGAATCACTCGAAAAAGATCTGCTTCA 1860  
QY 1861 AAGCAAGCTGAACCTTATTAAGCAGATTAAGCAATGGAACCTCGAAATTAATATTC 1920  
Db 1861 AAGCAAGCTGAACCTTATTAAGCAGATTAAGCAATGGAACCTCGAAATTAATATTC 1920  
QY 1921 ACAATTCAAAAGCACTTAAAAAGAAATAGGCTGAGAGGAGTCTTCAACAGGATATTC 1980  
Db 1921 ACAATTCAAAAGCACTTAAAAAGAAATAGGCTGAGAGGAGTCTTCAACAGGATATTC 1980  
QY 1981 ATGCGCTTGAATAGTACAGTGAAGATTAAGCAACCTAATTTGATCTGAATTTGCAA 2040  
Db 1981 ATGCGCTTGAATAGTACAGTGAAGATTAAGCAACCTAATTTGATCTGAATTTGCAA 2040  
QY 2041 TTGATAGTGTCTTGAAGTGAAGATTAAGCAACCTAATTTGATCTGAATTTGCAA 2100  
Db 2041 TTGATAGTGTCTTGAAGTGAAGATTAAGCAACCTAATTTGATCTGAATTTGCAA 2100  
QY 2101 GGCACAGCAGAAACCTAACAATCATGGAAGGTAAGAACTGCACTGAGGCAAGAAAG 2160  
Db 2101 GGCACAGCAGAAACCTAACAATCATGGAAGGTAAGAACTGCACTGAGGCAAGAAAG 2160  
QY 2161 GTTACCAAGCAAAATGAACAGACAACTAAGAAAGATGACAGGATATCTTCCAGAGCTGA 2220  
Db 2161 GTTACCAAGCAAAATGAACAGACAACTAAGAAAGATGACAGGATATCTTCCAGAGCTGA 2220  
QY 2221 AGTTAACAATGCACTGCTGTTTCTTACTAAGTGTCAAAATCCAGTGAACCTTAAAGAT 2280  
Db 2221 AGTTAACAATGCACTGCTGTTTCTTACTAAGTGTCAAAATCCAGTGAACCTTAAAGAT 2280  
QY 2281 TTGCAATCTAGCTTCCCAAGAGAAAGAAAGAAAGTAAAGTCAAGTAAAGTGT 2340  
Db 2281 TTGCAATCTAGCTTCCCAAGAGAAAGAAAGAAAGTAAAGTCAAGTAAAGTGT 2340  
QY 2341 CTAATTAATGCTGAAGACCCCAAGATCTCATGTTAAGTGAAGAAAGGTTTTCAGAACTG 2400  
Db 2341 CTAATTAATGCTGAAGACCCCAAGATCTCATGTTAAGTGAAGAAAGGTTTTCAGAACTG 2400  
QY 2401 AAGATCTGTGAGAGTGAAGTATTTATTTGATGTAACCTGATACATGATTAAGCACTGAG 2460  
Db 2401 AAGATCTGTGAGAGTGAAGTATTTATTTCAATGTAACCTGATACATGATTAAGCACTGAG 2460



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Db      4621 GCCCATCATTAGATGATAGGTGGTACATGACAGTTCCTCTGGGAGTCTTCAGAAATAGAA 4680
QY      4681 ACTACCATCATCTAAGAGAGAGCTCATTAAAGTGTGTGATGTGAGAGAGCAACAGCTGGAAG 4740
Db      4681 ACTACCATCATCTAAGAGAGAGCTCATTAAAGTGTGTGATGTGAGAGAGCAACAGCTGGAAG 4740
QY      4741 AGTCTGGGCGCACAGATTTGACGGAAACATCTTAATCTCCAGAGCAAGATCTAGAGGGAA 4800
Db      4741 AGTCTGGGCGCACAGATTTGACGGAAACATCTTAATCTCCAGAGCAAGATCTAGAGGGAA 4800
QY      4801 CCCCTTAACCTGGAATCTGGAATCAGCTCTTCTCTGATGACCTGTAATCTGATCTTCTG 4860
Db      4801 CCCCTTAACCTGGAATCTGGAATCAGCTCTTCTCTGATGACCTGTAATCTGATCTTCTG 4860
QY      4801 CCCCTTAACCTGGAATCTGGAATCAGCTCTTCTCTGATGACCTGTAATCTGATCTTCTG 4860
Db      4861 AAGCAGAGAGCCCGACAGTCTGCTGTGGCAACATACATCTTCAACCTCGACATGA 4920
QY      4861 AAGCAGAGAGCCCGACAGTCTGCTGTGGCAACATACATCTTCAACCTCGACATGA 4920
Db      4921 AAGTCCCGCAATTGAAAGTTGACAAATCTGCCAGAGTCCAGCTGCTCATACTACTG 4980
QY      4921 AAGTCCCGCAATTGAAAGTTGACAAATCTGCCAGAGTCCAGCTGCTCATACTACTG 4980
Db      4921 AAGTCCCGCAATTGAAAGTTGACAAATCTGCCAGAGTCCAGCTGCTCATACTACTG 4980
QY      4981 ATACTGCTGGGTATTAATGCAATGAGAAAGTGTGAGCAGGAGAAAGCCAGAAATGACAG 5040
Db      4981 ATACTGCTGGGTATTAATGCAATGAGAAAGTGTGAGCAGGAGAAAGCCAGAAATGACAG 5040
QY      5041 CTTCACAGAAAGAGGTCAACAAAGAAATGTCATGAGTGTGCTGCTGACCCCAAGAG 5100
Db      5041 CTTCACAGAAAGAGGTCAACAAAGAAATGTCATGAGTGTGCTGCTGACCCCAAGAG 5100
QY      5101 AATTATGCTGCTGTCACAGTTTGCAGAAACACCAACATCACTTAATCTAATTA 5160
Db      5101 AATTATGCTGCTGTCACAGTTTGCAGAAACACCAACATCACTTAATCTAATTA 5160
QY      5161 CTGAGAGAGTACTCATGTTGTTATGAAAACAGATGCTGATGTTGTGTGAACGACAC 5220
Db      5161 CTGAGAGAGTACTCATGTTGTTATGAAAACAGATGCTGATGTTGTGTGAACGACAC 5220
QY      5221 TGAATATTTTCTAGGAATTTGGGAGAGAAATGGGAGTACTTATTTCTGGGTGACCC 5280
Db      5221 TGAATATTTTCTAGGAATTTGGGAGAGAAATGGGAGTACTTATTTCTGGGTGACCC 5280
QY      5281 AGTCTATTAAGAAAGAAATCTGATAGAGCATGTTTGAAGTCAGAGAGATGTG 5340
Db      5281 AGTCTATTAAGAAAGAAATCTGATAGAGCATGTTTGAAGTCAGAGAGATGTG 5340
QY      5341 TCATGAGAGAAACCAACCAAGTCCAAAGCGACAGAAAGATCTCCAGAGCAGAAAGATCT 5400
Db      5341 TCATGAGAGAAACCAACCAAGTCCAAAGCGACAGAAAGATCTCCAGAGCAGAAAGATCT 5400
QY      5401 TCAGGGGGGCTAGAAATCTGTGTATGAGGCTTCACCAACATGCCACAGATCACTG 5460
Db      5401 TCAGGGGGGCTAGAAATCTGTGTATGAGGCTTCACCAACATGCCACAGATCACTG 5460
QY      5461 AATGATGATGACAGTGTGTGTGCTTCTGTGTGAGAGAGCTTTCATCAATTCACCTTG 5520
Db      5461 AATGATGATGACAGTGTGTGTGCTTCTGTGTGAGAGAGCTTTCATCAATTCACCTTG 5520
QY      5461 AATGATGATGACAGTGTGTGTGCTTCTGTGTGAGAGAGCTTTCATCAATTCACCTTG 5520
Db      5461 AATGATGATGACAGTGTGTGTGCTTCTGTGTGAGAGAGCTTTCATCAATTCACCTTG 5520
QY      5521 GCACAGGTGTCCACCAATTTGTTGTGACGCAATATGCTGGAACAGAGCAATGGCT 5580
Db      5521 GCACAGGTGTCCACCAATTTGTTGTGACGCAATATGCTGGAACAGAGCAATGGCT 5580
QY      5581 TCATGCAATTTGGGAGATGTGTGAGGCACTGTGTGACCCAGAGTGGGTGTGAGCA 5640
Db      5581 TCATGCAATTTGGGAGATGTGTGAGGCACTGTGTGACCCAGAGTGGGTGTGAGCA 5640
QY      5641 GTGTAGACTCTTACAGATGTCAGAGAGTGCACCTAATCTGATATACCCAGATCCCGACA 5700
Db      5641 GTGTAGACTCTTACAGATGTCAGAGAGTGCACCTAATCTGATATACCCAGATCCCGACA 5700
QY      5701 GCCACTACTGA 5711
Db      5701 GCCACTACTGA 5711

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RESULT 8
AAV46460
ID      AAV46460 standard; cDNA; 5711 BP.
XX
AC      AAV46460;
XX
CC      1g-NOV-1998 (first entry)
XX
DE      Human BRCA1 omi2 polymorphism #3 cDNA.
XX
KW      BRCA1; omi2; human; breast and ovarian cancer predisposing gene;
KM      polymorphism; susceptibility; anti-oncogene; tumour suppressor;
KM      chromosome 17q; ss.
XX
OS      Homo sapiens.
XX
FH      Key
FH      CDS
FT      120..5711
FT      /tag= a
FT      /product= "BRCA1 omi2 protein"
FT      variation
FT      2731
FT      /tag= b
FT      /note= "This polymorphic variation can be a C or T
XX      nucleotide"
XX
PN      US750400-A.
XX
PD      12-MAY-1998.
XX
PF      12-FEB-1997; 97US-0798691.
XX
PR      12-FEB-1996; 96US-0598591.
PR      12-FEB-1997; 97US-0798691.
XX
PA      (ONCO-) ONCORMED INC.
XX
PI      Allen AC, Alvares CP, Critz BS, Murphy PD, Olson SJ;
PI      Schelter DB, Zeng B;
XX
DR      WPI; 1998-296774/26.
XX
XX      BRCA1 omi2 gene coding sequences - useful for distinguishing between
PT      polymorphisms and mutation(s) in the screening for disposition to
XX      breast or ovarian cancer
XX
PS      Claim 2e; Page -; 54pp; English.
XX
CC      This sequence encodes a human BRCA1 (breast and ovarian cancer
CC      predisposing gene) omi2 gene in which a polymorphic variation occurs at
CC      nucleotide 2731. This sequence and other polymorphic variations of this
CC      sequence are useful for the identification of an individual who may or
CC      may not have an increased susceptibility to breast or ovarian cancer.
CC      The sequences used identify gene changes which are due to polymorphisms,
CC      rather than cancer causing mutations. BRCA1 is an anti-oncogene (tumour
CC      suppressor) which is involved in genetic inheritance of cancers,
CC      especially breast and ovarian cancer. It is found at human chromosome
CC      17q which is known to be linked to cancer susceptibility, especially
CC      breast cancer. Cells containing a mutation in this gene lose the
CC      wild-type function of BRCA1 and are more susceptible to cancers.
CC      NOTE: This sequence does not appear in the specification but has been
CC      created from the wild type BRCA1 omi2 gene represented in AAV46449.
XX
SQ      Sequence 5711 BP; 1956 A; 1098 G; 1274 G; 1382 T; 1 other;
XX
Query Match 100.0%; Score 5710.6; DB 19; Length 5711;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5710; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY      1 AGCTGCTGAGACTTCTCTGAGCCCGCACAGAGCTGTGGGTTTTCAGATAACTGGGCC 60
Db      1 AGCTGCTGAGACTTCTCTGAGCCCGCACAGAGCTGTGGGTTTCTCAGATAACTGGGCC 60

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|    |      |   |      |
|----|------|---|------|
| Qy | 61   | CTTGCGCTCAGAGAGCCTTCAACCTCTGCTCTGGGTAAAGTTCACTTGGAAACAGAAAGAA   | 120  |
| Db | 61   | CTTGCGCTCAGAGAGCCTTCAACCTCTGCTCTGGGTAAAGTTCACTTGGAAACAGAAAGAA   | 120  |
| Qy | 121  | TGGAATTTATCGCTCTTGCGGTGAAGAGTACAAAATGTCACTTAATGTATGACAGAAA      | 180  |
| Db | 121  | TGGAATTTATCGCTCTTGCGGTGAAGAGTACAAAATGTCACTTAATGTATGACAGAAA      | 180  |
| Qy | 181  | TCTTAGAGTGTCCATCTGTCTGTGAGTTGATCAAGAAACCTGTCTCCACAAAGTGTGACC    | 240  |
| Db | 181  | TCTTAGAGTGTCCATCTGTCTGTGAGTTGATCAAGAAACCTGTCTCCACAAAGTGTGACC    | 240  |
| Qy | 241  | ACATATTTTGCAAATTTTGCATGCTGAAACCTTCTCAACCAAGAAAGGGCTTCAACAGT     | 300  |
| Db | 241  | ACATATTTTGCAAATTTTGCATGCTGAAACCTTCTCAACCAAGAAAGGGCTTCAACAGT     | 300  |
| Qy | 301  | GTCTTTATGTAGAATATATATAACCAAAAGAGCCTACAAAGAAAGTACAGATTTATGTC     | 360  |
| Db | 301  | GTCTTTATGTAGAATATATATAACCAAAAGAGCCTACAAAGAAAGTACAGATTTATGTC     | 360  |
| Qy | 361  | AACTTGTGAAGAGCTATTTGAAATCAATTTGTGCTTTCAAGCTTGACACAGTTTGGAGT     | 420  |
| Db | 361  | AACTTGTGAAGAGCTATTTGAAATCAATTTGTGCTTTCAAGCTTGACACAGTTTGGAGT     | 420  |
| Qy | 421  | ATGCAAACAGCTATTAATTTTGCAAAAAGAAAAATTAATCTCTCCGAAACCTTAAGATG     | 480  |
| Db | 421  | ATGCAAACAGCTATTAATTTTGCAAAAAGAAAAATTAATCTCTCCGAAACCTTAAGATG     | 480  |
| Qy | 481  | AAGTTTCTATCATCCAAAGTATGGGCTACAGAAACCGTGCCAAAGACTTCTACAGAGTG     | 540  |
| Db | 481  | AAGTTTCTATCATCCAAAGTATGGGCTACAGAAACCGTGCCAAAGACTTCTACAGAGTG     | 540  |
| Qy | 541  | AAACCGAAAAATCTCTTCTTGCGAGAAACCAAGTCTCAAGTGTCAAATCTCTTAACCTTGGAA | 600  |
| Db | 541  | AAACCGAAAAATCTCTTCTTGCGAGAAACCAAGTCTCAAGTGTCAAATCTCTTAACCTTGGAA | 600  |
| Qy | 601  | CTGTGAGAACTCTAGAGCAAGAGGCGGATACAAACCTCAAAAGAGCTGTCTACACTTGG     | 660  |
| Db | 601  | CTGTGAGAACTCTAGAGCAAGAGGCGGATACAAACCTCAAAAGAGCTGTCTACACTTGG     | 660  |
| Qy | 661  | AATGGGATCTGATTTCTTCTGAAGATACCGTTAAAGGCAACTTAATGGCAGTGTGGAG      | 720  |
| Db | 661  | AATGGGATCTGATTTCTTCTGAAGATACCGTTAAAGGCAACTTAATGGCAGTGTGGAG      | 720  |
| Qy | 721  | ATCAAGAATTTGTTACAAATCAACCTCACAAGAACCAAGGATGAATCAAGTTTGGATTCTG   | 780  |
| Db | 721  | ATCAAGAATTTGTTACAAATCAACCTCACAAGAACCAAGGATGAATCAAGTTTGGATTCTG   | 780  |
| Qy | 781  | CAAAAAGAGCGCTTGTAATTTTCTGAGACGATGTAAACAATATCAGAAACATCATCAAC     | 840  |
| Db | 781  | CAAAAAGAGCGCTTGTAATTTTCTGAGACGATGTAAACAATATCAGAAACATCATCAAC     | 840  |
| Qy | 841  | CCAGTAAATATGATTTTGAACAACAACCTGAGAACGCTGAGAGGACATCCAGAAAAAGT     | 900  |
| Db | 841  | CCAGTAAATATGATTTTGAACAACAACAACCTGAGAACGCTGAGAGGACATCCAGAAAAAGT  | 900  |
| Qy | 901  | ATCAGGGTATGTTCTGTTCAAACTTGACATGTGAGCCATGTGGCACAAAATATCTCATGCCA  | 960  |
| Db | 901  | ATCAGGGTATGTTCTGTTCAAACTTGACATGTGAGCCATGTGGCACAAAATATCTCATGCCA  | 960  |
| Qy | 961  | GCTCATTTACAGATGAGAACAGCAGTTTATTAATCACTTAAGACAGAAATGATGTAAGAA    | 1020 |
| Db | 961  | GCTCATTTACAGATGAGAACAGCAGTTTATTAATCACTTAAGACAGAAATGATGTAAGAA    | 1020 |
| Qy | 1021 | AGGCTGAATTTCTGTATATAAGCAAAACGCTGGCTTAGCAAGAGGCCAATTAACGAT       | 1080 |
| Db | 1021 | AGGCTGAATTTCTGTATATAAGCAAAACGCTGGCTTAGCAAGAGGCCAATTAACGAT       | 1080 |
| Qy | 1081 | GGGCTGGAAGTAAAGAAACATGTATATGATGAGCGGAGCTCCAGACAGAAAAAGGTAG      | 1140 |
| Db | 1081 | GGGCTGGAAGTAAAGAAACATGTATATGATGAGCGGAGCTCCAGACAGAAAAAGGTAG      | 1140 |

|   |      |   |      |
|---|------|---|------|
| D | 2221 | AGTTTAACTGACCTGCTGCTCTTTTAACTAGTGTCTAAATACAGAGAACTTTAAAGAT    | 2280 |
| O | 2281 | TTGTCAATCTTAGGCTTCCAGAGAGAAAAAGAGAAATCAGAAACAGTTAAAGTGT       | 2340 |
| D | 2281 | TTGTCAATCTTAGGCTTCCAGAGAGAAAAAGAGAAATCAGAAACAGTTAAAGTGT       | 2340 |
| O | 2341 | CTAATATGCTGAAGACCCCAAGATCTCATGTTAAGTGAGAAAGGTTTTCAGAACTG      | 2400 |
| D | 2341 | CTAATATGCTGAAGACCCCAAGATCTCATGTTAAGTGAGAAAGGTTTTCAGAACTG      | 2400 |
| O | 2401 | AAAGATCTGTAGAGATGACGATTTTCAATGTGACCTGTACTGATTTATGCACTCAG      | 2460 |
| D | 2401 | AAAGATCTGTAGAGATGACGATTTTCAATGTGACCTGTACTGATTTATGCACTCAG      | 2460 |
| O | 2461 | AAAGATCTGTACTGGAAGTTAGCACTCAGGAGAAAGCAAAAACAGAACCAATTAAT      | 2520 |
| D | 2461 | AAAGATCTGTACTGGAAGTTAGCACTCAGGAGAAAGCAAAAACAGAACCAATTAAT      | 2520 |
| O | 2521 | GTGTAGTCACTGTGACGACATTTGAAAAACCCCAAGGACATTAATCACTGTTGTTCCAA   | 2580 |
| D | 2521 | GTGTAGTCACTGTGACGACATTTGAAAAACCCCAAGGACATTAATCACTGTTGTTCCAA   | 2580 |
| O | 2581 | ATAATAGAAATGACACAGAAAGGCTTTAAGTATCATTTGGGACATGAAGTTAACACAGTC  | 2640 |
| D | 2581 | ATAATAGAAATGACACAGAAAGGCTTTAAGTATCATTTGGGACATGAAGTTAACACAGTC  | 2640 |
| O | 2641 | GAGAAACAGACATGGAATGGAAGAAAGTGAATCTGATGCTCAGTATTTGCAAGATACAT   | 2700 |
| D | 2641 | GAGAAACAGACATGGAATGGAAGAAAGTGAATCTGATGCTCAGTATTTGCAAGATACAT   | 2700 |
| O | 2701 | TCAAGGTTTCAAGGCGCAGTCAATTTCTGTTTTCATATCCAGAGAAATGACAGAGAG     | 2760 |
| D | 2701 | TCAAGGTTTCAAGGCGCAGTCAATTTCTGTTTTCATATCCAGAGAAATGACAGAGAG     | 2760 |
| O | 2761 | AATGTGCAACATTTCTGTGCCACTCTGTGGTCTTTAAAGAAACAAAGTCCAAAAGTCACTT | 2820 |
| D | 2761 | AATGTGCAACATTTCTGTGCCACTCTGTGGTCTTTAAAGAAACAAAGTCCAAAAGTCACTT | 2820 |
| O | 2821 | TTGATGTGAACAAAGAGAAAGAAATGCAAGAAAGATGCTATATCAAGCCCTGATC       | 2880 |
| D | 2821 | TTGATGTGAACAAAGAGAGAAAGAAATGCAAGAAAGATGCTATATCAAGCCCTGATC     | 2880 |
| O | 2881 | AGACATTAATATCACTGACAGGCTTCTGTGGTGTGTCAGAAAGATTAAGCCAGTTGATA   | 2940 |
| D | 2881 | AGACATTAATATCACTGACAGGCTTCTGTGGTGTGTCAGAAAGATTAAGCCAGTTGATA   | 2940 |
| O | 2941 | ATGCCAATGTATGATCAAGAGAGGCTTGAAGTTTGTCTATCATCTCAGTTCAAGGCA     | 3000 |
| D | 2941 | ATGCCAATGTATGATCAAGAGAGGCTTGAAGTTTGTCTATCATCTCAGTTCAAGGCA     | 3000 |
| O | 3001 | ACGAAACCTGACATTAATCTCCAAATTAACATGACCTTTTACAAAACCATATCGTATAC   | 3060 |
| D | 3001 | ACGAAACCTGACATTAATCTCCAAATTAACATGACCTTTTACAAAACCATATCGTATAC   | 3060 |
| O | 3061 | CACCACTTTTCCCATCAAGTCAATTTGTAAATCTAATGTAAGAAAAATCTGTAGAG      | 3120 |
| D | 3061 | CACCACTTTTCCCATCAAGTCAATTTGTAAATCTAATGTAAGAAAAATCTGTGTAGAG    | 3120 |
| O | 3121 | AAAACTTTGAGGAACATTCATGTCACCTGAAGAGAAATGAGAAATGAGAACATTTCCA    | 3180 |
| D | 3121 | AAAACTTTGAGGAACATTCATGTCACCTGAAGAGAAATGAGAAATGAGAACATTTCCA    | 3180 |
| O | 3181 | GTAACAGTGAAGCAATTAAGCCGTAATTAACATTAAGAAAAATGTTTAAAGAACGACGT   | 3240 |
| D | 3181 | GTAACAGTGAAGCAATTAAGCCGTAATTAACATTAAGAAAAATGTTTAAAGAACGACGT   | 3240 |
| O | 3241 | CAAGCAATTAATTAAGATGAGTTCAGTACTATATGAAGGGCTCCAGTATTAATGAAA     | 3300 |
| D | 3241 | CAAGCAATTAATTAAGATGAGTTCAGTACTATATGAAGGGCTCCAGTATTAATGAAA     | 3300 |
| O | 3301 | TAGGTTCACTGATGAAGAACTTCAGACAGAACTAGGTGAAAACAGAGGCCAAAATTGA    | 3360 |
| D | 3301 | TAGGTTCACTGATGAAGAACTTCAGACAGAACTAGGTGAAAACAGAGGCCAAAATTGA    | 3360 |
| O | 3361 | ATGCTATGCTTAGATTAAGGGGTTTTCGCAACTGAGGTCTATTAACAAAGTCTTCTGGA   | 3420 |
| D | 3361 | ATGCTATGCTTAGATTAAGGGGTTTTCGCAACTGAGGTCTATTAACAAAGTCTTCTGGA   | 3420 |
| O | 3421 | GTAATGTGAAGCATCTGAAATTAAGAAAGCAAGAAATTAAGAAAGTACTGACCTGTTA    | 3480 |
| D | 3421 | GTAATGTGAAGCATCTGAAATTAAGAAAGCAAGAAATTAAGAAAGTACTGACCTGTTA    | 3480 |
| O | 3481 | ATAACATTTCTGCAATATCTGATTTGATTTGATTAACACTGAGGCTTGGGAAGTACTG    | 3540 |
| D | 3481 | ATAACATTTCTGCAATATCTGATTTGATTTGATTAACACTGAGGCTTGGGAAGTACTG    | 3540 |
| O | 3541 | ATGCATCTCAGGTTTGTTCAGACACCTGATGACCTGTAGATAGTGAATAAAG          | 3600 |
| D | 3541 | ATGCATCTCAGGTTTGTTCAGACACCTGATGACCTGTAGATAGTGAATAAAG          | 3600 |
| O | 3601 | AAAGTACTAGTTTGTCTGAAAAATGACATTAAGAAAGTCTGCTGTTTGAAGAAAGCG     | 3660 |
| D | 3601 | AAAGTACTAGTTTGTCTGAAAAATGACATTAAGAAAGTCTGCTGTTTGAAGAAAGCG     | 3660 |
| O | 3661 | TCCAGAAAGAGAGCTTACAGAGAGCTCAGGCTTTACCCATACATTTGCTCAG          | 3720 |
| D | 3661 | TCCAGAAAGAGAGCTTACAGAGAGCTCAGGCTTTACCCATACATTTGCTCAG          | 3720 |
| O | 3721 | GTTACGAAAGAGGGGCCAAGAAATTAAGTCTCAGAGAGAACTTATCTAGTGAGATG      | 3780 |
| D | 3721 | GTTACGAAAGAGGGGCCAAGAAATTAAGTCTCAGAGAGAACTTATCTAGTGAGATG      | 3780 |
| O | 3781 | AAAGCTTCTCCTGCTTCCAAACTTGTATTTTGTAAAGTAAACAAATATACCTTCTCAGT   | 3840 |
| D | 3781 | AAAGCTTCTCCTGCTTCCAAACTTGTATTTTGTAAAGTAAACAAATATACCTTCTCAGT   | 3840 |
| O | 3841 | CTACTAGGCAATGACACCGTTGCTACCGAGTGTCTGTAAAGAACCAAGAGAAATTAAT    | 3900 |
| D | 3841 | CTACTAGGCAATGACACCGTTGCTACCGAGTGTCTGTAAAGAACCAAGAGAAATTAAT    | 3900 |
| O | 3901 | TATCATTTGAAGAAATAGCTTAATTAAGTGAAGTGAACAGTAAATTAATGCAAGGATCTC  | 3960 |
| D | 3901 | TATCATTTGAAGAAATAGCTTAATTAAGTGAAGTGAACAGTAAATTAATGCAAGGATCTC  | 3960 |
| O | 3961 | AGGAAATCACTTATGAGAGAAACAAATGTTCTGATAGTGTGTTTCTTCAACAGTCA      | 4020 |
| D | 3961 | AGGAAATCACTTATGAGAGAAACAAATGTTCTGATAGTGTGTTTCTTCAACAGTCA      | 4020 |
| O | 4021 | GTAATTTGGAAGCTTGAATCAATTAACAAACCCAGAGATCTTTCTTGAATGGTCTT      | 4080 |
| D | 4021 | GTAATTTGGAAGCTTGAATCAATTAACAAACCCAGAGATCTTTCTTGAATGGTCTT      | 4080 |
| O | 4081 | CCAAACAAATGAGGCACTGCTGAAAGCAGGAGGTTGTCTGATGACAAAGAAATGG       | 4140 |
| D | 4081 | CCAAACAAATGAGGCACTGCTGAAAGCAGGAGGTTGTCTGATGACAAAGAAATGG       | 4140 |
| O | 4141 | TTTCAGATGATGAAGAAAGAGAAAGGCTTGAAGAAATTAATCAAGAGCAAAAGCA       | 4200 |
| D | 4141 | TTTCAGATGATGAAGAAAGAGAAAGGCTTGAAGAAATTAATCAAGAGCAAAAGCA       | 4200 |
| O | 4201 | TGATATCA  |      |

|    |      |              |                |              |           |             |            |         |        |        |       |    |     |   |
|----|------|--------------|----------------|--------------|-----------|-------------|------------|---------|--------|--------|-------|----|-----|---|
| OY | 4441 | ACCTGCCAATTC | CAGAACAAAGGCAT | CAGAAAAAGCAT | TATTA     | CTTCACAGAAA | AGTA       | 4500    |        |        |       |    |     |   |
| Db | 4441 | ACCTGCCAATTC | CAGAACAAAGGCAT | CAGAAAAAGCAT | TATTA     | CTTCACAGAAA | AGTA       | 4500    |        |        |       |    |     |   |
| OY | 4501 | GTGAATACCC   | TATAAGCCAGAT   | CCAGAAAGC    | CTTTCG    | CTGACAA     | GTTTAGGTG  | 4560    |        |        |       |    |     |   |
| Db | 4501 | GTGAATACCC   | TATAAGCCAGAT   | CCAGAAAGC    | CTTTCG    | CTGACAA     | GTTTAGGTG  | 4560    |        |        |       |    |     |   |
| OY | 4561 | CAGATAGTTCT  | TAACCGTAA      | AAATTAAGAA   | CCGAGAGT  | GGTAAAG     | GCATCCCTCT | TAAT    |        |        |       |    |     |   |
| Db | 4561 | CAGATAGTTCT  | TAACCGTAA      | AAATTAAGAA   | CCGAGAGT  | GGTAAAG     | GCATCCCTCT | TAAT    |        |        |       |    |     |   |
| OY | 4621 | GCCCATCAT    | TAGATATAG      | TAGGTGCAT    | GCACAGT   | TGCTCTG     | GGAGTCTT   | CAGAA   | TAGAA  |        |       |    |     |   |
| Db | 4621 | GCCCATCAT    | TAGATATAG      | TAGGTGCAT    | GCACAGT   | TGCTCTG     | GGAGTCTT   | CAGAA   | TAGAA  |        |       |    |     |   |
| OY | 4681 | ACTACCCATCT  | CAAGAGAGCT     | CATTAAAG     | TTTGAT    | TGTGAGAG    | CAACAGCTG  | GAAG    |        |        |       |    |     |   |
| Db | 4681 | ACTACCCATCT  | CAAGAGAGCT     | CATTAAAG     | TTTGAT    | TGTGAGAG    | CAACAGCTG  | GAAG    |        |        |       |    |     |   |
| OY | 4741 | AGCTGGGCC    | CACACATTTGA    | GGAAAC       | CTTACTTCC | CAAGGCA     | MAATCTA    | AGGGAA  |        |        |       |    |     |   |
| Db | 4741 | AGCTGGGCC    | CACACATTTGA    | GGAAAC       | CTTACTTCC | CAAGGCA     | MAATCTA    | AGGGAA  |        |        |       |    |     |   |
| OY | 4801 | CCCCCTTAC    | CTGGAACTG      | GAATCAG      | CCCTTCT   | CTGATG      | AGCCCTGA   | ATCTAT  | CTCTG  |        |       |    |     |   |
| Db | 4801 | CCCCCTTAC    | CTGGAACTG      | GAATCAG      | CCCTTCT   | CTGATG      | AGCCCTGA   | ATCTAT  | CTCTG  |        |       |    |     |   |
| OY | 4861 | AAGACAGAG    | CCCCCAGAGT     | CAGTCTG      | TGTGGC    | ACATAC      | CATCTT     | CAACCT  | CTGAT  | TGA    |       |    |     |   |
| Db | 4861 | AAGACAGAG    | CCCCCAGAGT     | CAGTCTG      | TGTGGC    | ACATAC      | CATCTT     | CAACCT  | CTGAT  | TGA    |       |    |     |   |
| OY | 4921 | AAGTCCCCCA   | ATTGAAGT       | GGCAGAT      | CTGCC     | CAGATC      | CAAGCTG    | CTCTCAT | ACTAGT |        |       |    |     |   |
| Db | 4921 | AAGTCCCCCA   | ATTGAAGT       | GGCAGAT      | CTGCC     | CAGATC      | CAAGCTG    | CTCTCAT | ACTAGT |        |       |    |     |   |
| OY | 4981 | ATACTCTG     | GGATATAT       | ATGCAAT      | TGAAAG    | AAAGTGT     | GACGAGG    | AGCAAG  | CAAA   | TTTGAC |       |    |     |   |
| Db | 4981 | ATACTCTG     | GGATATAT       | ATGCAAT      | TGAAAG    | AAAGTGT     | GACGAGG    | AGCAAG  | CAAA   | TTTGAC |       |    |     |   |
| OY | 5041 | CTTCAACAG    | AAAGGTC        | CAACAA       | AAATGTC   | CAATG       | TGTGTG     | GGCTG   | AGCC   | CAGAG  |       |    |     |   |
| Db | 5041 | CTTCAACAG    | AAAGGTC        | CAACAA       | AAATGTC   | CAATG       | TGTGTG     | GGCTG   | AGCC   | CAGAG  |       |    |     |   |
| OY | 5101 | AATTATCT     | CGTGTAC        | AAGTTGG      | CCAGAAAA  | CACACAT     | CATCA      | CTTTA   | CTAAT  | CTAAT  | T     |    |     |   |
| Db | 5101 | AATTATCT     | CGTGTAC        | AAGTTGG      | CCAGAAAA  | CACACAT     | CATCA      | CTTTA   | CTAAT  | CTAAT  | T     |    |     |   |
| OY | 5161 | CTGAAGA      | ACATCTAT       | GTGTTA       | TGA       | AAACG       | ATGCTG     | AAATGT  | GTGTAA | GGG    | AC    |    |     |   |
| Db | 5161 | CTGAAGA      | ACATCTAT       | GTGTTA       | TGA       | AAACG       | ATGCTG     | AAATGT  | GTGTAA | GGG    | AC    |    |     |   |
| OY | 5221 | TGAAATAT     | TTTTCTAG       | AAATG        | GGGAG     | AAAAAT      | GGGTAG     | TAA     | AGCTA  | TTT    | CTGGG | TG | ACC |   |
| Db | 5221 | TGAAATAT     | TTTTCTAG       | AAATG        | GGGAG     | AAAAAT      | GGGTAG     | TAA     | AGCTA  | TTT    | CTGGG | TG | ACC |   |
| OY | 5281 | AGCTATT      | AAAGAA         | AAAAAT       | GTCTGA    | TGAG        | ATGAT      | TTTTGA  | CTC    | AGAG   | AG    | AT | GTG |   |
| Db | 5281 | AGCTATT      | AAAGAA         | AAAAAT       | GTCTGA    | TGAG        | ATGAT      | TTTTGA  | CTC    | AGAG   | AG    | AT | GTG |   |
| OY | 5341 | TCAATGA      | AAACCA         | CCAGGTC      | CAAGCC    | AGCAAG      | AAATCC     | CAAG    | CA     | AAAG   | ATCT  |    |     |   |
| Db | 5341 | TCAATGA      | AAACCA         | CCAGGTC      | CAAGCC    | AGCAAG      | AAATCC     | CAAG    | CA     | AAAG   | ATCT  |    |     |   |
| OY | 5401 | TCAGGGG      | CTAGAA         | ATCTG        | TGCTA     | TG          | GGCCCTT    | CACCA   | ATG    | CCCA   | CAT   | CA | CTG |   |
| Db | 5401 | TCAGGGG      | CTAGAA         | ATCTG        | TGCTA     | TG          | GGCCCTT    | CACCA   | ATG    | CCCA   | AT    | CA | CTG |   |
| OY | 5461 | AATGAT       | AGTAC          | AGCTGT       | GTGTG     | CTTCT       | GTGTG      | TGA     | AGAG   | CTT    | CAT   | CA | CTT | G |
| Db | 5461 | AATGAT       | AGTAC          | AGCTGT       | GTGTG     | CTTCT       | GTGTG      | TGA     | AGAG   | CTT    | CAT   | CA | CTT | G |

|    |      |  |      |
|----|------|--|------|
| QY | 5521 | GCACAGGTGTCCACCCCAATTGTGGTGTGTGACGCCAGATGCTTGACACAGAGACAAATGGCT  | 5580 |
| Db | 5521 | GCAACAGGTGTCCACCCCAATTGTGGTGTGTGACGCCAGATGCTTGACACAGAGACAAATGGCT | 5580 |
| QY | 5581 | TCCATGCAATTGGGCAGATGTGTAGGACACCTGTGTGTGACCCGAGAGTGGGTGTGGACA     | 5640 |
| Db | 5581 | TCCATGCAATTGGGCAGATGTGTAGGACACCTGTGTGTGACCCGAGAGTGGGTGTGGACA     | 5640 |
| QY | 5641 | GTGTAGCACTTACCAAGTCCAGAGAGTGCACACCTTACCTGATACCCCAAGTCCCCACA      | 5700 |
| Db | 5641 | GTGTAGCACTTACCAAGTCCAGAGAGTGCACACCTTACCTGATACCCCAAGTCCCCACA      | 5700 |
| QY | 5701 | GCCACTACTGA  | 5711 |
| Db | 5701 | GCCACTACTGA  | 5711 |

| XX | AAV46461   | standard; cDNA; 5711 BP.                            |
|----|--|---|
| XX | AAV46461;  |   |
| XX | 18-NOV-1998  | (first entry)                                       |
| XX | Human BRCA1 omi2 polymorphism #4 cDNA.                                   |   |
| XX | BRCA1; omi2; human; breast and ovarian cancer predisposing gene;         |   |
| KW | polymorphism; susceptibility; anti-oncogene; tumour suppressor;          |   |
| KW | chromosome 17q; ss.  |   |
| XX |  |   |
| OS | Homo sapiens.  |   |
| XX |  |   |
| FH | Key  | Location/Qualifiers                                 |
| FH | CDS  | 120..5711   |
| FT |  | /*tag= a  |
| FT |  | /product= "BRCA1 omi2 protein"                      |
| FT | variation  | 3232  |
| FT |  | /*tag= b  |
| FT |  | /note= "This polymorphic variation can be an A or G |
| FT |  | nucleotide"   |
| XX |  |   |
| PN | US5750400-A.   |   |
| XX |  |   |
| PD | 12-MAY-1998.   |   |
| XX |  |   |
| PE | 12-FEB-1997;   | 97US-0798691.                                       |
| XX |  |   |
| PR | 12-FEB-1996;   | 96US-0598591.                                       |
| XX | 12-FEB-1997;   | 97US-0798691.                                       |
| XX |  |   |
| PA | (ONCO-) ONCORMED INC.  |   |
| XX |  |   |
| PI | Allen AC, Alvares CP, Critz BS, Murphy PD, Olson SJ;                     |   |
| PI | Schelter DB, Zeng B;   |   |
| XX |  |   |
| DR | WPI; 1998-296774/26.   |   |
| XX |  |   |
| PT | BRCA1 omi gene coding sequences - useful for distinguishing between      |   |
| PT | polymorphisms and mutation(s) in the screening for disposition to        |   |
| PT | breast or ovarian cancer   |   |
| XX |  |   |
| PS | Claim 2e; Page -; 54pp; English.   |   |
| XX |  |   |
| CC | This sequence encodes a human BRCA1 (breast and ovarian cancer           |   |
| CC | predisposing gene) omi2 gene in which a polymorphic variation occurs at  |   |
| CC | nucleotide 3332. This sequence and other polymorphic variations of this  |   |
| CC | sequence are useful for the identification of an individual who may or   |   |
| CC | may not have an increased susceptibility to breast or ovarian cancer.    |   |
| CC | The sequences used identify gene changes which are due to polymorphisms, |   |
| CC | rather than cancer causing mutations. BRCA1 is an anti-oncogene (tumour  |   |
| CC | suppressor) which is involved in genetic inheritance of cancers,         |   |
| CC | especially breast and ovarian cancer. It is found at human chromosome    |   |
| CC |  |   |



4261 ACTGCTCAGGGGTAATCTCTCAAGGTGACATTTTAACTCTACGCGAGGGAATACCATGCG 4320  
4321 AACATAACCTGATAAGGCTCCAGCAGGAAATGCTGAATCAGAACTGTGTGAAACAGC 4380  
4322 AACATAACCTGATAAGGCTCCAGCAGGAAATGCTGAATCAGAACTGTGTGAAACAGC 4380  
4381 ATGGAGGCCAGCCTTTCTAAGAGCTACCTTCCATCATAGTACTCTCTGCTGAGG 4440  
4381 ATGGAGGCCAGCCTTTCTAAGAGCTACCTTCCATCATAGTACTCTCTGCTGAGG 4440  
4441 ACCTGGGAATCCAGAACAGACATCAGAAAAGCAGATTTAACTTCAAGAAAAGT 4500  
4441 ACCTGGGAATCCAGAACAGACATCAGAAAAGCAGATTTAACTTCAAGAAAAGT 4500  
4501 GTGAATAACCTATAGGCGAGAAATCCAGAAAGCCTTTCTGCTGAACAATTGAGTGTCTG 4560  
4501 GTGAATAACCTATAGGCGAGAAATCCAGAAAGCCTTTCTGCTGAACAATTGAGTGTCTG 4560  
4561 CAGATAGTTTACCAAGTAAATAAAGAACAGAGTGGAAAGTCAATCCCTCTTAAAT 4620  
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4621 GCCCATCATTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4680  
4621 GCCCATCATTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4680  
4681 ACTACCATCTCAAGAGAGAGCTCATTAAGGTTGATGATGATGATGATGATGATGATGATGAT 4740  
4681 ACTACCATCTCAAGAGAGAGCTCATTAAGGTTGATGATGATGATGATGATGATGATGATGAT 4740  
4741 AGTGTGGGCCACAGATTTGACGAAACATCTTACTTCCAAAGGCAAGATCTGAGAGGA 4800  
4741 AGTGTGGGCCACAGATTTGACGAAACATCTTACTTCCAAAGGCAAGATCTGAGAGGA 4800  
4801 CCCCTTACCTGAGATCTGAGATGAGCTCTTCTGATGAGCCTGAACTGATCTTCTG 4860  
4801 CCCCTTACCTGAGATCTGAGATGAGCTCTTCTGATGAGCCTGAACTGATCTTCTG 4860  
4801 CCCCTTACCTGAGATCTGAGATGAGCTCTTCTGATGAGCCTGAACTGATCTTCTG 4860  
4861 AAGACAGAGGCCAGAGTCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4920  
4861 AAGACAGAGGCCAGAGTCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4920  
4921 AAGTCCCCCAATGAAAGTTCAGAAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4980  
4921 AAGTCCCCCAATGAAAGTTCAGAAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4980  
4981 ATACTGTGGGTATTAATGCAATGGAAGAGTGAAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAG 5040  
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5101 AATTATGCTG 5160  
5101 AATTATGCTG 5160  
5161 CTGAAGAGACTACTG 5220  
5161 CTGAAGAGACTACTG 5220  
5221 TGAATAATTTTCTAAGAAATGCGGAGAGAAATGGGATGATGATGATGATGATGATGATGATGATGATGATGATG 5280  
5221 TGAATAATTTTCTAAGAAATGCGGAGAGAAATGGGATGATGATGATGATGATGATGATGATGATGATGATGATG 5280  
5281 AGTCTATTAAAGAAAGAAATGCTGAATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5340  
5281 AGTCTATTAAAGAAAGAAATGCTGAATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5340  
5341 TCAATGGAAGAAACCAAGAGTCAAGAGGAG 5400  
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5461 AATG 5520  
5461 AATG 5520  
5521 GCACAGGTCCACCAATTTG 5580  
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5581 TCCATGCAATTTGGGAGATG 5640  
5581 TCCATGCAATTTGGGAGATG 5640  
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5641 GTGTAGCACTTACCAAGTCCAG 5700  
5701 GCCACTACTGA 5711  
5701 GCCACTACTGA 5711

RESULT 2  
US-08-798-691-1  
Sequence 1, Application US/08798691  
Patent No. 5750400  
GENERAL INFORMATION:  
APPLICANT: Murphy, Patricia D.  
APPLICANT: Allen, Antoinette C.  
APPLICANT: Alvares, Christopher P.  
APPLICANT: Critz, Brenda S.  
APPLICANT: Olson, Sheri J.  
APPLICANT: Schelter, Denise B.  
TITLE OF INVENTION: Coding Sequences of the Human  
NUMBER OF SEQUENCES: 72  
CORRESPONDENCE ADDRESS:  
ADDRESSER: ONCORMED  
STREET: 200 Perry Parkway  
CITY: Galtersberg  
STATE: MD  
COUNTRY: USA  
ZIP: 20877  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/798,691  
FILING DATE: 12-Feb-97  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Thomas Gallegos  
REGISTRATION NUMBER: 32,692  
REFERENCE/DOCKET NUMBER: PA-0054CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 301-527-2051  
TELEFAX: 301-208-6997  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5711 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
ORIGINAL SOURCE:



MAP POSITION: 17q21  
US-08-598-591-1

Query Match 100.0%; Score 5711; DB 1; Length 5711;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 5711; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTCGTGAAGTCTCTGACCCCGGACGAGGCTGGGTTCTCAGATTAATGGGCC 60  
DB 1 AGCTCGTGAAGTCTCTGACCCCGGACGAGGCTGGGTTCTCAGATTAATGGGCC 60  
QY 61 CCTGCGCTCAGAGAGCCCTTCACTCTGCTGGGTTAAAGTTCAATTGGAACAGAAAGAA 120  
DB 61 CCTGCGCTCAGAGAGCCCTTCACTCTGCTGGGTTAAAGTTCAATTGGAACAGAAAGAA 120  
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DB 121 TGAATTTATCTGCTCTTGGCGTTGAGAGAGTACAAAATGTCATTAATGCTATGAGAAA 180  
QY 181 TCTTAGAGTGTCCCATCTGTCTGAGAGTTCAGAGAACTGTCTCCAGAAAGTGAC 240  
DB 181 TCTTAGAGTGTCCCATCTGTCTGAGAGTTCAGAGAACTGTCTCCAGAAAGTGAC 240  
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DB 241 ACATATTTTGAATTTTGGATGCTGAAACTTCTCAACAGAGAAAGAGGCTTCAAGT 300  
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DB 301 GTCCCTTATGTATGAAGATGATATTAACAAAGAGGCTTCAAGAAAGTATGATGTC 360  
QY 361 AACTGTGTGAAGAGCTTTGAAATTCATTTGCTTTTCACTGAGTGAACAGTTTGAAGT 420  
DB 361 AACTGTGTGAAGAGCTTTGAAATTCATTTGCTTTTCACTGAGTGAACAGTTTGAAGT 420  
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DB 481 AAGTTTTCATATCTCAAAAGATGAGGCTTCAAGAAAGGCTTCAAGATG 540  
QY 541 AACCCGAAATTCCTTCTTGAAGAAACAGTCTCAAGTCCAACTCTCAACCTTGGA 600  
DB 541 AACCCGAAATTCCTTCTTGAAGAAACAGTCTCAAGTCCAACTCTCAACCTTGGA 600  
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DB 721 ATCAAGAAATGTTAACAATACCCCTCAAGGAACAGAGATGAATAGTTGGATCTG 780  
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QY 841 CCAAGTATATGATTTGAACACCACTGAGAAAGCTGAGAGGCTTCAAGAAAGT 900  
DB 841 CCAAGTATATGATTTGAACACCACTGAGAAAGCTGAGAGGCTTCAAGAAAGT 900  
QY 901 ATGAGGATGATTTCTGTTCAAACTTGAAGTGAAGGATGAGGCAATATGATGCA 960  
DB 901 ATGAGGATGATTTCTGTTCAAACTTGAAGTGAAGGATGAGGCAATATGATGCA 960  
QY 961 GCTCATTACAGCATGAGAAAGAGGATTTATTACTCACTAAAGACAGATGATGAGAA 1020  
DB 961 GCTCATTACAGCATGAGAAAGAGGATTTATTACTCACTAAAGACAGATGATGAGAA 1020

DB 961 GCTCATTACAGCATGAGAAAGAGGATTTATTACTCACTAAAGACAGATGATGAGAA 1020  
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DB 1021 AGGCTGAATTTCTGATTAATAAAGCAACAGCTTGGCTTGAAGAGGCAACATTAACAT 1080  
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DB 1141 ATCTGAATGCTGATTCCTCTGTGAGAGAAAGATGAATAGCAGAAATGCGATGCT 1200  
QY 1201 CAGAGAAATCTTAAGATCTGAAGATGTTCTTGGATTAACATTAATAGAGCTTGA 1260  
DB 1201 CAGAGAAATCTTAAGATCTGAAGATGTTCTTGGATTAACATTAATAGAGCTTGA 1260  
QY 1261 AAGTTAATGAGTGTCTTCCAGAAAGTATGAACCTGTTAGGTTCTGATGATCAGATGATG 1320  
DB 1261 AAGTTAATGAGTGTCTTCCAGAAAGTATGAACCTGTTAGGTTCTGATGATCAGATGATG 1320  
QY 1321 GGGAGTCTGAATCAAAATGCCAAAGTACCTGATGATGAGCGTTCAATAGGATAGT 1380  
DB 1321 GGGAGTCTGAATCAAAATGCCAAAGTACCTGATGATGAGCGTTCAATAGGATAGT 1380  
QY 1381 AATATTTGCTGTTCTTCAAGAAATATGATCTTACCTGAGTATCTCATGAGGCTTAA 1440  
DB 1381 AATATTTGCTGTTCTTCAAGAAATATGATCTTACCTGAGTATCTCATGAGGCTTAA 1440  
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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 12, 2003, 23:57:10 ; Search time 283 seconds  
(without alignments)  
6188.802 Million cell updates/sec

Title: US-09-734-672-1

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Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

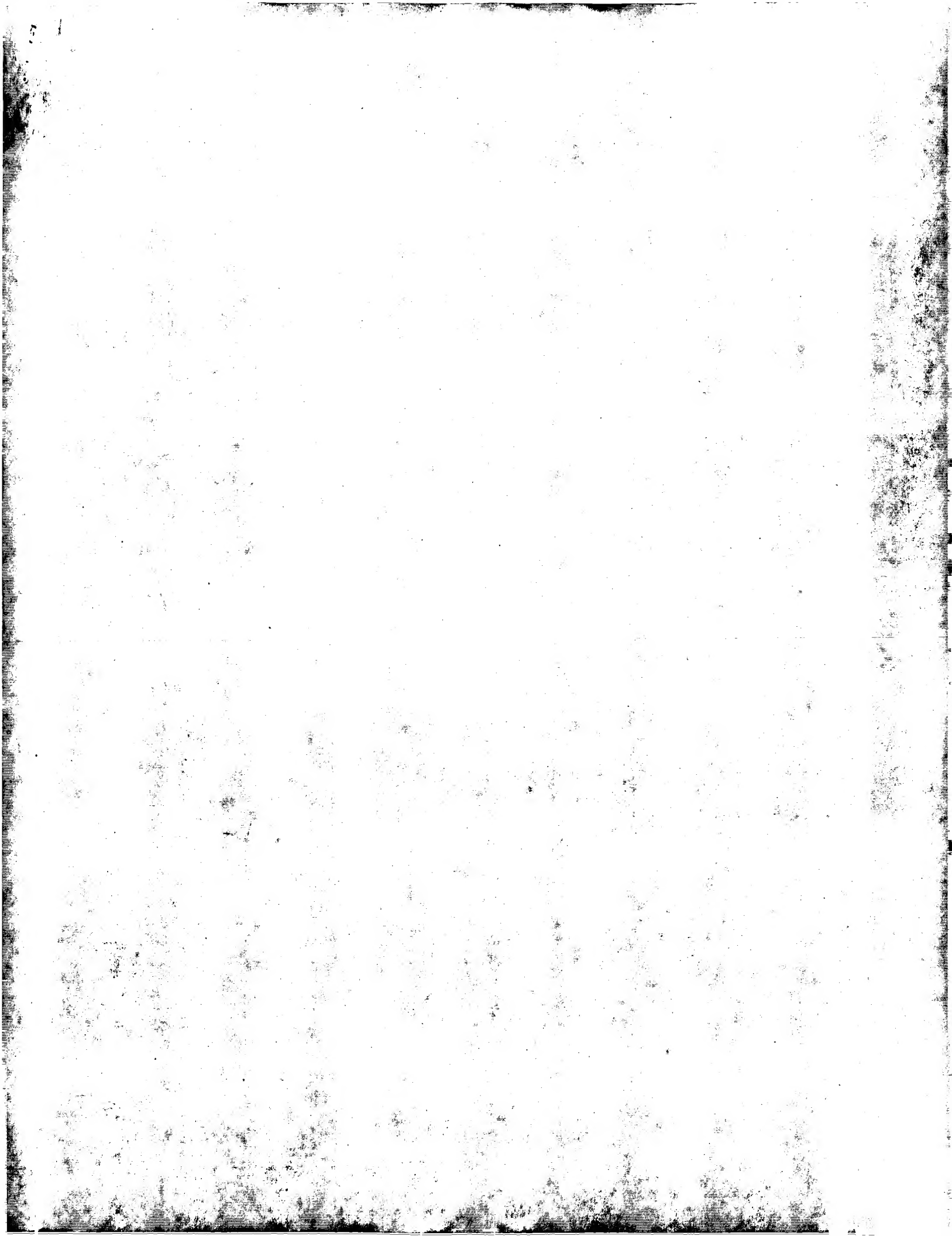
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# ALIGNMENTS

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Sequence 1, Application US/08598591  
Patent No. 5654155  
GENERAL INFORMATION:  
APPLICANT: Allen, Antoinette C.  
APPLICANT: Alvares, Christopher P.  
APPLICANT: Critz, Brenda S.  
APPLICANT: Murphy, Patricia D.  
APPLICANT: Olson, Sheri J.  
APPLICANT: Schelter, Denise B.  
APPLICANT: Zeng, Bin  
TITLE OF INVENTION: A Consensus Sequence of the Human BRCA1 Gene  
Patent No. 5654155  
NUMBER OF SEQUENCES: 74  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
STREET: 699 Prince St.  
CITY: Alexandria  
STATE: VA  
COUNTRY: USA  
ZIP: 22314  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/598,591  
FILING DATE: herewith  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Swecker, Robert S.  
REGISTRATION NUMBER: 19,885  
REFERENCE/DOCKET NUMBER: 020160-282  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-836-6620  
TELEFAX: 703-836-2021  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5711 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
STRAIN: BRCA1  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: 17



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 VERSION BG257190.1 GI:12767019  
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 SOURCE human.  
 ORGANISM Homo sapiens  
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 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 938)  
 NIH-MGC http://mgi.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgaabbs-r@mail.nih.gov  
 Tissue Procurement: ATCC  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed By: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
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 Note: this is a NIH\_MGC Library."

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 Job time : 6809 secs



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ACCESSION BF791668

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AUTHORS NIH-MGC http://mgs.nci.nih.gov/.
TITLES   National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL  Unpublished (1999)
COMMENT  Contact: Robert Strausberg, Ph.D.
          Email: cgabbs-r@mail.nih.gov
          Tissue Procurement: ATCC
          CDNA Library Preparation: Life Technologies, Inc.
          DNA Sequencing by: Incyte Genomics, Inc.
          Clone distribution: MGC clone distribution information can be
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| REFERENCE | Mammalia; Eutheria; Primates; Carnivori; Hominiidae; Homo.                                       |
| AUTHORS   | 1 (bases 1 to 739)   |
| TITLE     | NCI-CGAP <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> . |
| JOURNAL   | National Cancer Institute, Cancer Genome Anatomy Project (CGAP)                                  |
| COMMENT   | Tumor Gene Index   |
|           | Unpublished (1997)   |
|           | Contact: Robert Strausberg, Ph.D.  |

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 single-stranded DNA preparation of NCI CGAP Sub5 was used  
 as a tracer in a subtractive hybridization with a driver  
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 clone id: 2732833-2737415, 3068040-3065191), 25% of the  
 driver population), a pool of clones from NCI CGAP Sub4  
 (IMAGE clone ids 2735592-2729326: 25% of the driver  
 population), NCI CGAP Sub6 (pool Air-AU, IMAGE ids  
 2729699-2733190: 25% of the driver population), and  
 NCI CGAP Sub7 (IMAGE ids 3069192-3072238, 3081664-3084555  
 of the driver population). Subtraction was  
 performed as previously described (Bonaldo, Lennon &  
 Soares (1996): Normalization and Subtraction: Two  
 Approaches To Facilitate Gene Discovery. Genome Research  
 7, 991-806.

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|------------|--------------|---------|-------|----------|
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| Query Match               | 12.0% | Score 686.6;        | DB 12;    | Length 739; |
| Best Local Similarity     | 99.1% | Pred. No. 4.9e-151; |           |             |
| Matches 689; Conservative | 0;    | Mismatches 6;       | Indels 0; | Gaps 0;     |

|    |      |   |      |
|----|------|---|------|
| Qy | 1386 | TCTGTTTCTTCAGAGAAAATAGACTTACGTGCGCAGTGAATCCCTCAGAGCCTTAATATGT | 1445 |
| Db | 698  | TCTGTTCCNTCAGAGAAAATAGACTATCTGCGCAGTGAATCCCTCAGAGCCTTAATATGT  | 639  |
| Qy | 1446 | AAAAGTGAAGAGTTCACCTCCCAATCAGTAGAGAGTAATATTGAAGACAAATATTGGG    | 1505 |
| Db | 638  | AAAAGTGAAGAGTTCACCTCCCAATCAGTAGAGAGTAATATTGAAGACAAATATTGGG    | 579  |
| Qy | 1506 | AAAACTATCGGAGAGAGCAAGCCTCCCAACTTAAGCGATGTAACTGAATACTTAAT      | 1565 |
| Db | 578  | AAAACTATCGGAGAGAGCAAGCCTCCCAACTTAAGCGATGTAACTGAATACTTAAT      | 519  |
| Qy | 1566 | ATAGAGAGATTTGTACTGAGCGCACAGATAATACAAAGCGTCCCTCACAATTAATA      | 1622 |
| Db | 518  | ATAGAGAGATTTGTACTGAGCGCACAGATAATACAAAGCGTCCCTCACAATTAATA      | 459  |
| Qy | 1626 | AAGCGTAAAAAGAGACTTACATCAGAGCCTTCATCCTGAGATTTTATCAGAGAAACAGAT  | 1685 |
| Db | 458  | AAGCGTAAAAAGAGACTTACATCAGAGCCTTCATCCTGAGATTTTATCAGAGAAACAGAT  | 399  |
| Qy | 1686 | TTGGCAGTTCMAAAGACTCTCGAATATGAATATCGGGACCTAACCAACGAGCGAGAT     | 1743 |
| Db | 398  | TTGGCAGTTCMAAAGACTCTCGAATATGAATATCGGGACCTAACCAACGAGCGAGAT     | 339  |

|    |      |   |      |
|----|------|---|------|
| Qy | 1446 | GGTCAAGTATGAAATATTACTAATAGTGGTCATGAGAAATAAACAAAAGGTATTCATT      | 1805 |
| Db | 338  | GGTCAAGTATGAAATATTACTAATAGTGGTCATGAGAAATAAACAAAAGGTATTCATT      | 279  |
| Qy | 1806 | CAGAAATGAGAAAAATCCTTAACCCAAATGAATCACTCGAAAAAGAAATTCGTTTCAAAACG  | 1865 |
| Db | 278  | CAGAAATGAGAAAAATCCTTAACCCAAATGAATCACTCGAAAAAGAAATTCGTTTCAAAACG  | 219  |
| Qy | 1866 | AAAGCTGAACCTATAGCAGCAGTATAGCAATATGAACTCGAATTTAAATATCCACAAT      | 1925 |
| Db | 218  | AAAGCTGAACCTATAGCAGCAGTATAGCAATATGAACTCGAATTTAAATATCCACAAT      | 159  |
| Qy | 1926 | TCAAAAGCACCCTAAAAAGAAATAGGCTGAGAGAGAAAGTCTTCTACACGACATATTCATGCG | 1985 |
| Db | 158  | TCAAAAGCACCCTAAAAAGAAATAGGCTGAGAGAGAAAGTCTTCTACACGACATATTCATGCG | 99   |
| Qy | 1986 | CTTGAACCTAGTACGTAGAAATCTTAAGGCCACCTAATTTGTACTGAATTGGCAAAATTGAT  | 2045 |
| Db | 98   | CTTGAACCTAGTACGTAGAAATCTTAAGGCCACCTAATTTGTACTGAATTGGCAAAATTGAT  | 39   |
| Qy | 2046 | AGTTGTTCTAGCAGTGAAGATTAAGAAAAAAA 2080                           |      |
| Db | 38   | AGTTGTTCTAGCAGTGAAGATTAAGAAAAAAA 4                              |      |

|            |  |
|------------|--|
| RESULT     | 13   |
| BM800251   |  |
| LOCUS      | 987 bp mRNA linear EST 05-MAR-2002   |
| DEFINITION | AJ6800251 ACENOCOURT 6415998 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:5511286<br>5' , mRNA sequence. |

|           |              |             |
|-----------|--------------|-------------|
| ACCESSION | EM800251     | GI:19117074 |
| VERSION   | EM800251.1   |             |
| KEYWORDS  | EST.         |             |
| SOURCE    | human.       |             |
| ORGANISM  | Homo sapiens |             |

|           |  |
|-----------|--|
| REFERENCE |  |
| AUTHORS   |  |
| TITLE     |  |
| JOURNAL   |  |
| COMMENT   |  |
|           | <p>NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a>.<br/> National Institutes of Health, Mammalian Gene Collection (MGC)<br/> Unpublished (1999)<br/> Contact: Robert Strausberg, Ph.D.</p> |

Email: c9apbs-r@mail.nih.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINTL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LINTL at:  
<http://image.llnl.gov>  
plate: LLAMA2212 row: 1 column: 07  
High quality sequence stop: 692.

| FEATURES            | SOURCE  | LOCATION/QUALITY  |
|---------------------|---------|---|
| 1.                  | 987     | /organism="Homo sapiens"  |
|                     |         | /db_xref="taxon:9606"   |
|                     |         | /clone="IMAGE:5531286"  |
|                     |         | /clone_1b="NH MGC 71"   |
|                     |         | /tissue_type="leiomysarcoma"  |
|                     |         | /lab_host="DH10B (phage-resistant)"   |
|                     |         | /note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. |
| Average insert size | 2.1 kb. | "   |
| BASE COUNT          | 342 a   | 181 c 222 g 238 t 4 others  |
| ORIGIN              |         |   |

Query Match 12.0%; Score 686.4; DB 14; Length 987;  
 Best Local Similarity 85.8%; Pred. No. 6,1e-151;  
 Matches 87; Conservative 14; Indels 131; Gaps 5;

398 TCAGCTTGACACAGGTTTGAGTATGCAACAGCTTAATTTTGCAAAAAAGGAATAA 457

398 TCAGCTGACACAGGTTTGAGTATGCAACAGCTATAATTTTGCAGAAAAAGAAATAA 457

```

Db      301 TGAACAGAGGCTCTGAGAGCTGCTCAGGGCTATCCCTCAGAGTGACATTTTAACAC 360
Qy      4301 TCACAGAGGATACCTGACACATTAACCTGATTAAGCTCCAGAGAGAAATGGCTAGCT 4360
Db      361 TCACAGAGGATACCTGACACATTAACCTGATTAAGCTCCAGAGAGAAATGGCTAGCT 420
Qy      4361 AGAGCTGTGTAAACAGCATGGAGCCAGCTTCAACAGCTACCTCCATCATTAAG 4420
Db      421 AGAGCTGTGTAAACAGCATGGAGCCAGCTTCAACAGCTACCTCCATCATTAAG 480
Qy      4421 TGACTCTTCTGCTCCCTTGAAGACCTGCGAAATCCAGAAACAAAGCAGATCAGAAAAGAGT 4480
Db      481 TGACTCTTCTGCTCCCTTGAAGACCTGCGAAATCCAGAAACAAAGCAGATCAGAAAAGAGT 540
Qy      4481 ATTAACTTCACAGAAAAGTGTGAATACCTATTAAGCCAGATCCAGAGGCTTTCTGC 4540
Db      541 ATTAACTTCACAGAAAAGTGTGAATACCTATTAAGCCAGATCCAGAGGCTTTCTGC 600
Qy      4541 TGACAAGTTGAGGTGTCTGCAGATAGTTCTACAGATTAATAAGACAGAGAGTGA 4600
Db      601 TGACAAGTTGAGGTGTCTGCAGATAGTTCTACAGATTAATAAGACAGAGAGTGA 660
Qy      4601 AAGCTCATCCCTCTTAATGCCCCCATCATTAAGATGATAGTGG 4643
Db      661 AANNCAT-CCCTCTTAATGCCATCATTAAGATGATAGTGG 702

```

RESULT 11  
Bg777447 747 bp mRNA linear EST 15-MAY-2001  
LOCUS 602664758P1 NIH\_MGC\_60 Homo sapiens cDNA clone IMAGE:4804551 5',

DEFINITION mRNA sequence.  
Bg777447.1 GI:14047764

ACCESSION Bg777447  
VERSION Bg777447.1  
KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 747)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgabbs-remail.nih.gov  
Tissue Procurement: DCTD/DRP  
CDNA Library Preparation: CLONETECH Laboratories, Inc.  
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.lnl.gov

Plate: LCM1651 row: c column: 16  
High quality sequence stop: 725.

FEATURES  
Location/Qualifiers

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1..747
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4804551"
/clone_id="NIH MGC 60"
/tissue_type="adenocarcinoma"
/lab_host="DH10B (TI phage-resistant)"
/note="Organ: prostate; Vector: pDNR-LIB (Clontech);
Site_1: SfiI (ggcgccctgggc); Site_2: SfiI (ggcgatcaggcc
); Double-stranded cDNA was prepared from cell line RNA.
5' and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CACGGCATTAGGCC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGCGGAGCGCGGCGGAGG-3' (30)BN-3'
(where B = A, C, or G and N = A, C, G, or T). Average
insert size 1.5 kb (range 0.9-4.0 kb). 14/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech

```

Laboratories (Palo Alto, CA). Note: this is a NIH\_MGC  
Library."

Query Match 12.0%; Score 687.6; DB 12; Length 747;  
Best Local Similarity 97.7%; Pred. No. 2,9e-151;  
Matches 729; Conservative 0; Mismatches 14; Indels 3; Gaps 3;

```

BASE COUNT      232 a      160 c      162 g      193 t
ORIGIN
1 AGTCGCTGAGACTTCTTGAGACCCGACCCAGGCTGTGGGCTTCTCAGATACTGGCC 60
3 AGCTCCCTGAGACTTCTTGAGACCCGAGGGA-CAGCTGTGGGGTTCCTCAGATACTGGCC 61
61 CCGGCGCTCAGAGAGGCTTCACTGCTGCTGGGGAAGTTCATTTGGAACAGAGAGAA 120
62 CCGGCGCTCAGAGAGGCTTCACTGCTGCTGGGGAAGTTCATTTGGAACAGAGAGAA 121
121 TGGATTATCTGCTCTTGGCGTTGAAGAGTACAAATGTCAATTAATGCTATGCAAGAA 180
122 TGGATTATCTGCTCTTGGCGTTGAAGAGTACAAATGTCAATTAATGCTATGCAAGAA 181
181 TCTTAAGTGTCCCATCTGTCTGGAAGTATCAAGAACCTGTCTCAGAAAGTGGACC 240
182 TCTTAAGTGTCCCATCTGTCTGGAAGTATCAAGAACCTGTCTCAGAAAGTGGACC 241
241 ACATATTTTGCAAAATTTTGAGTCTGAACCTTCAACAGAGAGAGAGGCTTCAAGT 300
242 ACATATTTTGCAAAATTTTGAGTCTGAACCTTCAACAGAGAGAGAGGCTTCAAGT 301
301 GTCCCTTATGTAAGATATATATACCAAGAGGCTTCAAGAGAGATTTAGTC 360
302 GTCCCTTATGTAAGATATATATACCAAGAGGCTTCAAGAGAGATTTAGTC 361
361 AACTTGTGAAGAGCTATTGAA-AATCATTTGTGCTTTTCAAGCTTACACAGTTTGGAG 419
362 AACTTGTGAAGAGCTATTGAA-AATCATTTGTGCTTTTCAAGCTTACACAGTTTGGAG 421
420 TATGCAACAGCTATATTTTGGCAAAAAGAAATTAACCTCTGCAACATCTAAAGAT 479
422 TATGCAACAGCTATATTTTGGCAAAAAGAAATTAACCTCTGCAACATCTAAAGAT 481
480 GAAGTTTCTATCATCCAAAGTATGAGCTACAGAAACCGTCCAAAGAGCTTCTACAGAT 539
482 GAAGTTTCTATCATCCAAAGTATGAGCTACAGAAACCGTCCAAAGAGCTTCTACAGAT 541
540 GAACCCGAAAATCTCTTCTTGCAGAAACCAAGTCTAGTGTCAACTCTTAACTTTGGA 559
542 GAACCCGAAAATCTCTTCTTGCAGAAACCAAGTCTAGTGTCAACTCTTAACTTTGGA 601
600 ACTGTGAGAACTCTGAGCAAAAGAGCGGATTAACAACCTCAAAAGCGTCTGTCATT 659
602 ACTGTGAGAACTCTGAGCAAAAGAGCGGATTAACAACCTCAAAAGCGTCTGTCATT 661
660 GAATGGAGTCTGATCTTCTGGAAGTACCGTTAATTAAGCAACTTATTTGCACTGT- 718
662 GAATGGAGTCTGATCTTCTGGAAGTACCGTTAATTAAGCAACTTATTTGCACTGT- 719
719 AGATCAAGAAATGTTTCAAAATCAACC 744
722 AGATCAAGAAATGTTTCAAAATCAACC 747

```

RESULT 12

BF508987/c 739 bp mRNA linear EST 06-DEC-2000  
LOCUS UI-H-B1a-act-b-06-0-UI.s1 NCI CGAP\_Sub8 Homo sapiens cDNA clone  
IMAGE:3085787 3', mRNA sequence.

ACCESSION BF508987  
VERSION BF508987.1 GI:11592285  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/HLN at: <http://image.llnl.gov>  
 Plate: LHM13341 row: 0 column: 21  
 High quality sequence stop: 669.  
 Location/Qualifiers

## FEATURES

source

1..878  
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 /db\_xref="taxon:9606"  
 /clone="IMAGE:606516"  
 /clone\_1ib="NIH MGC 72"  
 /tissue\_type="melanotic melanoma"  
 /lab\_host="DH10B (phage-resistant)"  
 /note="Organ: skin; Vector: pCMV-SportS; Site\_1: NotI; Site\_2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 2 kb. Library constructed by Life Technologies."

BASE COUNT 261 a 180 c 190 g 227 t  
 ORIGIN

Query Match 12.4%; Score 706.2; DB 14; Length 878;  
 Best Local Similarity 98.8%; Pred. No. 1.2e-155;

Matches 754; Conservative 0; Mismatches 3; Indels 6; Gaps 4;

30 CAGGCTGGGGTTTCTCAGATTAAGTGGCCCTGGCTCAGAGGCTTACCTCTGC 89  
 13 CAGGCTGGGGTTTCTCAGATTAAGTGGCCCTGGCTCAGAGGCTTACCTCTGC 72  
 90 TCTGGTAAAGTTCATTTGAACAGAAAGAAATGATTTATCTCTTGGCGTTGAAGA 149  
 73 TCTGGTAAAGTTCATTTGAACAGAAAGAAATGATTTATCTCTTGGCGTTGAAGA 132  
 150 GTACAAAATGTCATTAATGCTATGAGAAATCTTGAAGTCCATCTGTCTGAGTTG 209  
 133 GTACAAAATGTCATTAATGCTATGAGAAATCTTGAAGTCCATCTGTCTGAGTTG 192  
 210 ATCAAGAACTGTCTCCACAAAGTGTGACCAATATTTTGCATTTGATGCTGAAA 269  
 193 ATCAAGAACTGTCTCCACAAAGTGTGACCAATATTTTGCATTTGATGCTGAAA 252  
 270 CTTCCACCCGAAAGAGGGCTTACAGTGTCTCTTATGTAAGATATATACCAA 329  
 253 CTTCCACCCGAAAGAGGGCTTACAGTGTCTCTTATGTAAGATATATACCAA 312  
 330 AGGAGCTTACAAAGAGTACGAGATTAGTCAACTGTGAGAGCTATTTGAAGATCAT 389  
 313 AGGAGCTTACAAAGAGTACGAGATTAGTCAACTGTGAGAGCTATTTGAAGATCAT 372  
 390 TGTGCTTTACGCTTGACACAGGTTTGAAGTATGCAACAGCTATATTTGCAAAAAG 449  
 373 TGTGCTTTACGCTTGACACAGGTTTGAAGTATGCAACAGCTATATTTGCAAAAAG 432  
 450 GAAATTAATCTCTCTGGAACATCTAAAGATGAAGTTTCTATCATCCAAAGTATGGCTAC 509  
 433 GAAATTAATCTCTCTGGAACATCTAAAGATGAAGTTTCTATCATCCAAAGTATGGCTAC 492  
 510 AGAAACCGGCAAAAGAGCTTCTACAGAGTGAACCCGAAATCTCTTGCAGAGAAAC 569  
 493 AGAAACCGGCAAAAGAGCTTCTACAGAGTGAACCCGAAATCTCTTGCAGAGAAAC 549  
 570 AGTCTCAAGTGTCAACCTCTTAACCTTGGAACCTGTGAGAACTCTGAGCAAAAGCAGG 629  
 550 AGTCTCAAGTGTCAACCTCTTAACCTTGGAACCTGTGAGAACTCTGAGCAAAAGCAGG 609  
 630 ATCAAACTCAAAAGAGCTCTGTCTACATTTGAATTTGGATCTGATTTCTTGAAGATACC 689  
 610 ATCAAACTCAAAAGAGCTCTGTCTACATTTGAATTTGGATCTGATTTCTTGAAGATACC 669  
 690 GTTATATAGGCAACTTATTTGAGT-GTGGAGATCAAGAAATGTTTAAATCAATCAATCAATCA 748  
 670 GTTATATAGGCAACTTATTTGAGTGTGGAGATCAAGAAATGTTTAAATCAATCAATCAATCA 729  
 749 AGGAACA-GGGATGAATCAG-TTGTGATCTGCAAAAAAG 789

DB 730 AGGACCAAGGAGTAAATCAGTTTGGATTTCTGCACAAAAAG 772

RESULT 10

AUI25312

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

AUI25312 702 bp mRNA linear EST 01-AUG-2002  
 AUI25312 NT2RM4 Homo sapiens CDNA clone NT2RM4001388 5', mRNA  
 sequence.  
 AUI25312  
 AUI25312.1 GI:10950028  
 EST.  
 human.  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 1 (bases 1 to 702)  
 Ota,T., Makamatsu,A., Ozawa,M., Ishii,S., Saio,K., Yamamoto,J.,  
 Nakamura,Y., Nishikawa,T., Nagai,T., Suzuki,Y., Sugano,S. and  
 Isogai,T.  
 HRI human CDNA project (Ota,T., Makamatsu,A., Ozawa,M., Ishii,S.,  
 Saio,K., Yamamoto,J., Nakamura,Y., Nishikawa,T., Nagai,T., Suzuki,  
 Y., Sugano,S., Isogai,T.)  
 Unpublished (2000)  
 Contact: Takao Isogai  
 Genomics Laboratory  
 Helix Research Institute  
 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan  
 Tel: 81-438-52-3875  
 Fax: 81-438-52-3886  
 Email: genomics@hri.co.jp  
 HRI human CDNA project, 5'- & 3'-end one pass sequencing: Helix  
 Research Institute; CDNA library construction: Department of  
 Virology, Institute of Medical Science, University of Tokyo, and  
 Helix Research Institute.

TITLE

JOURNAL

COMMENT

FEATURES

source

1..702  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="NT2RM4001388"  
 /clone\_1ib="NT2RM4"  
 /cell\_type="teratocarcinoma"  
 /cell\_line="NT2"  
 /note="Vector: pME18SF13; mRNA from uninduced NT2 neuronal  
 precursor cells"  
 BASE COUNT 235 a 142 c 163 g 159 t 3 others  
 ORIGIN

Query Match 12.0%; Score 688; DB 9; Length 702;  
 Best Local Similarity 99.4%; Pred. No. 2.2e-151;

Matches 699; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

3941 AATATTGGCAAGGATCTCAGAAACATCACCTTAGTGAAGAAACAAATGTTCTGTAG 4000  
 1 AATATTGGCAAGGATCTCAGAAACATCACCTTAGTGAAGAAACAAATGTTCTGTAG 60  
 4001 CTGTTTCTTCCACAGTCAAGTGAATTGGAAGATTTGAACTGCAATCAATCAATCAATCA 4060  
 61 CTGTTTCTTCCACAGTCAAGTGAATTGGAAGATTTGAACTGCAATCAATCAATCAATCA 120  
 4061 TCCCTTCTTGAATTTGGTTCTTCCAAACAAATGAGCATCAGTCTGAAAGCCAGGAGTTGG 4120  
 121 TCCCTTCTTGAATTTGGTTCTTCCAAACAAATGAGCATCAGTCTGAAAGCCAGGAGTTGG 180  
 4121 TCTGAGTGAAGAAATTTGTTTCAAGTATGAAAGAAAGAGAAACGGGCTTGAAGAAA 4180  
 181 TCTGAGTGAAGAAATTTGTTTCAAGTATGAAAGAAAGAGAAACGGGCTTGAAGAAA 240  
 4181 TAACTCAAGAAAGAAAGCATGATTTCAACTTATGTTGAAGCCAGCATCTGGGTGTAGAG 4240  
 241 TAACTCAAGAAAGAAAGCATGATTTCAACTTATGTTGAAGCCAGCATCTGGGTGTAGAG 300  
 4241 TGAACAAGCTCTCTGAGAGACTCTCAGGCTATCTCTCAGAGTGAATTTTAAACAC 4300

Db 541 CTTATTTGGGTGACCCAGCTCTATTAAAGAAAATCTGATAGCATGATTTTGA 600  
QY 5324 AGTCAGAGAGATGTGTCATAGAGAAAACCAAGGTCACAAAGCAGCAAGAGATC 5383  
Db 601 AGTCAGAGAGATGTGTCATAGAGAAAACCAAGGTCACAAAGCAGCAAGAGATC 660  
QY 5384 CCAGAGAGAAAATCTTCAGGGGGGCTAGAAATCTGTGTCATAGGGCCCTTCACCAAT 5443  
Db 661 CCAGAGAGAAAATCTTCAGGGGGGCTAGAAATCTGTGTCATAGGGCCCTTCACCAAT 720  
QY 5444 GCCCAGACATCACTGGAATG 5465  
Db 721 GCCCAGACATCACTGGAATG 742

RESULT 8  
BQ422380 899 bp mRNA linear EST 23-MAY-2002  
LOCUS AGENCOURT 7802085 NIH\_MGC\_92 Homo sapiens cDNA clone IMAGE:6042052  
DEFINITION 5', mRNA sequence.  
ACCESSION BQ422380.1 GI:21117695  
VERSION BQ422380  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 899)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapds-remail.nih.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.lnl.gov  
Plate: LLM13280 row: n column: 05  
High quality sequence stop: 597.  
Location/Qualifiers  
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/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:6042052"  
/clone\_lid="NIH MGC\_92"  
/tissue="embryonal carcinoma, cell line"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: testis; Vector: pCMV-Sport6; Site\_1: NotI;  
Site\_2: SalI; Cloned unidirectionally; oligo-dT primed.  
Average insert size 2.5 kb. Library enriched for  
full-length clones and constructed by Life Technologies.  
Note: this is a NIH MGC Library."

BASE COUNT 291 a 182 c 192 g 230 t 4 others  
ORIGIN

Query Match 12.9%; Score 734.6; DB 14; Length 899;  
Best Local Similarity 97.1%; Pred. No. 2.4e-162;  
Matches 824; Conservative 0; Mismatches 11; Indels 14; Gaps 7;

QY 30 CAGCGTGTGGGGTTTCACATACCTGCGCCCTCGCTCAGAGGCTTACCTCTGC 89  
Db 16 CAGCGTGTGGGGTTTCACATACCTGCGCCCTCGCTCAGAGGCTTACCTCTGC 75  
QY 90 TCTGGTAAAGTTCATTCAGAGAGAAAGAAATGATTTATGCTTCTCGGCTGAAGAA 149  
Db 76 TCTG-----GTTATTCAGAGAGAAAGAAATGATTTATGCTTCTCGGCTGAAGAA 129  
QY 150 GTACAAATGTCATTAATGCTATGACAGAAAATCTTAGAGTCTCCCATCTGCTGAGAGTTG 209

Db 130 GTACAAATGTCATTAATGCTATGACAGAAAATCTTAGAGTCTCCCATCTGCTGAGAGTTG 189  
QY 210 ATCAAGAACTCTCTCCCAAGAGTGTGACCAATATTTTGAAGATTTGACATGAGAA 269  
Db 190 ATCAAGAACTCTCTCCCAAGAGTGTGACCAATATTTTGAAGATTTGACATGAGAA 249  
QY 270 CTCTCAACAGAGAAAGAGGCTTCAAGTGTCTTTATGTGAATGATATATACCAA 329  
Db 250 CTCTCAACAGAGAAAGAGGCTTCAAGTGTCTTTATGTGAATGATATATACCAA 309  
QY 330 AGAGGCTTCAAGAGAAAGTACGAGATTAGTCAACTTTGAGAGCTATTGAATCATT 389  
Db 310 AGAGGCTTCAAGAGAAAGTACGAGATTAGTCAACTTTGAGAGCTATTGAATCATT 369  
QY 390 TGTGCTTTTCAAGTGTGACAGGTTGGAGTATGCAACGCTATATTTTGAAGAAAG 449  
Db 370 TGTGCTTTTCAAGTGTGACAGGTTGGAGTATGCAACGCTATATTTTGAAGAAAG 429  
QY 450 GAAATATACCTCTCTGACATCTTAAAGATGAAATTTCTATCTCAAGATATGGCTAC 509  
Db 430 GAAATATACCTCTCTGACATCTTAAAGATGAAATTTCTATCTCAAGATATGGCTAC 489  
QY 510 AGAACCCTGTCACAAAGACTTCTACAGAGTGAACCCGAAATCTTCTGACAGAAAC 569  
Db 490 AGAACCCTGTCACAAAGACTTCTACAGAGTGAACCCGAAATCTTCTGACAGAAAC 546  
QY 570 AGTCTAGTCTCCACTCTCTTACCTTGAACCTGTGAACTGTGAGCAAGCAAGCGG 629  
Db 547 AGTCTAGTCTCCACTCTCTTACCTTGAACCTGTGAACTGTGAGCAAGCAAGCGG 606  
QY 630 ATCAACCTTCAAGAGAGCTGTCTACATTTGAATTTGGATCTTCTGAGAGATAC 689  
Db 607 ATCAACCTTCAAGAGAGCTGTCTACATTTGAATTTGGATCTTCTGAGAGATAC 666  
QY 690 GTTAATAGGCACTTATTCAGTGTGGAGATCAAGATTTGACAAATCACCCTCAA 749  
Db 667 GTTAATAGGCACTTATTCAGTGTGGAGATCAAGATTTGACAAATCACCCTCAA 726  
QY 750 GGAACCA-GGAGTGAATACGTTGATTTCTGAAAAAGGCTGC-TTGGAATTTCTG 807  
Db 727 GGAACCAAGGAGTGAATACGTTGATTTCTGAAAAAGGCTGTGGAATTTCTG 786  
QY 808 AGACGATGTAAACA-ATACTGAACATC-ATCAACCAGTAAATATGA-TTGAACACCA 864  
Db 787 AGACGATGTGTAAANAATCTGAATCAATCAATCAACCAAGTAAATATGATTTGAACACCA 846  
QY 865 CTGAGAAAC 873  
Db 847 CTGAGAAAC 855

RESULT 9  
BQ215100 878 bp mRNA linear EST 02-MAY-2002  
LOCUS AGENCOURT 7591049 NIH\_MGC\_72 Homo sapiens cDNA clone IMAGE:605516  
DEFINITION 5', mRNA sequence.  
ACCESSION BQ215100  
VERSION BQ215100.1 GI:20396500  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 878)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapds-remail.nih.gov  
Tissue Procurement: ATCC/DCTP  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation

/cell\_type="retinoblastoma"  
/cell\_line="Y79"  
/note="Vector: PM18SFL3"  
BASE COUNT 255 a 146 c 185 g 194 t 3 others  
ORIGIN

Query Match 13.3%; Score 761.8; DB 9; Length 783;  
Best Local Similarity 99.2%; Pred. No. 8.8e-169;  
Matches 774; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 3579 TTAGATGATGCTGAATTAAGAGAGTACTAGTTTGTGGAATAATGACATTAGAGAACT 3638  
Db 1 TTAGATGATGCTGAATTAAGAGAGTACTAGTTTGTGGAATAATGACATTAGAGAACT 60

QY 3639 TCTGCTGTTTTCAGCAAAAGCGTCCAGAAAGAGAGAGTCTAGAGAGTCTTCTC 3698  
Db 61 TCTGCTGTTTTCAGCAAAAGCGTCCAGAAAGAGAGAGTCTAGAGAGTCTTCTC 120

QY 3699 ACCCTACACATTTGGCTCAGGTTACCGAAGAGGGGCCAAGAAATTAGAGTCTCAGAA 3758  
Db 121 ACCCTACACATTTGGCTCAGGTTACCGAAGAGGGGCCAAGAAATTAGAGTCTCAGAA 180

QY 3759 GAGAACTTATCTAGTGAAGAGTGAAGGCTTCCCTGCTCCACACTGTTATTTGTATA 3818  
Db 181 GAGAACTTATCTAGTGAAGAGTGAAGGCTTCCCTGCTCCACACTGTTATTTGTATA 240

QY 3819 GTAAACAATATCTCTCTCAGTCTACTAGAGTACGACCGTGTCTACCGAGTGTCTCT 3878  
Db 241 GTAAACAATATCTCTCTCAGTCTACTAGAGTACGACCGTGTCTACCGAGTGTCTCT 300

QY 3879 AAGAACACAGAGAGAGATTTATTCATTGAAAGATAGCTTAAATGACTGCTAGTAA 3938  
Db 301 AAGAACACAGAGAGAGATTTATTCATTGAAAGATAGCTTAAATGACTGCTAGTAA 360

QY 3939 GTAATATTTGGCAAGAGCATCTCAGAGACATCACTTAGAGAGAAACAAATGTTCTGT 3998  
Db 361 GTAATATTTGGCAAGAGCATCTCAGAGACATCACTTAGAGAGAAACAAATGTTCTGT 420

QY 3999 AGCTTGTCTTCTTCACAGTCAAGTGAATTTGAAGAATTGACTGCAATTAACAACCCAG 4058  
Db 421 AGCTTGTCTTCTTCACAGTCAAGTGAATTTGAAGAATTGACTGCAATTAACAACCCAG 480

QY 4059 GATCTTTCTTGTATGTTGTTCTTCCAAACAATGAGGCATCAGTCTGAAGCCAGGAGTT 4118  
Db 481 GATCTTTCTTGTATGTTGTTCTTCCAAACAATGAGGCATCAGTCTGAAGCCAGGAGTT 540

QY 4119 GGTGAGTGAACAAGAAATGTTGTTTCAGATGATGAAGAAAGAGAAAGCGGCTTGAAGAA 4178  
Db 541 GGTGAGTGAACAAGAAATGTTGTTTCAGATGATGAAGAAAGAGAAAGCGGCTTGAAGAA 600

QY 4179 AATATCAAGAAGAGCAAGATGATTCAACTTAGTGAAGAGCATCTGGTGTGAG 4238  
Db 601 AATATCAAGAAGAGCAAGATGATTCAACTTAGTGAAGAGCATCTGGTGTGAG 660

QY 4239 AGTGAACAAGCGTCTTGAAGAGTCTCAGGCTATCTCTCAAGTGAACATTTTAA-C 4297  
Db 661 AGTGAACAAGCGTCTTGAAGAGTCTCAGGCTATCTCTCAAGTGAACATTTTAA-C 720

QY 4298 CACTCAGAGAGGATACCATGCAACATTAACCTGATTAAGCTCCAGCAGAGAAATGGCTGA 4357  
Db 721 CACTCAGAGAGGATACCATGCAACATTAACCTGATTAAGCTCCAGCAGAGAAATGGCTGA 780

RESULT 7  
BG681276 743 bp mRNA linear EST 01-MAY-2001  
LOCUS BG681276  
DEFINITION 602627125F1 NCI\_CGAP\_Skin4 Homo sapiens cDNA clone IMAGE:475187 5',  
mRNA sequence.  
ACCESSION BG681276  
VERSION BG681276.1 GI:13912673  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
1 (bases 1 to 743)  
NIH-MGC <http://mgs.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: James Cleaver, M.D.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LUMI)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LUMI at:  
<http://image.llnl.gov>  
Plate: LUMI0609 row: a column: 08  
High quality sequence stop: 741.  
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/lab\_host="DH10B (T1 phage-resistant)"  
/note="Organ: skin; Vector: pCMV-SPORT6; Site: 1: NotI;  
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dr.  
Average insert size 1.5kb. Library constructed by Life  
Technologies. Note: this is a NCI\_CGAP Library."  
BASE COUNT 233 a 156 c 182 g 172 t  
ORIGIN

Query Match 13.0%; Score 740.4; DB 12; Length 743;  
Best Local Similarity 99.9%; Pred. No. 9.7e-164;  
Matches 741; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4724 GGAGCAACAGCTGGAAGAGTGGGCGCACAGATTTGACGGAACATCTTATGCGAAG 4783  
Db 1 GGAGCAACAGCTGGAAGAGTGGGCGCACAGATTTGACGGAACATCTTATGCGAAG 60

QY 4784 GCAAGATTAAGGGAACCCCTTACCTGGAATCTGGAATCAGCTCTTCTCTGATGACC 4843  
Db 61 GCAAGATTAAGGGAACCCCTTACCTGGAATCTGGAATCAGCTCTTCTCTGATGACC 120

QY 4844 TGAATCTGATCTCTTCTGGAAGCAGAGCCCGAGTCACTCGTTTGGCAACATACATC 4903  
Db 121 TGAATCTGATCTCTTCTGGAAGCAGAGCCCGAGTCACTCGTTTGGCAACATACATC 180

QY 4904 TTCAACCTCTGATTTGAAGATTCCCAATTGAAGTTGCAAGATCTGCCAGATCCAGC 4963  
Db 181 TTCAACCTCTGATTTGAAGATTCCCAATTGAAGTTGCAAGATCTGCCAGATCCAGC 240

QY 4964 TGTGCTCATATCTGATATCTGTGGTATATGCAATGGAAGAAAGTGTGACAGGA 5023  
Db 241 TGTGCTCATATCTGATATCTGTGGTATATGCAATGGAAGAAAGTGTGACAGGA 300

QY 5024 GAAGCGAATTTGACAGTTCACAGAAAGGTCACAAAGAATGTCATGGGAGTGC 5083  
Db 301 GAAGCGAATTTGACAGTTCACAGAAAGGTCACAAAGAATGTCATGGGAGTGC 360

QY 5084 TGGCCTGACCCAGAGAATTTATGCTGTGTAACAATTTGCCAGAAACACCAATCAC 5143  
Db 361 TGGCCTGACCCAGAGAATTTATGCTGTGTAACAATTTGCCAGAAACACCAATCAC 420

QY 5144 TTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 5203  
Db 421 TTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 480

QY 5204 TGTGTGGAACGGACATGAATATTTTTCAGAAATTGGCGGAGGAAATGGTACTTTG 5263  
Db 481 TGTGTGGAACGGACATGAATATTTTTCAGAAATTGGCGGAGGAAATGGTACTTTG 540

QY 5264 CTATTTCTGGGTGACCACTCTATTTAAAGAAATAATCTGAATGAGCATGATTTTGA 5323



QY 2879 ACAGACA 2885  
 Db 971 AACGAAA 977

RESULT 5  
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 LOCUS  
 DEFINITION AUI22476 MAMMAL Homo sapiens cDNA clone MAMMA1002447 5', mRNA  
 sequence.  
 ACCESSION AUI22476  
 VERSION AUI22476.1 GI:10937746  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 845)  
 Oca.T., Nishikawa.T., Suzuki.Y., Ishii.S., Saito.K., Kawai.Y.,  
 Yamamoto.J., Wakamatsu.A., Nakamura.Y., Nagai.T., Sugano.S. and  
 Isogai.T.  
 HRI human cDNA project  
 Unpublished (2000)  
 Contact: Takao Isogai  
 Genomics Laboratory  
 Helix Research Institute  
 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan  
 Tel: 81-438-52-3975  
 Fax: 81-438-52-3986  
 Email: genomics@hri.co.jp  
 HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix  
 Research Institute; cDNA library construction: Department of  
 Virology, Institute of Medical Science, University of Tokyo, and  
 Helix Research Institute.  
 Location/Qualifiers  
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BASE COUNT 279 a 172 c 191 g 200 t 3 others

ORIGIN

Query Match 14.2%; Score 811.8; DB 9; Length 845;  
 Best Local Similarity 99.1%; Pred. No. 1.4e-180;  
 Matches 836; Conservative 0; Mismatches 5; Indels 3; Gaps 2;

QY 3819 GTAAACAATTAACCTTCTCACTCTACAGGATGACACCGTGGTCTACCGAGTCTGTCT 3878  
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QY 3879 AAGAACAAGAGAGATTTATTTATTCATTGAGAAATAGCTTAATGACTGAGTAACAG 3938  
 Db 61 AAGAACAAGAGAGATTTATTTATTCATTGAGAAATAGCTTAATGACTGAGTAACAG 120

QY 3939 GTAATATTGGCAAGGATCTCAGGAACATCACTTATGAGAGAAACAAATGTTCTGCT 3998  
 Db 121 GTAATATTGGCAAGGATCTCAGGAACATCACTTATGAGAGAAACAAATGTTCTGCT 180

QY 3999 AGCTGTTTCTTACAGTGCAGGATTTGGAAGTGAAGTGAACAAATTAACCAACAG 4058  
 Db 181 AGCTGTTTCTTACAGTGCAGGATTTGGAAGTGAAGTGAACAAATTAACCAACAG 240

QY 4059 GATCCTTCTTGAATGTTCTTCCAAACAATGAGGATCAGTCTGAAGCGAGGAGTT 4118  
 Db 241 GATCCTTCTTGAATGTTCTTCCAAACAATGAGGATCAGTCTGAAGCGAGGAGTT 300

QY 4119 GGTCTGAGTGCAAGAAATGTTCTTCAAGTATGAAGAAAGGAGCGGCTTGAGAA 4178  
 Db 301 GGTCTGAGTGCAAGAAATGTTCTTCAAGTATGAAGAAAGGAGCGGCTTGAGAA 360

QY 4179 AATAATCAAGAAAGAGCAATGATTCNAATCTTAGTGAGACAGCATCTGGTGTGAG 4238  
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QY 4239 AGTGAACAAGCGCTCTCTGAGAGCTGCTCAGGGCTATCTCTCAGAGTGAATTTTACC 4298  
 Db 421 AGTGAACAAGCGCTCTCTGAGAGCTGCTCAGGGCTATCTCTCAGAGTGAATTTTACC 480

QY 4299 ACTCAGACAGAGGATATCCATGCAACTAATACCTGATTAAGTCCAGAGAGAAATGGCTGAA 4358  
 Db 481 ACTCAGACAGAGGATATCCATGCAACTAATACCTGATTAAGTCCAGAGAGAAATGGCTGAA 540

QY 4359 CTGAAAGCTGTGTTAGAACAGCATGGAGAGCGACCTTCTTAACAGTACCTTCATCATTA 4418  
 Db 541 CTGAAAGCTGTGTTAGAACAGCATGGAGAGCGACCTTCTTAACAGTACCTTCATCATTA 600

QY 4419 AGTGAAGCTGTGCTGCTTGAAGACCTGCGAATTCAGAAACAAAGCAATCAGAAAAAGCA 4478  
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QY 4479 GTATTAACTTCAAGAAAGATAGTGAATATCCCTTAAGCCAGAAATCCAGAAAGGCTTTCT 4538  
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QY 4539 GCTGACAGATTGAGGTGCTGAGATAGTCTTACCAAGTAAATTAAGAACACAGGA -G 4596  
 Db 721 GCTGACAGATTGAGGTGCTGAGATAGTCTTACCAAGTAAATTAAGAACACAGGAAGT 780

QY 4597 TGGAAAGGTCA-TCCCTCTTAAATGCCATCTTATGATGATAGTGTGATCATGACAGT 4655  
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QY 4656 TGCT 4659  
 Db 841 TGCT 844

RESULT 6  
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 LOCUS  
 DEFINITION AUI42729 Y79AA1 Homo sapiens cDNA clone Y79AA1000792 5', mRNA  
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 ACCESSION AUI42729  
 VERSION AUI42729.1 GI:11004250  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 783)  
 Oca.T., Nishikawa.T., Suzuki.Y., Ishii.S., Saito.K., Kawai.Y.,  
 Yamamoto.J., Wakamatsu.A., Nakamura.Y., Nagai.T., Sugano.S. and  
 Isogai.T.  
 HRI human cDNA project  
 Unpublished (2000)  
 Contact: Takao Isogai  
 Genomics Laboratory  
 Helix Research Institute  
 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan  
 Tel: 81-438-52-3975  
 Fax: 81-438-52-3986  
 Email: genomics@hri.co.jp  
 HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix  
 Research Institute; cDNA library construction: Department of  
 Virology, Institute of Medical Science, University of Tokyo, and  
 Helix Research Institute.  
 Location/Qualifiers  
 1..783  
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 /clone="Y79AA1000792"  
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 Db 4435 CCCAAGTCAGCTCGTGTGGCAACATACCTTCTCACTGTGATTGAAGTTCCCA 494  
 QY 4931 ATTGAAGTTGAGATCTGCCAGTCCAGTGTGCTGCTCAATACATGATCTCTGG 4990  
 Db 495 ATTGAAGTTGAGATCTGCCAGTCCAGTGTGCTGCTCAATACATGATCTCTGG 554  
 QY 4991 GTATATGCAATGAGAAAGTGTGAGCAGGAGAGAACCAATGACAGCTTCAACAG 5050  
 Db 555 TTATATGCAATGAGAAAGTGTGAGCAGGAGAGAACCAATGACAGCTTCAACAG 614  
 QY 5051 AAGGTCACAAAGAAATGTCATGTGTGTCTGCTGAGCCCGAAGAAATTAATGCT 5110  
 Db 615 AAGGTCACAAAGAAATGTCATGTGTGTCTGCTGAGCCCGAAGAAATTAATGCT 674  
 QY 5111 CGTGACAAAGTTGCGAGAAACACCACTCTTAATCTAATCTAATCTAATCTAATGAC 5170  
 Db 675 CGTGACAAAGTTGCGAGAAACACCACTCTTAATCTAATCTAATCTAATGAC 734  
 QY 5171 TACTCATGTTGTTATGAAACAGATGCTGATTTGTGTGAACGAGACATGAATATTT 5230  
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 Db 795 TCTAGCAATTCGCGAGAGAAATGGGTAGTATGCTATTTCTGGGTGACCCAGTCTATTA 854  
 QY 5291 AGAAGAAATGCTGATGACATGATTTTGAAGTCAGAGAGATGTGG--TCAATGGA 5348  
 Db 855 AGAAGAAATGCTGATGACATGATTTTGAAGTCAGAGAGATGTGGTCAATGGA 914  
 QY 5349 AGAAGAAATGCTGATGACATGATTTTGAAGTCAGAGAGATGTGGTCAATGGA 914  
 Db 915 AGAAGAAATGCTGATGACATGATTTTGAAGTCAGAGAGATGTGGTCAATGGA 939

RESULT 4  
 BM452288 1089 bp mRNA linear EST 05-FEB-2002  
 LOCUS AGENCOURT\_6386302 NIH\_MGC\_72 Homo sapiens cDNA clone IMAGE:5526666  
 DEFINITION 5', mRNA sequence.  
 ACCESSION BM452288  
 VERSION BM452288.1 GI:18501328  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 1089)  
 NIH-MGC http://mgi.nci.nih.gov/  
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
 TITLE Unpublished (1999)  
 JOURNAL Contact: Robert Strausberg, Ph.D.  
 Email: cga@bbs-rcmail.nih.gov  
 Tissue Procurement: ATCC/DC/DTP  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation (LLNL)  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: L14M12200 row: k column: 19  
 High quality sequence stop: 667.  
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 /tissue\_type="melanotic melanoma"  
 /lab\_host="DH10B (phage-resistant)"  
 /note="Organ: skin; Vector: pCMV-SPORT6; Site\_1: NotI;

BASE COUNT 389 a 212 c 248 g 240 t  
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 Query Match 14.8%; Score 844.6; DB 13; Length 1089;  
 Best Local Similarity 96.2%; Pred. No. 2.8e-188;  
 Matches 930; Conservative 0; Mismatches 29; Indels 8; Gaps 6;  
 Site\_2: SalI; Cloned unidirectionally. Primer: Oligo dT.  
 Average insert size 2 kb. Library constructed by Life  
 Technologies."  
 QY 1925 TTCAAAGACCTTAAGAAATAGGCTGAGAGAGAGCTTCTCCAGGCAATATTCATGC 1984  
 Db 13 TTCAAAGACCTTAAGAAATAGGCTGAGAGAGAGCTTCTCCAGGCAATATTCATGC 72  
 QY 1985 GCTTGAACCTAGTACAGTAAATCTAAGCCCACTAATTTGACTGAATTCAGAAATGA 2044  
 Db 73 GCTTGAACCTAGTACAGTAAATCTAAGCCCACTAATTTGACTGAATTCAGAAATGA 132  
 QY 2045 TAGTTGTTCTAGCACTGAGATTAAGAAAAAAGTACCAACCAATGCGAGTACGCA 2104  
 Db 133 TAGTTGTTCTAGCACTGAGATTAAGAAAAAAGTACCAACCAATGCGAGTACGCA 192  
 QY 2105 CAGCAGAAACCTCACTCAGTAAAGAGTAAAGAACTTGCAACCTGAGCCAGAGATTA 2164  
 Db 193 CAGCAGAAACCTCACTCAGTAAAGAGTAAAGAACTTGCAACCTGAGCCAGAGATTA 252  
 QY 2165 CAGCAGAAATGACAGACAGTAAAGACATGACAGCATCTTCCAGAGCTGAAGTT 2224  
 Db 253 CAGCAGAAATGACAGACAGTAAAGACATGACAGCATCTTCCAGAGCTGAAGTT 312  
 QY 2225 AACAAATGCACTGCTTTCTTTACTAAGTGTTCAAATACAGTGAACCTTAAGAAATTTGT 2284  
 Db 313 AACAAATGCACTGCTTTCTTTACTAAGTGTTCAAATACAGTGAACCTTAAGAAATTTGT 372  
 QY 2285 CAATCTTACCTTCCAAAGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGTCTAA 2344  
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 QY 2345 TAATGCTGAAGACCCCAAGATCTCATGTTAAGTGAAGAGGTTTGGCAACTGAAG 2404  
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 QY 2405 ATCTGTAGAGATGACAGTATTTCAATGTTGTACTGTTATGAGCACTGAGAAAG 2464  
 Db 493 ATCTGTAGAGATGACAGTATTTCAATGTTGTACTGTTATGAGCACTGAGAAAG 552  
 QY 2465 TATCTGCTTACTGGAAGTTAGCACTTGAAGAGCAAAAAACAAGCAATTAATGTGT 2524  
 Db 553 TATCTGCTTACTGGAAGTTAGCACTTGAAGAGCAAAAAACAAGCAATTAATGTGT 612  
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 QY 2585 TAGAATGACACAGAGGCTTTAAGTATCACTTGGGACATGAAGTTAACCACTGCGGA 2644  
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 QY 2645 AACAGCATTAAGAAAT-GGAAGAAAGTGAACCTGACATTTGGCAATTCATTA 2703  
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 QY 2704 AGGTTTCAAGAGGCGAGCATTTGCTGCTGTTTCAAAATCCAGAAATGCGAAGAGAAAT 2763  
 Db 793 A-GTTTCAAGAGGCGAGCATTTGCTGCTGTTTCAAAATCC-GGAAGAAATGCGAAGAGAT 850  
 QY 2764 GTGCAACATTTCTGCGCCACTCTGGGTCC--TTAAAGAAACAAGTCCAAAGTCACTTTT 2822  
 Db 851 GTGCAACATTTCTGCGCCACTCTGGGTCC--TTAAAGAAACAAGTCCAAAGTCACTTTT 910  
 QY 2823 GAATGTGAACAAA---GGAAGAAATCAAGAAAGATAGCTTA-TATCAAGCTGT 2878  
 Db 911 GAATGTGAACAAA---GGAAGAAATCAAGAAAGATAGCTTA-TATCAAGCTTT 970

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|----|------|--|------|
| Db | 1081 | GGGCTGGAAAGAAAGAAACATGTAATGATAGACCGGACTCCAGCAGACAGAAAAAAGGTAG  | 1140 |
| Oy | 1141 | ATCTGAATGCTGATCCCTGTGTGTGAGAGAAAAAGATGGAATTAAGCAGAAATCGCCATGCT | 1200 |
| Db | 1141 | ATCTGAATGCTGATCCCTGTGTGTGAGAGAAAAAGATGGAATTAAGCAGAAATCGCCATGCT | 1200 |
| Oy | 1201 | CAGGAATCCTAGAGATACGTAGAGATGTTCTCTGGATTAACCTTAATGCGAGCAATTGAGA  | 1260 |
| Db | 1201 | CAGGAATCCTAGAGATACGTAGAGATGTTCTCTGGATTAACCTTAATGCGAGCAATTGAGA  | 1260 |
| Oy | 1261 | AAGTTAATGAGTGTGTTTCCAGAAAGTGTGAACCTTTAGTTCTGATGACTCACATGATG    | 1320 |
| Db | 1261 | AAGTTAATGAGTGTGTTTCCAGAAAGTGTGAACCTTTAGTTCTGATGACTCACATGATG    | 1320 |
| Oy | 1321 | GGGAGCTCGAATCAATGCCCAAAGTAGCTGATGTAATTGGACGTTCTTAATAGGTAGATG   | 1380 |
| Db | 1321 | GGGAGCTCGAATCAATGCCCAAAGTAGCTGATGTAATTGGACGTTCTTAATAGGTAGATG   | 1380 |
| Oy | 1381 | AATATCTCGTCTTCCAGAGAAAAAGACCTTAAGGCGCAGATGCTCATGAGGCTTTAA      | 1440 |
| Db | 1381 | AATATCTCGTCTTCCAGAGAAAAAGACCTTAAGGCGCAGATGCTCATGAGGCTTTAA      | 1440 |
| Oy | 1441 | TATGTAAAGTGAAGAGATTCACTTCCAATCAGTAGAGATTAATTGAAGACAAAATAT      | 1500 |
| Db | 1441 | TATGTAAAGTGAAGAGATTCACTTCCAATCAGTAGAGATTAATTGAAGACAAAATAT      | 1500 |
| Oy | 1501 | TTGGGAAAACTTATGGAGAAAGGACACCTTCCCACTTAAAGCATGTAACTGAAATC       | 1560 |
| Db | 1501 | TTGGGAAAACTTATGGAGAAAGGACACCTTCCCACTTAAAGCATGTAACTGAAATC       | 1560 |
| Oy | 1561 | TAAATATAGAGACATTTGTACTGACGACAGATATATCAAGAGCGTCCCTCAAAATA       | 1620 |
| Db | 1561 | TAAATATAGAGACATTTGTACTGACGACAGATATATCAAGAGCGTCCCTCAAAATA       | 1620 |
| Oy | 1621 | AATTAAACGTTAAAGAGACCTTACATCAGGCGCTTCACTGAGGATTTTATCAAGAAAG     | 1680 |
| Db | 1621 | AATTAAACGTTAAAGAGACCTTACATCAGGCGCTTCACTGAGGATTTTATCAAGAAAG     | 1680 |
| Oy | 1681 | CAGATTTTGGCAGTCTAAAAGACCTCTGAAATGATTAATCAGGAACTTAACCAAACGGAGC  | 1740 |
| Db | 1681 | CAGATTTTGGCAGTCTAAAAGACCTCTGAAATGATTAATCAGGAACTTAACCAAACGGAGC  | 1740 |
| Oy | 1741 | AGAAATGCTCAAGTGTATGATATTACTTAATAGTGTGATGAGAAATTAACCAAAAGGTGATT | 1800 |
| Db | 1741 | AGAAATGCTCAAGTGTATGATATTACTTAATAGTGTGATGAGAAATTAACCAAAAGGTGATT | 1800 |
| Oy | 1801 | CTATTTCAGATGAGAAAAATCCTTAACCCAAATGAATCACTCGAAAAAGAAATCTGCTTTCA | 1860 |
| Db | 1801 | CTATTTCAGATGAGAAAAATCCTTAACCCAAATGAATCACTCGAAAAAGAAATCTGCTTTCA | 1860 |
| Oy | 1861 | AAACGAAAGCTGACCTTATAGCAGCAGATTAAGCAATATGTGAATCTGAAATTAATATCC   | 1920 |
| Db | 1861 | AAACGAAAGCTGACCTTATAGCAGCAGATTAAGCAATATGTGAATCTGAAATTAATATCC   | 1920 |
| Oy | 1921 | ACAAATTCAAAAGCCTTAATAAAGATAGGCTGAGAGAGAAGCTTCTACAGGCAATATTC    | 1980 |
| Db | 1921 | ACAAATTCAAAAGCCTTAATAAAGATAGGCTGAGAGAGAAGCTTCTACAGGCAATATTC    | 1980 |
| Oy | 1981 | ATGCGCTTGAACCTAGTAGTCACTAGTAATACTTAAGCCCACTTAATTGTACTGAATTGCAA | 2040 |
| Db | 1981 | ATGCGCTTGAACCTAGTAGTCACTAGTAATACTTAAGCCCACTTAATTGTACTGAATTGCAA | 2040 |
| Oy | 2041 | TTGATATAGTTCTTCAAGCAGTGAAGAGATTAAGAAAAAAGTACAAACCA             | 2090 |
| Db | 2041 | TTGATATAGTTCTTCAAGCAGTGAAGAGATTAAGAAAAAAGTACAAACCA             | 2090 |
| Db | 2041 | TTGATATAGTTCTTCAAGCAGTGAAGAGATTAAGAAAAAAGTACAAACCA             | 2090 |

|            |   |
|------------|---|
| RESULT 3   |   |
| BQ068830   |   |
| LOCUS      |   |
| DEFINITION | BQ068830 962 bp mRNA linear EST 02-APR-2002   |
| ACCESSION  | AGENCOURT 6740238 NIH_MGC_47 Homo sapiens cDNA clone IMAGE:5802685<br>5' mRNA Sequence. |
|            | BQ068830  |

|           |   |                   |
|-----------|---|-------------------|
| VERSION   | BC068830.1  | GI:19897888       |
| KEYWORDS  | EST.  |                   |
| SOURCE    | human.  |                   |
| ORGANISM  | Homo sapiens  |                   |
| REFERENCE | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo. |                   |
| AUTHORS   | 1 (bases 1 to 962)  |                   |
| TITLE     | National MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .  |                   |
| JOURNAL   | National Institutes of Health, Mammalian Gene Collection (MGC)  |                   |
| COMMENT   | Unpublished (1999)  |                   |
|           | Contact: Robert Strausberg, Ph.D.   |                   |
|           | Email: <a href="mailto:cgabbs-remail.nih.gov">cgabbs-remail.nih.gov</a>   |                   |
|           | Tissue Procurement: ATCC  |                   |
|           | cDNA Library Preparation: Rabin Laboratory  |                   |
|           | cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  |                   |
|           | DNA Sequencing by: Agencourt Bioscience Corporation   |                   |
|           | Clone distribution: MGC clone distribution information can be   |                   |
|           | found through the I.M.A.G.E. Consortium/LNL at:   |                   |
|           | <a href="http://image.lnl.gov">http://image.lnl.gov</a>   |                   |
|           | Plate: LUCM2037   | row: h column: 14 |
|           | High quality sequence. stop: H700.  |                   |

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FEATURES
source
Location/Qualifiers
1..962
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/clone_image="5802685"
/clone_id="NIH_MGC_47"
/tissue_type="neuroblastoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: brain; Vector: pOTR1; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
BASE COUNT
302 a 195 c 235 g 229 t 1 others
ORIGIN

```

| Query Match | Best Local Similarity | 15.1%  | Score 861.4 | DB 14      | Length 962 |
|-------------|-----------------------|--|-------------|------------|------------|
| Matches     | 890                   | Conservative   | 0           | Mismatches | 33         |
|             |                       |  |             | Indels     | 2          |
|             |                       |  |             | Gaps       | 1          |
| QY          | 4451                  | TCGAAACAAAGCACCATCAGAAAAAGCAGTATTAACTTCACAGAAAAGTAGTAATACC       |             |            | 4510       |
| Db          | 15                    | TTCCGGACAGAGCCACATCAGAAAAAGCAGTATTAACTTCACAGAAAAGTAGTAATACC      |             |            | 74         |
| QY          | 4511                  | TATTAAGCCAGAAATCCAGAAAGCCCTTCTCGCGCAAGATTGAGGTGTCGAGATAGTCC      |             |            | 4570       |
| Db          | 75                    | TATTAAGCCAGAAATCCAGAAAGCCCTTCTCGCGCAAGATTGAGGTGTCGAGATAGTCC      |             |            | 134        |
| QY          | 4571                  | TACCAAGTAAAAATAAAGAACCCAGAGAGTGAAAGGTCAATCCCTTTCTAAATGCCATCATY   |             |            | 4630       |
| Db          | 135                   | TACCAAGTAAAAATAAAGAACCCAGAGAGTGAAAGGTCAATCCCTTTCTAAATGCCATCATY   |             |            | 194        |
| QY          | 4631                  | AGATGATATGGTGTGTCATATGCACAGTGTCTCTGGGAGTCTTCAGAAATAGAACTAACCATC  |             |            | 4690       |
| Db          | 195                   | AGATGATATGGTGTGTCATATGCACAGTGTCTCTGGGAGTCTTCAGAAATAGAACTAACCATC  |             |            | 254        |
| QY          | 4691                  | TCAAGAGAGAGCTCATTAAGTTGTTGATGTGTGAGAGCAACAGCTGGAAGAGTCTGGGCC     |             |            | 4750       |
| Db          | 225                   | TCAAGAGAGAGCTCATTAAGTTGTTGATGTGTGAGAGCAACAGCTGGAAGAGTCTGGGCC     |             |            | 314        |
| QY          | 4751                  | ACACGATTTCGCGAAACATCTTAACTTCCCAAGSCAAGATCTAAGAGGAACCCCTTAACT     |             |            | 4810       |
| Db          | 315                   | ACACGATTTCGCGAAACATCTTAACTTCCCAAGSCAAGATCTAAGAGGAACCCCTTAACT     |             |            | 374        |
| QY          | 4811                  | GGAATCTGGAAATCAAGCCCTTCTCTGATATGACCCGGAATCTGATCTCTTCTGAAAGCAGAGC |             |            | 4870       |
| Db          | 375                   | GGAATCTGGAAATCAAGCCCTTCTCTGATATGACCCGGAATCTGATCTCTTCTGAAAGCAGAGC |             |            | 434        |

QY 1861 AAAGAAAGCTGAACCTATAGCAGCAGATATAGCAATATGCAATTAATATCC 1920  
DB 1865 AAAGAAAGCTGAACCTATAGCAGCAGATATAGCAATATGCAATTAATATCC 1924  
QY 1921 ACAATTCAAAAGCACCCTTAAAAAGATAGGCTGAGAGAACTCTTACCAGCATATTC 1980  
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DB 1985 ATGGCGCTGAAGCTAGTACAGTAAATCTAAGCCACCTAATGTACTGAATGCAAA 2044  
QY 2041 TTGATAGTGTGTCTAGCAGTGAAGATTAAGAAAAAAGTACAAACCAA 2091  
DB 2045 TTGATAGTGTGTCTAGCAGTGAAGATTAAGAAAAAAGTACAAACCAA 2095

RESULT 2  
BC030969  
LOCUS BC030969  
DEFINITION Homo sapiens, similar to breast cancer 1, early onset, clone  
IMAGE:4804551, mRNA.  
ACCESSION BC030969  
VERSION BC030969.1 GI:21411299  
KEYWORDS HTC.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 2090)  
AUTHORS Strausberg, R.  
TITLE Direct Submission  
JOURNAL Submitted (03-JUN-2002) National Institutes of Health, Mammalian  
Gene Collection (MGC), Cancer Genomics Office, National Cancer  
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
USA  
REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
COMMENT Contact: GSC help desk  
Email: [gsc@bbs-rcmail.nih.gov](mailto:gsc@bbs-rcmail.nih.gov)  
Tissue Procurement: DCTD/DTF  
cDNA Library Preparation: CLONTECH Laboratories, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Sequencing Group at the Stanford Human Genome  
Center, Stanford University School of Medicine, Stanford, CA 94305  
Web site: <http://www.shgc.stanford.edu>  
Contact: (Dickson, Mark) [mdickson@stanford.edu](mailto:mdickson@stanford.edu)  
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,  
R. M.  
FEATURES  
source  
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/note="Vector: pDNR-LIB"  
BASE COUNT 754 a 385 c 444 g 507 t  
ORIGIN  
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Matches 2075; Conservative 0; Mismatches 14; Indels 1; Gaps 1;  
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DB 2 AGCTGCTGAGACTTCTGGAACCCGACACAGGCTGTGGGTTTCTCAGATACTGGGC 60  
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DB 61 CCTGGCTCAGAGAGCCCTTCAACCTCTGCTGTGGGTAAAGTTCATTGGAACAGAAAGAA 120  
QY 121 TGGATTTATCTGCTCTTCCGCTTGAAGAGTACAAAATGTCATTAATGCTATGCAAGAAA 180  
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QY 121 TGGATTTATCTGCTCTTCCGCTTGAAGAGTACAAAATGTCATTAATGCTATGCAAGAAA 180  
DB 121 TGGATTTATCTGCTCTTCCGCTTGAAGAGTACAAAATGTCATTAATGCTATGCAAGAAA 180  
QY 181 TCTTGAATGTCCTCATCTGCTGAGATTGATCAAGAACTGTCTCCAAAGTGTACC 240  
DB 181 TCTTGAATGTCCTCATCTGCTGAGATTGATCAAGAACTGTCTCCAAAGTGTACC 240  
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DB 361 AACTTGTGAAGAGCTATTTGAAAATCAATTGTGCTTTTCAAGCTTGACACAGTTTGGAGT 420  
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QY 721 ATCAAGATTTGTTCAAAATCAACCCCTCAAGAGACCAAGGATGAATCAAGTTGGATCTG 780  
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/BLINL at: <http://image.llnl.gov>  
Series: IRAL Plate: 19 Row: a Column: 18  
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA 91: 6552298  
This clone has the following problem: incomplete processing.

## FEATURES

source

location/qualifiers

1..2101

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/issue\_type="Bladder, carcinoma"

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/lab\_host="DH10B"

/note="Vector: pDNr-LIB"

BASE COUNT 756 a 385 c 452 g 508 t

ORIGIN

Query Match

Best Local Similarity 99.4%; Pred. No. 0;

Matches 2079; Conservative 0; Mismatches 11; Indels 1; Gaps 1;

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Db 1805 CTATTGAGATGAGAAATCTTAACCAATAGATCACTCGAAAAAGAAATCTGCTTTCA 1864
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 12, 2003, 23:46:15 ; Search time 6805 Seconds  
(without alignments)  
13591.833 Million cell updates/sec

Title: US-09-734-672-3

Perfect score: 5711  
Sequence: 1 AGCTGCTGAGACTTCTG.....TCCCCACAGCCACTACTGA 5711

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

BEST: \*  
1: em\_escba:\*  
2: em\_escbm:\*  
3: em\_escin:\*  
4: em\_escmu:\*  
5: em\_escov:\*  
6: em\_escpl:\*  
7: em\_escro:\*  
8: em\_escr1:\*  
9: gb\_esc1:\*  
10: gb\_esc2:\*  
11: gb\_esc3:\*  
12: gb\_esc4:\*  
13: gb\_esc5:\*  
14: gb\_esc6:\*  
15: em\_escfun:\*  
16: em\_escm:\*  
17: gb\_gss:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_inv:\*  
20: em\_gss\_dln:\*  
21: em\_gss\_vrt:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_mam:\*  
24: em\_gss\_mus:\*  
25: em\_gss\_other:\*  
26: em\_gss\_pro:\*  
27: em\_gss\_rtd:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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|------------|--------|-------------|--------|-------|--------------------|
| 1          | 2061.4 | 36.1        | 2101   | 11    | BC012577 Homo sapi |
| 2          | 2055.6 | 36.0        | 2090   | 11    | BC030969 Homo sapi |
| 3          | 861.4  | 15.1        | 962    | 14    | BC068830 AGENCOURT |
| 4          | 844.6  | 14.8        | 1089   | 13    | BM452288 AGENCOURT |
| 5          | 811.8  | 14.2        | 845    | 9     | AU122476           |
| 6          | 761.8  | 13.3        | 783    | 9     | AU142729           |

| Result | LOCUS    | DEFINITION | ACCESSION | VERSION | KEYWORDS    | SOURCE       | ORGANISM     | REFERENCE | AUTHORS           | TITLE  | JOURNAL  | REMARK | COMMENT |
|--------|----------|------------|-----------|---------|-------------|--------------|--------------|-----------|-------------------|--|--|--------|---------|
| 1      | BC012577 | 2101 bp    | BC012577  | 1       | GI:15214876 | Homo sapiens | Homo sapiens | 1         | (bases 1 to 2101) | Submitted (15-AUG-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA | NIH-MGC Project URL: <a href="http://mgc.nci.nih.gov">http://mgc.nci.nih.gov</a><br>Contact: MGC help desk<br>Email: <a href="mailto:cgabs-remail.nih.gov">cgabs-remail.nih.gov</a><br>Tissue Procurement: ATCC<br>CDNA Library Preparation: CLONTECH Laboratories, Inc.<br>DNA Sequencing by: The I.M.A.G.E. Consortium (LMU)<br><a href="http://www.systemsbio.org">http://www.systemsbio.org</a><br>contact: <a href="mailto:amadansystemsbiology.org">amadansystemsbiology.org</a><br>Anup Madan, Rachel Dickhoff, Jessica Fahy, Stephanie Ford, Julia Greene, Mark Kettelman and Anuradha Madan |        |         |

## ALIGNMENTS

| Result | LOCUS    | DEFINITION | ACCESSION | VERSION | KEYWORDS    | SOURCE       | ORGANISM     | REFERENCE | AUTHORS           | TITLE  | JOURNAL  | REMARK | COMMENT |
|--------|----------|------------|-----------|---------|-------------|--------------|--------------|-----------|-------------------|--|--|--------|---------|
| 1      | BC012577 | 2101 bp    | BC012577  | 1       | GI:15214876 | Homo sapiens | Homo sapiens | 1         | (bases 1 to 2101) | Submitted (15-AUG-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA | NIH-MGC Project URL: <a href="http://mgc.nci.nih.gov">http://mgc.nci.nih.gov</a><br>Contact: MGC help desk<br>Email: <a href="mailto:cgabs-remail.nih.gov">cgabs-remail.nih.gov</a><br>Tissue Procurement: ATCC<br>CDNA Library Preparation: CLONTECH Laboratories, Inc.<br>DNA Sequencing by: The I.M.A.G.E. Consortium (LMU)<br><a href="http://www.systemsbio.org">http://www.systemsbio.org</a><br>contact: <a href="mailto:amadansystemsbiology.org">amadansystemsbiology.org</a><br>Anup Madan, Rachel Dickhoff, Jessica Fahy, Stephanie Ford, Julia Greene, Mark Kettelman and Anuradha Madan |        |         |



QY 4561 CAGATAGTCTACCACTAAAAATAAGAACCCAGAGTGGAAAAGTCACTCCCTTCTAAT 4620  
DB 4561 CAGATAGTCTACCACTAAAAATAAGAACCCAGAGTGGAAAAGTCACTCCCTTCTAAT 4620  
QY 4621 GCCCATCATTAGATGATAGTGTGATGACAGTTCCTCTGAGAGTCTTTCAGAAATAGA 4680  
DB 4621 GCCCATCATTAGATGATAGTGTGATGACAGTTCCTCTGAGAGTCTTTCAGAAATAGA 4680  
QY 4681 ACTACCATCTCAAGAGAGAGCTCATTAGGTTGTTATGTTGAGAGCAACAGCTGGAAG 4740  
DB 4681 ACTACCATCTCAAGAGAGAGCTCATTAGGTTGTTATGTTGAGAGCAACAGCTGGAAG 4740  
QY 4741 AGCTGGGGCCACACGATTTGAGGAAACCTTACTTGGCAAGCAAGATCTAGAGGAA 4800  
DB 4741 AGCTGGGGCCACACGATTTGAGGAAACCTTACTTGGCAAGCAAGATCTAGAGGAA 4800  
QY 4801 CCCCTTACCTGGAATCTGGAATCAGCCTCTTCTGTATGACCCTGAATCTGATCTTCTG 4860  
DB 4801 CCCCTTACCTGGAATCTGGAATCAGCCTCTTCTGTATGACCCTGAATCTGATCTTCTG 4860  
QY 4861 AAGACAGAGCCCGAGAGTCACTGCTGTTGGCAACATACCATCTCAACTCTGCAATTGA 4920  
DB 4861 AAGACAGAGCCCGAGAGTCACTGCTGTTGGCAACATACCATCTCAACTCTGCAATTGA 4920  
QY 4921 AAGTCCCAATTGAAGTTGAGATCTGCCCCAGAGTCCAGCTGCTGCTCACTACTACTG 4980  
DB 4921 AAGTCCCAATTGAAGTTGAGATCTGCCCCAGAGTCCAGCTGCTGCTCACTACTACTG 4980  
QY 4981 ATACTGCTGGGTATATGCAATGGAAGAAAGTGTGAGCAGAGGAGAAAGCCAGAAATTGACAG 5040  
DB 4981 ATACTGCTGGGTATATGCAATGGAAGAAAGTGTGAGCAGAGGAGAAAGCCAGAAATTGACAG 5040  
QY 5041 CTTCAACAGAAAGGTCACAAAGAAATGTCATGCTGCTGCTGAGCTGAGCCCAAGAG 5100  
DB 5041 CTTCAACAGAAAGGTCACAAAGAAATGTCATGCTGCTGCTGAGCTGAGCCCAAGAG 5100  
QY 5101 AATTATGCTCGTGAAGTTGCAAGAAACACACATCACTTAACCTAATCTAATTA 5160  
DB 5101 AATTATGCTCGTGAAGTTGCAAGAAACACACATCACTTAACCTAATCTAATTA 5160  
QY 5161 CTGAAGAGACTACTCATGTTGTTATGAAACAGATGCTGAGTTGTGTGAAAGGAGAC 5220  
DB 5161 CTGAAGAGACTACTCATGTTGTTATGAAACAGATGCTGAGTTGTGTGAAAGGAGAC 5220  
QY 5221 TGAATATTTTCTAGGAATTCGCGAGAGAAATGGGTAGTACTAATTTCTGGGTGACC 5280  
DB 5221 TGAATATTTTCTAGGAATTCGCGAGAGAAATGGGTAGTACTAATTTCTGGGTGACC 5280  
QY 5281 AGTCTATTAAAGAAAGAAATGCTGAATGAGATGATTTTGAAGTCAAGAGAGATGTG 5340  
DB 5281 AGTCTATTAAAGAAAGAAATGCTGAATGAGATGATTTTGAAGTCAAGAGAGATGTG 5340  
QY 5341 TCAATGGAAGAAACCAAGGTCCAAAGGAGCAAGAGATCCAGACAGAAAGATCT 5400  
DB 5341 TCAATGGAAGAAACCAAGGTCCAAAGGAGCAAGAGATCCAGACAGAAAGATCT 5400  
QY 5401 TCAGGGGGCTAGAAATCTGTTGCTATGAGCCCTTACCAACATGCCACAGATCAACTG 5460  
DB 5401 TCAGGGGGCTAGAAATCTGTTGCTATGAGCCCTTACCAACATGCCACAGATCAACTG 5460  
QY 5461 AATGATGATGAGAGCTGTGAGTCTTCTGTGTTGAAGAGAGCTTTCATCAATCACTT 5520  
DB 5461 AATGATGATGAGAGCTGTGAGTCTTCTGTGTTGAAGAGAGCTTTCATCAATCACTT 5520  
QY 5521 GCAAGAGTGTCAACCAATTTGTGTTGTGAGCCAGATGCTGAGACAGAGCAATGCT 5580  
DB 5521 GCAAGAGTGTCAACCAATTTGTGTTGTGAGCCAGATGCTGAGACAGAGCAATGCT 5580  
QY 5581 TCCATGCAATTTGGGAGATGTGAGGCACTGTGTTGACCCGAGAGTGGGTGTTGACA 5640  
DB 5581 TCCATGCAATTTGGGAGATGTGAGGCACTGTGTTGACCCGAGAGTGGGTGTTGACA 5640

QY 5641 GTGTAGCACTTACAGATGCTCCAGAGCTGGACACTTACTGATATCCAGATCCCCACA 5700  
DB 5641 GTGTAGCACTTACAGATGCTCCAGAGCTGGACACTTACTGATATCCAGATCCCCACA 5700  
QY 5701 GCCACTACTGA 5711  
DB 5701 GCCACTACTGA 5711

Search completed: June 13, 2003, 00:36:31  
Job time : 1122 secs

|    |      |   |       |
|----|------|---|-------|
| Db | 2341 | CTAATATATCTGAAGACCCCAAGATCTCATGTTAACTGAGAAAGGGTTTGCAACTG      | 24000 |
| Qy | 2401 | AAAGATCTGTAGAGATAGCACTATTTCAATTGTACTGTGACTGATTAATGGCACTCAGG   | 24600 |
| Db | 2401 | AAAGATCTGTAGAGATAGCACTATTTCAATTGTACTGTGACTGATTAATGGCACTCAGG   | 24600 |
| Qy | 2461 | AAAGTATCTCTTACTCTGGAAGTTAGCACTCTGAGGAGGCCAAAACAGACCAATAAT     | 25200 |
| Db | 2461 | AAAGTATCTCTTACTCTGGAAGTTAGCACTCTGAGGAGGCCAAAACAGACCAATAAT     | 25200 |
| Qy | 2521 | GTGTAGTCAAGTGTGAGCACTTGGAAACCCCAAGGGACTAATTCATGTTGTTTCAAG     | 25800 |
| Db | 2521 | GTGTAGTCAAGTGTGAGCACTTGGAAACCCCAAGGGACTAATTCATGTTGTTTCAAG     | 25800 |
| Qy | 2581 | ATATATAGAAATGACA CAGAGGCTTTAAGTATCCATTGGGACATGAAGTTAAACAACATC | 26400 |
| Db | 2581 | ATATATAGAAATGACA CAGAGGCTTTAAGTATCCATTGGGACATGAAGTTAAACAACATC | 26400 |
| Qy | 2641 | GGGAAACAAAGCATAGAAATGGAAGAAAGTGAACCTTAGTCAGTATTTGCGAATACAT    | 27000 |
| Db | 2641 | GGGAAACAAAGCATAGAAATGGAAGAAAGTGAACCTTAGTCAGTATTTGCGAATACAT    | 27000 |
| Qy | 2701 | TCAAGTTTCAAGGGCCAGTATTTGCTCTGTTTTCAAATCCAGAAATCGAAGAGG        | 27600 |
| Db | 2701 | TCAAGTTTCAAGGGCCAGTATTTGCTCTGTTTTCAAATCCAGAAATCGAAGAGG        | 27600 |
| Qy | 2761 | AATGTGCAAACTTCTCTGCCCACTCTGGGTCTTTAAAGAAACAAAGTCCAAAGTCACTT   | 28200 |
| Db | 2761 | AATGTGCAAACTTCTCTGCCCACTCTGGGTCTTTAAAGAAACAAAGTCCAAAGTCACTT   | 28200 |
| Qy | 2821 | TTGAATGTGACAAAGAAAGAAATCAAGAAAGATGAGTCTAATATCAAGCCTGAC        | 28800 |
| Db | 2821 | TTGAATGTGACAAAGAAAGAAATCAAGAAAGATGAGTCTAATATCAAGCCTGAC        | 28800 |
| Qy | 2881 | AGACGTTAATTCACCTGAGGCTTTCCTGTGGTGTGCAGAAATAGCCAGTGTGATA       | 29400 |
| Db | 2881 | AGACGTTAATTCACCTGAGGCTTTCCTGTGGTGTGCAGAAATAGCCAGTGTGATA       | 29400 |
| Qy | 2941 | ATGCCAAATGTATGTCAAAAGAGGCTCTAGGTTTGTCTATCATCTCAGTTCAAGAGCA    | 30000 |
| Db | 2941 | ATGCCAAATGTATGTCAAAAGAGGCTCTAGGTTTGTCTATCATCTCAGTTCAAGAGCA    | 30000 |
| Qy | 3001 | ACGAAACTGEGACTCATCTCCAAATTAACATGACCTTTTACAAAAACCATATCGTATAC   | 30600 |
| Db | 3001 | ACGAAACTGEGACTCATCTCCAAATTAACATGACCTTTTACAAAAACCATATCGTATAC   | 30600 |
| Qy | 3061 | CACCACTTTTCCCATCAAGTATTTGTTAAAACTTAATGTAAAGAAATCTGCTAGAGG     | 31200 |
| Db | 3061 | CACCACTTTTCCCATCAAGTATTTGTTAAAACTTAATGTAAAGAAATCTGCTAGAGG     | 31200 |
| Qy | 3121 | AAAACTTTGAGGACATTCATATGTCAACCTGAAGAAAGAAATGAGAACTTCCAA        | 31800 |
| Db | 3121 | AAAACTTTGAGGACATTCATATGTCAACCTGAAGAAAGAAATGAGAACTTCCAA        | 31800 |
| Qy | 3181 | GTACAGTGAACAATTAAGCGGTAATTAACATTAGAGAAATGTTTAAAGAGCACT        | 32400 |
| Db | 3181 | GTACAGTGAACAATTAAGCGGTAATTAACATTAGAGAAATGTTTAAAGAGCACT        | 32400 |
| Qy | 3241 | CAAGCAATTTATATGATGATGTTCCAGTATTAATGAAGTGGGCTCCAGTATTAATGAA    | 33000 |
| Db | 3241 | CAAGCAATTTATATGATGATGTTCCAGTATTAATGAAGTGGGCTCCAGTATTAATGAA    | 33000 |
| Qy | 3301 | TAGGTTCAGTATGAAAACATTCAGAGAACTGAGTAAAGAGAGGCAAAATTTGA         | 33600 |
| Db | 3301 | TAGGTTCAGTATGAAAACATTCAGAGAACTGAGTAAAGAGAGGCAAAATTTGA         | 33600 |
| Qy | 3361 | ATGCTATGCTTATGATTAAGGGTTTTCGAACCTGAGGTCTAATTAACAAAGTCTTCTGAA  | 34200 |
| Db | 3361 | ATGCTATGCTTATGATTAAGGGTTTTCGAACCTGAGGTCTAATTAACAAAGTCTTCTGAA  | 34200 |
| Qy | 3421 | GTAATTTGACATCTCTGAATTAATAAAAGCAAGATATGAAGATGTTCAAGCTGTTA      | 34800 |
| Db | 3421 | GTAATTTGACATCTCTGAATTAATAAAAGCAAGATATGAAGATGTTCAAGCTGTTA      | 34800 |

|    |      |   |      |
|----|------|---|------|
| Db | 3421 | GTAAATGTAAGCTACCTGAAATTAATAAAGCAAGAATTAAGAAAGTAGTTCAGACTCTTA    | 3148 |
| Qy | 3481 | ATACAGATTTCTCTCCATATCTGAATTTACATACTTAAGAACAGCTTATGGGAATGTC      | 3540 |
| Db | 3481 | ATACAGATTTCTCTCCATATCTGAATTTACATACTTAAGAACAGCTTATGGGAATGTC      | 3540 |
| Qy | 3541 | ATGCATCTCAGGTTGGTCTGAGACACCTGTATGACCTGTTAGATGATGGGAAATAAAG      | 3600 |
| Db | 3541 | ATGCATCTCAGGTTGGTCTGAGACACCTGTATGACCTGTTAGATGATGGGAAATAAAG      | 3600 |
| Qy | 3601 | AAGATACTAGTTTGTGCTGAAATAATACATTAAGAAAGTTCGCTGTTTTAGCAAAACG      | 3660 |
| Db | 3601 | AAGATACTAGTTTGTGCTGAAATAATACATTAAGAAAGTTCGCTGTTTTAGCAAAACG      | 3660 |
| Qy | 3661 | TCCAGAAAGAGAGCTTAGCAGAGAGTCCAGCCCTTTCACCCATACATTTGGCTCAG        | 3720 |
| Db | 3661 | TCCAGAAAGAGAGCTTAGCAGAGAGTCCAGCCCTTTCACCCATACATTTGGCTCAG        | 3720 |
| Qy | 3721 | GTTACCGAAGAGGGGCCCAAGAAATTAAGTCTCAGAAAGAACTTAATGAGAGATG         | 3780 |
| Db | 3721 | GTTACCGAAGAGGGGCCCAAGAAATTAAGTCTCAGAAAGAACTTAATGAGAGATG         | 3780 |
| Qy | 3781 | AAGAGCTTCCCTGCTCCAAACACTTGTATTGTGTAAGTAATAACAATACCTTCAGT        | 3840 |
| Db | 3781 | AAGAGCTTCCCTGCTCCAAACACTTGTATTGTGTAAGTAATAACAATACCTTCAGT        | 3840 |
| Qy | 3841 | CTACTAGGCATAGCACCGTTGCTACCGAGTGCTGTCTTAAGAACACAGAGAGAAATTAT     | 3900 |
| Db | 3841 | CTACTAGGCATAGCACCGTTGCTACCGAGTGCTGTCTTAAGAACACAGAGAGAAATTAT     | 3900 |
| Qy | 3901 | TATCATTTAAGAAATAGCTTAATATGATCTGCAGTAACCAAGTAATTTGGCAAGGCACTTC   | 3960 |
| Db | 3901 | TATCATTTAAGAAATAGCTTAATATGATCTGCAGTAACCAAGTAATTTGGCAAGGCACTTC   | 3960 |
| Qy | 3961 | AGGAACATCACCTTAGTATGAGGAAACAATAATTTCTGACGTTGTTTTCTTCAAGTGCA     | 4020 |
| Db | 3961 | AGGAACATCACCTTAGTATGAGGAAACAATAATTTCTGACGTTGTTTTCTTCAAGTGCA     | 4020 |
| Qy | 4021 | GTGAATTTGGAAGACTTGACTGCAATAACAACCCAGAGATCCTTTCTTGAATTTGGTTCTT   | 4080 |
| Db | 4021 | GTGAATTTGGAAGACTTGACTGCAATAACAACCCAGAGATCCTTTCTTGAATTTGGTTCTT   | 4080 |
| Qy | 4081 | CCAAACAATAGGCAATCAGTCTTAAGGCCAGGAGTTGGTCTGATGACAAAGAAATTGG      | 4140 |
| Db | 4081 | CCAAACAATAGGCAATCAGTCTTAAGGCCAGGAGTTGGTCTGATGACAAAGAAATTGG      | 4140 |
| Qy | 4141 | TTTCAGATGATGAAGAAAGAGAGACGGGCTTTGGAAGAAATTAATCAAGAAAGACAAAGCA   | 4200 |
| Db | 4141 | TTTCAGATGATGAAGAAAGAGAGACGGGCTTTGGAAGAAATTAATCAAGAAAGACAAAGCA   | 4200 |
| Qy | 4201 | TGSAATTCMAACTTAGTGAAGCACATCTGGGTTGAGATGAAACAACGCTCTGTAAG        | 4260 |
| Db | 4201 | TGSAATTCMAACTTAGTGAAGCACATCTGGGTTGAGATGAAACAACGCTCTGTAAG        | 4260 |
| Qy | 4261 | ACTGCTCAGGGCTATCCTCTCAGATGACATTTTAACCACTCAGCAGAGGATACCATGC      | 4320 |
| Db | 4261 | ACTGCTCAGGGCTATCCTCTCAGATGACATTTTAACCACTCAGCAGAGGATACCATGC      | 4320 |
| Qy | 4321 | AACTTAACCTGATTAAGCTCCAGAGAGAAATTTGGCTGAACCTAAGAGCTGTGGAACAGC    | 4380 |
| Db | 4321 | AACTTAACCTGATTAAGCTCCAGAGAGAAATTTGGCTGAACCTAAGAGCTGTGGAACAGC    | 4380 |
| Qy | 4381 | ATGGAGCGACCTTTCTTAACAGTACCTTCATCATTAATGACTCTTTCGCCCTTGAGG       | 4440 |
| Db | 4381 | ATGGAGCGACCTTTCTTAACAGTACCTTCATCATTAATGACTCTTTCGCCCTTGAGG       | 4440 |
| Qy | 4441 | ACCTGCGAATCCAGAACAAAGCACATCAGAAAAAGCAGATTAATTAACCTTCACAGAAAAATG | 4500 |
| Db | 4441 | ACCTGCGAATCCAGAACAAAGCACATCAGAAAAAGCAGATTAATTAACCTTCACAGAAAAATG | 4500 |
| Qy | 4501 | GTGAATACCCCTATAAGCCAGAAATCCAGAAAGCCTTTCTGCTGACAAAGTTTGAGTGTCTG  | 4560 |
| Db | 4501 | GTGAATACCCCTATAAGCCAGAAATCCAGAAAGCCTTTCTGCTGACAAAGTTTGAGTGTCTG  | 4560 |

QY 181 TCTTAGAGTGTCCATCTGTCTGAGATTGATCAAGGAACTGTCTCCACAAAGTGTGACC 240  
DB 181 TCTTAGAGTGTCCATCTGTCTGAGATTGATCAAGGAACTGTCTCCACAAAGTGTGACC 240  
QY 241 ACATATTTTGCAAAATTTTGATGCTGAACTTCTCAACCGAAGAAAGGCGCTTCACAGT 300  
DB 241 ACATATTTTGCAAAATTTTGATGCTGAACTTCTCAACCGAAGAAAGGCGCTTCACAGT 300  
QY 301 GTTCCTTTATGTAGAAATGATATTAACCAAAAGAGCCTACAGAAAGTACAGATTTTATGTC 360  
DB 301 GTTCCTTTATGTAGAAATGATATTAACCAAAAGAGCCTACAGAAAGTACAGATTTTATGTC 360  
QY 361 AACTTGTGAAAGCTATTGAAATCATTTGTCTTTACGCTTGACAAGTGTGGAGT 420  
DB 361 AACTTGTGAAAGCTATTGAAATCATTTGTCTTTACGCTTGACAAGTGTGGAGT 420  
QY 421 ATGCAAAAGCTTAATTTTGGCAAAAAGGAAATAACTCTCTGAACATCTTAAGAGATG 480  
DB 421 ATGCAAAAGCTTAATTTTGGCAAAAAGGAAATAACTCTCTGAACATCTTAAGAGATG 480  
QY 481 AAGTTTCTATCATCAAAAGTATGGGCTACAGAAACCGTGCCAAAGACCTTCTACAGATG 540  
DB 481 AAGTTTCTATCATCAAAAGTATGGGCTACAGAAACCGTGCCAAAGACCTTCTACAGATG 540  
QY 541 AACCCGAAAATCCTTCTCTGAGGAAACCAAGTCTCAAGTCTCAACTCTCTAACCTTGGA 600  
DB 541 AACCCGAAAATCCTTCTCTGAGGAAACCAAGTCTCAAGTCTCAACTCTCTAACCTTGGA 600  
QY 601 CTGTGAAACTCTGAGGAAACCAAGCAGGATACAACTCTCAAAAGAGTCTGTCTACATG 660  
DB 601 CTGTGAAACTCTGAGGAAACCAAGCAGGATACAACTCTCAAAAGAGTCTGTCTACATG 660  
QY 661 AATTGGATCTGATTTCTTGAAGATACCGTTAATAAGCACTTAATTGAGTGGAG 720  
DB 661 AATTGGATCTGATTTCTTGAAGATACCGTTAATAAGCACTTAATTGAGTGGAG 720  
QY 721 ATCAAAATTTGTACAAATCAACCCCTCAAGGAAACCAAGGATGAATCACTTTGATTCG 780  
DB 721 ATCAAAATTTGTACAAATCAACCCCTCAAGGAAACCAAGGATGAATCACTTTGATTCG 780  
QY 781 CAAAAAAGGCTGTGGAATTTTCTGAGCGAGTGAACAAATATCTGAACATCATCAAC 840  
DB 781 CAAAAAAGGCTGTGGAATTTTCTGAGCGAGTGAACAAATATCTGAACATCATCAAC 840  
QY 841 CCAGTAATATGATTTGAACACCACTGAGAGGCTGAGGAGCAATCCAGAAAGT 900  
DB 841 CCAGTAATATGATTTGAACACCACTGAGAGGCTGAGGAGCAATCCAGAAAGT 900  
QY 901 ATAGAGTATGTTCTGTTTCAAACTTGATGAGGCAATGTCACAAATCATCATGCCA 960  
DB 901 ATAGAGTATGTTCTGTTTCAAACTTGATGAGGCAATGTCACAAATCATCATGCCA 960  
QY 961 GCTCATTAAGCATGAGAACAGAGTTTATTACTCACTAAAGACAGAAATGTAGAAA 1020  
DB 961 GCTCATTAAGCATGAGAACAGAGTTTATTACTCACTAAAGACAGAAATGTAGAAA 1020  
QY 1021 AGGCTGAATTTCTGTAATTAAGCAAAACAGCTGCTTAGCAAGAGCCAACTAATACAGAT 1080  
DB 1021 AGGCTGAATTTCTGTAATTAAGCAAAACAGCTGCTTAGCAAGAGCCAACTAATACAGAT 1080  
QY 1081 GGGCTGGAAGTAAAGAAACATGTAATGATGAGCGGACTCCAGACACAGAAAAAGGTAG 1140  
DB 1081 GGGCTGGAAGTAAAGAAACATGTAATGATGAGCGGACTCCAGACACAGAAAAAGGTAG 1140  
QY 1141 ATCTGATGCTGATCCCTGTGTGAGAGAAAGAAATGAAATAGCAGAACTGCTGCT 1200  
DB 1141 ATCTGATGCTGATCCCTGTGTGAGAGAAAGAAATGAAATAGCAGAACTGCTGCT 1200  
QY 1201 CAGAGAACTCTAGAGATCTGAAGATGTTCTTGATATACATTAATAGCAGATTCAG 1260  
DB 1201 CAGAGAACTCTAGAGATCTGAAGATGTTCTTGATATACATTAATAGCAGATTCAG 1260

QY 1261 AAGTTAATGAGTGGTTTCCAGAGATGAATGAATGTTAGTGTCTGATGACTCAGATGATG 1320  
DB 1261 AAGTTAATGAGTGGTTTCCAGAGATGAATGAATGTTAGTGTCTGATGACTCAGATGATG 1320  
QY 1321 GGGAGCTGAATCAATGCGCAAGATGATGATATGGAACGTTCTAAATGAGATGATG 1380  
DB 1321 GGGAGCTGAATCAATGCGCAAGATGATGATATGGAACGTTCTAAATGAGATGATG 1380  
QY 1381 AATATTCTGTTCTTCCAGAGAAATAGATTTCTGCGCAGTATCTCTAGAGCTTTAA 1440  
DB 1381 AATATTCTGTTCTTCCAGAGAAATAGATTTCTGCGCAGTATCTCTAGAGCTTTAA 1440  
QY 1441 TATGTAAAGTAAAGAGTTCCTCCAAATCGTAGAGTATATTAAGACAAATAT 1500  
DB 1441 TATGTAAAGTAAAGAGTTCCTCCAAATCGTAGAGTATATTAAGACAAATAT 1500  
QY 1501 TTGGGAAAACTATGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1560  
DB 1501 TTGGGAAAACTATGCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1560  
QY 1561 TAATTATAGAGCATTTGTTACTGAGCCAGATTAATACAGAGGCTCCCTCACAATA 1620  
DB 1561 TAATTATAGAGCATTTGTTACTGAGCCAGATTAATACAGAGGCTCCCTCACAATA 1620  
QY 1621 AATTAAAGGCTAAAGAGACCTACATCAGGCTTATCTGAGATTTTATCAAGAAAG 1680  
DB 1621 AATTAAAGGCTAAAGAGACCTACATCAGGCTTATCTGAGATTTTATCAAGAAAG 1680  
QY 1681 CAGATTGCGACATTAAGAAAGCTCCTGAATGATTAATCAGGAACTAAACGAGAC 1740  
DB 1681 CAGATTGCGACATTAAGAAAGCTCCTGAATGATTAATCAGGAACTAAACGAGAC 1740  
QY 1741 AGAATGCTCAAGTGAATATTAATTAATGCTGATGAGATTAATAACAAAGTGTAT 1800  
DB 1741 AGAATGCTCAAGTGAATATTAATTAATGCTGATGAGATTAATAACAAAGTGTAT 1800  
QY 1801 CTATTCCAGATGAGAAAAATCTTAACCCAAATGAATCACTCGAAAAAGAAATCGCTTCA 1860  
DB 1801 CTATTCCAGATGAGAAAAATCTTAACCCAAATGAATCACTCGAAAAAGAAATCGCTTCA 1860  
QY 1861 AAAAGAAAGCTGAACCTATTAAGCAGCAGTATTAAGCAATATGGAATCGAAATTAATATCC 1920  
DB 1861 AAAAGAAAGCTGAACCTATTAAGCAGCAGTATTAAGCAATATGGAATCGAAATTAATATCC 1920  
QY 1921 ACAATTCAAAGCAGCTTAAGAAATGAGCTGAGAGGAAAGTCTTACAGGCAATATTC 1980  
DB 1921 ACAATTCAAAGCAGCTTAAGAAATGAGCTGAGAGGAAAGTCTTACAGGCAATATTC 1980  
QY 1981 ATGCGCTGAATAGTATGATGATGATTAAGGCACTTAATGATGATGATGATGATGATG 2040  
DB 1981 ATGCGCTGAATAGTATGATGATGATTAAGGCACTTAATGATGATGATGATGATGATG 2040  
QY 2041 TTGATATGTTGTTCTAGCAGTGAAGATTAAGAAAAAGTAAACCAATATCCAGTCA 2100  
DB 2041 TTGATATGTTGTTCTAGCAGTGAAGATTAAGAAAAAGTAAACCAATATCCAGTCA 2100  
QY 2101 GGCACAGCAAAACCTACATCATGTAAGAGGTAAGAACTGCACTGAGGCAAGAAAG 2160  
DB 2101 GGCACAGCAAAACCTACATCATGTAAGAGGTAAGAACTGCACTGAGGCAAGAAAG 2160  
QY 2161 GTAAACAGCAAAATGAACAGACAGTAAAGACATGACAGGATCTTCCAGAGCTGA 2220  
DB 2161 GTAAACAGCAAAATGAACAGACAGTAAAGACATGACAGGATCTTCCAGAGCTGA 2220  
QY 2221 AATTAAACAATGACCTGTTCTTTTACTAAGTGTCAATATCCAGTGAATTAAGAAAT 2280  
DB 2221 AATTAAACAATGACCTGTTCTTTTACTAAGTGTCAATATCCAGTGAATTAAGAAAT 2280  
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DB 2281 TTGTCATCTGAGCTTCCAAAGAAAGAAAGAAAGAAAGAAAGAAAGTAT 2340  
QY 2341 CTAATATGCTGAAGACCCCAAGATCTCATGTTAAGTGAAGAAAGGTTTGCAAACTG 2400



QY 2641 GGGAAACAGCATAGAAATGGAAGAAAGTGAAGTGAAGTCTGAGTATTTGGCAATATCAT 2700  
Db 2641 GGGAAACAGCATAGAAATGGAAGAAAGTGAAGTGAAGTGAAGTCTGAGTATTTGGCAATATCAT 2700  
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QY 2761 AATGTGCACATTTCTGCGCCACTCTGGGCTTTAAAGAAACAAAGTCCAAAGTCACTT 2820  
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QY 2821 TTGAATGTGAACAAAGGAAAGAAATCAAGAGAAAGATGCTTAATATCAACCTGTAC 2880  
Db 2821 TTGAATGTGAACAAAGGAAAGAAATCAAGAGAAAGATGCTTAATATCAACCTGTAC 2880  
QY 2881 AGACAGTTAATATCACTGACAGGCTTCTGTGGTGTGAGAAAGATTAAGCCAGTTGATA 2940  
Db 2881 AGACAGTTAATATCACTGACAGGCTTCTGTGGTGTGAGAAAGATTAAGCCAGTTGATA 2940  
QY 2941 ATGCCAAATGTATATCAAGAGAGGCTTAGTGTCTATCATCTCAGTTCAAGGCA 3000  
Db 2941 ATGCCAAATGTATATCAAGAGAGGCTTAGTGTCTATCATCTCAGTTCAAGGCA 3000  
QY 3001 AGCAAACTGACATTAATCACTCCAAATPAACATGGAATTTTAAACCAATATCTATAC 3060  
Db 3001 AGCAAACTGACATTAATCACTCCAAATPAACATGGAATTTTAAACCAATATCTATAC 3060  
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Db 3061 CACCACTTTTCCCATCAAGTCACTTTGTAACTAAATGTAAAGAAATCTCTAGAG 3120  
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Db 3181 GTACAGGACCAAAATTAAGCGTAATPAACATTAAGAAATGTTTTAAAGAGCCAGCT 3240  
QY 3241 CAAGCAATATTAATGAAGTTCAGTACTAATGAAGGAGCTCCAGTATTAATGA 3300  
Db 3241 CAAGCAATATTAATGAAGTTCAGTACTAATGAAGGAGCTCCAGTATTAATGA 3300  
QY 3301 TAGGTTCCAGTATGAAGAAATTCAGAGCAAGTCTAGAGAAACAGAGGCGCAAAATTGA 3360  
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QY 3361 ATGCTATGCTTAATTAAGGGGTTTTGCACTGAGGCTATTAACAAAGTCTTCGGA 3420  
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QY 3421 GTAATGTGAAGCATCTCGAATTAAGAAAGCAAGATATGAAGAGTGTCAAGCTGTA 3480  
Db 3421 GTAATGTGAAGCATCTCGAATTAAGAAAGCAAGATATGAAGAGTGTCAAGCTGTA 3480  
QY 3481 ATACAGATTTCTCTCCATATCTGATTTCAATTAATTAAGAAACAGCTATGGAAGTGT 3540  
Db 3481 ATACAGATTTCTCTCCATATCTGATTTCAATTAATTAAGAAACAGCTATGGAAGTGT 3540  
QY 3541 ATGATCTCAGGTTTGTCTGAGACACCTGATGACCTGTAGATGATGGAATTAAG 3600  
Db 3541 ATGATCTCAGGTTTGTCTGAGACACCTGATGACCTGTAGATGATGGAATTAAG 3600  
QY 3601 AAGATCTAGTTTGTCTGAAATATGACATTAAGGAAAGTCTGCTGTTTAAAGAAAGCG 3660  
Db 3601 AAGATCTAGTTTGTCTGAAATATGACATTAAGGAAAGTCTGCTGTTTAAAGAAAGCG 3660  
QY 3661 TTCAGAAAGAGAGCTTAGAGAGAGTCCCTTCAACCATACATTTGGCTCAGG 3720  
Db 3661 TTCAGAAAGAGAGCTTAGAGAGAGTCCCTTCAACCATACATTTGGCTCAGG 3720

QY 3721 GTTACGAGAGAGAGGCGCAAGAAATTAAGAGTCCAGAAAGAGAACTTATCTAGAGAGATG 3780  
Db 3721 GTTACGAGAGAGAGGCGCAAGAAATTAAGAGTCCAGAAAGAGAACTTATCTAGAGAGATG 3780  
QY 3781 AAGAGCTTCCCTGCTTCCAAACATTTGTTATTTGTAAGTAACAATATACCTTCACT 3840  
Db 3781 AAGAGCTTCCCTGCTTCCAAACATTTGTTATTTGTAAGTAACAATATACCTTCACT 3840  
QY 3841 CTAATAGGATAGACCCGTTGCTACCGAGTGTCTGTAAAGAACAGAGAGAAATTTAT 3900  
Db 3841 CTAATAGGATAGACCCGTTGCTACCGAGTGTCTGTAAAGAACAGAGAGAAATTTAT 3900  
QY 3901 TATCATTTGAAGATAGCTTAATTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 3960  
Db 3901 TATCATTTGAAGATAGCTTAATTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 3960  
QY 3961 AGGAACATACCTTAGTGAAGAAACAAATGTTCTGCTAGCTTGTCTTCAAGTGA 4020  
Db 3961 AGGAACATACCTTAGTGAAGAAACAAATGTTCTGCTAGCTTGTCTTCAAGTGA 4020  
QY 4021 GTGAATTTGAAGATTTGACTGCAATATCAACACCAAGATCTTCTGATTTGTTCT 4080  
Db 4021 GTGAATTTGAAGATTTGACTGCAATATCAACACCAAGATCTTCTGATTTGTTCT 4080  
QY 4081 CCAGAAATGAGAGATCAGTCTGAAGAGCAGAGAGTGTGCTGAGTGAAGAGAAATGG 4140  
Db 4081 CCAGAAATGAGAGATCAGTCTGAAGAGCAGAGAGTGTGCTGAGTGAAGAGAAATGG 4140  
QY 4141 TTTCAAGATGATGAAGAAAGAGAGAGCGGCTTGAAGAAATTAATCAAGAGCAAGAG 4200  
Db 4141 TTTCAAGATGATGAAGAAAGAGAGAGCGGCTTGAAGAAATTAATCAAGAGCAAGAG 4200  
QY 4201 TGGATTTCAAACTTAAGTGAAGAGATCTGAGTGTGAAGTGAAGTGAAGTGAAGTGAAG 4260  
Db 4201 TGGATTTCAAACTTAAGTGAAGAGATCTGAGTGTGAAGTGAAGTGAAGTGAAGTGAAG 4260  
QY 4261 ACTGCTCAGAGGCTATCTCTCAGAGTGAATTTTAACTGAGCAGAGAGATACCATGC 4320  
Db 4261 ACTGCTCAGAGGCTATCTCTCAGAGTGAATTTTAACTGAGCAGAGAGATACCATGC 4320  
QY 4321 AACATTAACCTGATTAAGAGTCCAGAGAGAAATGCTGAATCTGAAGCTGTGTTAAG 4380  
Db 4321 AACATTAACCTGATTAAGAGTCCAGAGAGAAATGCTGAATCTGAAGCTGTGTTAAG 4380  
QY 4381 ATGGAGCCAGGCTTCTAATCAGTACCTTCAATCAATGAAGTCTTCTGCTTGAAG 4440  
Db 4381 ATGGAGCCAGGCTTCTAATCAGTACCTTCAATCAATGAAGTCTTCTGCTTGAAG 4440  
QY 4441 ACCGCGAATCCAGAAACAAAGCAATCAGAAAGAGCTATTAATCTTCAAGAAAGTA 4500  
Db 4441 ACCGCGAATCCAGAAACAAAGCAATCAGAAAGAGCTATTAATCTTCAAGAAAGTA 4500  
QY 4501 GTGAATACCTTATTAAGCCAGAAATCCAGAAAGAGCTTCTCTGCAAGTGTGAGTGTG 4560  
Db 4501 GTGAATACCTTATTAAGCCAGAAATCCAGAAAGAGCTTCTCTGCAAGTGTGAGTGTG 4560  
QY 4561 CAGATAGTCTTCAACCTAATTAAGAAACAGAGAGTGAAGAGTATCCCTTCTAAT 4620  
Db 4561 CAGATAGTCTTCAACCTAATTAAGAAACAGAGAGTGAAGAGTATCCCTTCTAAT 4620  
QY 4621 GCCCATCATTTAGATGATAGTGTGATCAGAGTGTCTCTGAGAGTCTTCAAGATGA 4680  
Db 4621 GCCCATCATTTAGATGATAGTGTGATCAGAGTGTCTCTGAGAGTCTTCAAGATGA 4680  
QY 4681 ACTAACCATCTCAAGAGAGCTCATTAAGTGTGTGATGAGAGCAACAGCTGGAAG 4740  
Db 4681 ACTAACCATCTCAAGAGAGCTCATTAAGTGTGTGATGAGAGCAACAGCTGGAAG 4740  
QY 4741 AGCTGAGGAGCAACGATTTGAAGAGAAACATTTACTTGCAGAGCAAGATCTAGAGGAA 4800  
Db 4741 AGCTGAGGAGCAACGATTTGAAGAGAAACATTTACTTGCAGAGCAAGATCTAGAGGAA 4800  
QY 4801 CCCCTTACCTGGAATCTGGAATCAGCTCTTCTGTGATGACCTGATCTGATCTTCTG 4860

Db 421 ATGAAAAGCCTATATTTTGGCAAAAAGAAAATAACTCTCTGAAACATCTAAAAGATG 480  
Qy 481 AAGTTTCTATCATCCAAAGTATGGGCTACAGAAAACGCTGCCAAAAGACTTCTACAGAGTG 540  
Db 481 AAGTTTCTATCATCCAAAGTATGGGCTACAGAAAACGCTGCCAAAAGACTTCTACAGAGTG 540  
Qy 541 AACCAGAAATCTCTTCTTGACAGAAAACGAGTCTGAGTCCAGCTCTTAACTTGGAA 600  
Db 541 AACCAGAAATCTCTTCTTGACAGAAAACGAGTCTGAGTCCAGCTCTTAACTTGGAA 600  
Qy 601 CTGTGAGAACTCTGAGACAAAGCAGCGATCAACCTTAAAGAGCTGTGTCTACATTTG 660  
Db 601 CTGTGAGAACTCTGAGACAAAGCAGCGATCAACCTTAAAGAGCTGTGTCTACATTTG 660  
Qy 661 AATTGGAGTCTGATCTCTGAGATACCGTTAATAGGCACTTATTGACGTGGAG 720  
Db 661 AATTGGAGTCTGATCTCTGAGATACCGTTAATAGGCACTTATTGACGTGGAG 720  
Qy 721 ATCAAGAAATGTTTACAAATCACCCCTCAAGAAACGAGATGAAATCAGTTTGAATTCTG 780  
Db 721 ATCAAGAAATGTTTACAAATCACCCCTCAAGAAACGAGATGAAATCAGTTTGAATTCTG 780  
Qy 781 CAAAAAGGCTGCTTGTGATTTTCTGAGACGAGATGTAACAATCTGMACTCATCAAC 840  
Db 781 CAAAAAGGCTGCTTGTGATTTTCTGAGACGAGATGTAACAATCTGMACTCATCAAC 840  
Qy 841 CCAGTAATATGATTTTGAACACCACTGAGAAACGCTGAGAGGCACTCCAGAAAAGT 900  
Db 841 CCAGTAATATGATTTTGAACACCACTGAGAAACGCTGAGAGGCACTCCAGAAAAGT 900  
Qy 901 ATCAGGGAGTCTGCTTTCAAACTTGATGAGACCAATGTTGCAACAATCTCATGCA 960  
Db 901 ATCAGGGAGTCTGCTTTCAAACTTGATGAGACCAATGTTGCAACAATCTCATGCA 960  
Qy 961 GCTCTATTAACAGATGAGAAACAGCAGTTTATCTACTAATAAGACGAATGATGAGAA 1020  
Db 961 GCTCTATTAACAGATGAGAAACAGCAGTTTATCTACTAATAAGACGAATGATGAGAA 1020  
Qy 1021 AAGCTGAATCTGTATATAAAGCAAAACAGCTGCTTGAAGAGAGCCAACTAACAGAT 1080  
Db 1021 AAGCTGAATCTGTATATAAAGCAAAACAGCTGCTTGAAGAGAGCCAACTAACAGAT 1080  
Qy 1081 GGGCTGGAAGTAAAGAAACATGTAATGATAGCGGAGCTCCAGCAGAAAAAAGTAG 1140  
Db 1081 GGGCTGGAAGTAAAGAAACATGTAATGATAGCGGAGCTCCAGCAGAAAAAAGTAG 1140  
Qy 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAAAGATGGAATAGCAGAACTGCCATGCT 1200  
Db 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAAAGATGGAATAGCAGAACTGCCATGCT 1200  
Qy 1201 CAGAGAACTCTAGAGATCTAGAGATGTTCTTGATTAACACTAATATGACAGATTCAGA 1260  
Db 1201 CAGAGAACTCTAGAGATCTAGAGATGTTCTTGATTAACACTAATATGACAGATTCAGA 1260  
Qy 1261 AAGTTAATGAGTGGTTTTCCAGAAAGTAGAATCTGTAAGTTCTGATGACCTACATGATG 1320  
Db 1261 AAGTTAATGAGTGGTTTTCCAGAAAGTAGAATCTGTAAGTTCTGATGACCTACATGATG 1320  
Qy 1321 GGGAGTCTGAATCAAAAGCCAAAGTAGTATGTTTGAAGCTTTTAAATGAGGATGATG 1380  
Db 1321 GGGAGTCTGAATCAAAAGCCAAAGTAGTATGTTTGAAGCTTTTAAATGAGGATGATG 1380  
Qy 1381 AATATCTGCTTCTTCCAGAGAAATAGACTTACTGGCAGATGCTCATGAGGCTTTAA 1440  
Db 1381 AATATCTGCTTCTTCCAGAGAAATAGACTTACTGGCAGATGCTCATGAGGCTTTAA 1440  
Qy 1441 TATGTAAAGTGAAGAGTCTCAATCAATCAGTAGAGATTAATTAAGACAAATAT 1500  
Db 1441 TATGTAAAGTGAAGAGTCTCAATCAATCAGTAGAGATTAATTAAGACAAATAT 1500  
Qy 1501 TTGGGAAAACCTATCGGAAGAGGCAAGCTTCCCACTTAAAGCATGTAATCTGAAATC 1560  
Db 1501 TTGGGAAAACCTATCGGAAGAGGCAAGCTTCCCACTTAAAGCATGTAATCTGAAATC 1560

Db 1501 TTGGGAAAACCTATCGGAAGAGGCAAGCTTCCCACTTAAAGCATGTAATCTGAAATC 1560  
Qy 1561 TAAATATGAGACATTTGTTTCTAGGCAACAGATATATACAAGACGTCCTCCCAACAATA 1620  
Db 1561 TAAATATGAGACATTTGTTTCTAGGCAACAGATATATACAAGACGTCCTCCCAACAATA 1620  
Qy 1621 AATTAAAGCTTAAAGAGACCTACATGAGCTTCACTGAGATTTTATCAAGAAAG 1680  
Db 1621 AATTAAAGCTTAAAGAGACCTACATGAGCTTCACTGAGATTTTATCAAGAAAG 1680  
Qy 1681 CAGATTTGGAGCTTCAAAAAGCTCTGTAATGATTAATTCAGGAACTTAACCAAGAGC 1740  
Db 1681 CAGATTTGGAGCTTCAAAAAGCTCTGTAATGATTAATTCAGGAACTTAACCAAGAGC 1740  
Qy 1741 AGAATGCTCAAGTATGATTAATTAATGATGCTCATGAGATTAATTAAGAGTATTC 1800  
Db 1741 AGAATGCTCAAGTATGATTAATTAATGATGCTCATGAGATTAATTAAGAGTATTC 1800  
Qy 1801 CTATTCAGATGAGAAAAATCTTAAACCAATAGAAATCACTCGAAAAAGAAATCTGCTTCA 1860  
Db 1801 CTATTCAGATGAGAAAAATCTTAAACCAATAGAAATCACTCGAAAAAGAAATCTGCTTCA 1860  
Qy 1861 AAAGGAAAGCTGAACCTTAAAGCAGAGTATTAAGCAATAGGAACTCGAAATTAATTC 1920  
Db 1861 AAAGGAAAGCTGAACCTTAAAGCAGAGTATTAAGCAATAGGAACTCGAAATTAATTC 1920  
Qy 1921 ACAATTCAAAAGCACTTAAAGAAATAGGCTGAGAGAGAGTCTTCAACGAGCATATTC 1980  
Db 1921 ACAATTCAAAAGCACTTAAAGAAATAGGCTGAGAGAGAGTCTTCAACGAGCATATTC 1980  
Qy 1981 ATGGCTTTGAACCTAGTATGAGAAATCTAAGCCCACTTAATGTAATGTAATTCGAA 2040  
Db 1981 ATGGCTTTGAACCTAGTATGAGAAATCTAAGCCCACTTAATGTAATGTAATTCGAA 2040  
Qy 2041 TTGATAGTGTCTTCAAGAGTGAAGATTAAGAAAAAAGTCAACCAATCCAGTCA 2100  
Db 2041 TTGATAGTGTCTTCAAGAGTGAAGATTAAGAAAAAAGTCAACCAATCCAGTCA 2100  
Qy 2101 GGCACAGCAGAAACCTTCAACTCATGGAAGTAAAGAACTGGAACCTGAGCAAGAAAG 2160  
Db 2101 GGCACAGCAGAAACCTTCAACTCATGGAAGTAAAGAACTGGAACCTGAGCAAGAAAG 2160  
Qy 2161 GTAAACAAGCCAAATGAACAGACAAATGAAGACATGACAGGATCTTCCAGAGCTGA 2220  
Db 2161 GTAAACAAGCCAAATGAACAGACAAATGAAGACATGACAGGATCTTCCAGAGCTGA 2220  
Qy 2221 AGTTAACAAATGACACCTGTCTTTTACTAAGTGTTCAAATACCAATGAACTTAAGAT 2280  
Db 2221 AGTTAACAAATGACACCTGTCTTTTACTAAGTGTTCAAATACCAATGAACTTAAGAT 2280  
Qy 2281 TTGTCAATCTAGGCTTCCAAAGAGAAAGAAAGAAAGAAAGAAAGTAAAGT 2340  
Db 2281 TTGTCAATCTAGGCTTCCAAAGAGAAAGAAAGAAAGAAAGAAAGTAAAGT 2340  
Qy 2341 CTAATATGCTGAAGACCCCAAGATCTCATGTTAAGTGAAGAAAGGTTTTGCAAACTG 2400  
Db 2341 CTAATATGCTGAAGACCCCAAGATCTCATGTTAAGTGAAGAAAGGTTTTGCAAACTG 2400  
Qy 2401 AAAGATCTGTAAGAGTGAAGATTTTCACTGATCTGATGATTAATGCACTCAG 2460  
Db 2401 AAAGATCTGTAAGAGTGAAGATTTTCACTGATCTGATGATTAATGCACTCAG 2460  
Qy 2461 AAAGATCTGTAAGAGTGAAGATTTTCACTGATCTGATGATTAATGCACTCAG 2520  
Db 2461 AAAGATCTGTAAGAGTGAAGATTTTCACTGATCTGATGATTAATGCACTCAG 2520  
Qy 2521 GTGTGAGTCAAGTGAAGATTTGAAACCCCAAGGAGCTAATTCATGTTGTTCCAAAG 2580  
Db 2521 GTGTGAGTCAAGTGAAGATTTGAAACCCCAAGGAGCTAATTCATGTTGTTCCAAAG 2580  
Qy 2581 ATATATGAATGACACAGAAAGCTTTAAGTATCATTTGGAGCATGAAGTTAACACAGTC 2640  
Db 2581 ATATATGAATGACACAGAAAGCTTTAAGTATCATTTGGAGCATGAAGTTAACACAGTC 2640





|    |      |                                 |                                |                  |                 |      |
|----|------|---------------------------------|--------------------------------|------------------|-----------------|------|
| OY | 3001 | AGGAAACCTGACCTCACTTATCCAAATPAA  | CATGGA                         | CTTTTACAA        | AAACCAATGCTATAC | 3060 |
| Db | 3001 | ACGAACTGCACTCACTTACTCCAAATPAA   | CATGGA                         | CTTTTACAA        | AAACCAATGCTATAC | 3060 |
| OY | 3061 | CACCACTTTTCCATCAAGTCATTTGTTTAA  | AACTPAATGTA                    | AGAAAAATCGCTAGAG | 3120            |      |
| Db | 3061 | CACCACTTTTCCCATCAAGTCATTTGTTTAA | AACTPAATGTA                    | AGAAAAATCGCTAGAG | 3120            |      |
| OY | 3121 | AAACTTTGAGGAACATTCAATGCTCACTGAA | AGAAATGGGAAATGGAACATTCCAA      | 3180             |                 |      |
| Db | 3121 | AAACTTTGAGGAACATTCAATGCTCACTGAA | AGAAATGGGAAATGGAACATTCCAA      | 3180             |                 |      |
| OY | 3181 | GTACAGTGACCAATTTAGCCGTAATTAAC   | TATAGAGAAAATGTTTTTAAAGAC       | CACT 3240        |                 |      |
| Db | 3181 | GTACAGTGACCAATTTAGCCGTAATTAAC   | TATAGAGAAAATGTTTTTAAAGAC       | CACT 3240        |                 |      |
| OY | 3241 | CAAGCAATATTAATAGAGTAGGTTCCAGT   | ACTAATGAATGGGCTCCAGTATTAATGA   | 3300             |                 |      |
| Db | 3241 | CAAGCAATATTAATAGAGTAGGTTCCAGT   | ACTAATGAATGGGCTCCAGTATTAATGA   | 3300             |                 |      |
| OY | 3301 | TAGGTTCCAGTATGAAAAATTCAAGCAGAA  | CTAGTAAGAAACAGAGGCCAAATTTGA    | 3360             |                 |      |
| Db | 3301 | TAGGTTCCAGTATGAAAAATTCAAGCAGAA  | CTAGTAAGAAACAGAGGCCAAATTTGA    | 3360             |                 |      |
| OY | 3361 | ATGCTATGTTGATTTAGGGGTTTTGCAAC   | CTGAGGCTATPAACAAAGCTCTCTGGAA   | 3420             |                 |      |
| Db | 3361 | ATGCTATGTTGATTTAGGGGTTTTGCAAC   | CTGAGGCTATPAACAAAGCTCTCTGGAA   | 3420             |                 |      |
| OY | 3421 | GTAATTGTAGCATCTGTAATAAATAAGCA   | GAATATGAAGATAGTTCAGACTGTA      | 3480             |                 |      |
| Db | 3421 | GTAATTGTAGCATCTGTAATAAATAAGCA   | GAATATGAAGATAGTTCAGACTGTA      | 3480             |                 |      |
| OY | 3481 | ATACAGATTTCTCTCCATATCTGATTTCA   | GATTAAGAACAGCTATGGGAAGTATGC    | 3540             |                 |      |
| Db | 3481 | ATACAGATTTCTCTCCATATCTGATTTCA   | GATTAAGAACAGCTATGGGAAGTATGC    | 3540             |                 |      |
| OY | 3541 | ATGCATCTCAGGTTGTTCTGAGACACCT    | GAAGACCTGTAGATAGCTGAATTAAG     | 3600             |                 |      |
| Db | 3541 | ATGCATCTCAGGTTGTTCTGAGACACCT    | GAAGACCTGTAGATAGCTGAATTAAG     | 3600             |                 |      |
| OY | 3601 | AAGATCTAGTTTGTCTGAAAAATGACATTA  | AGGAAGTTGCTGTGTTTTAGCAAAAGCG   | 3660             |                 |      |
| Db | 3601 | AAGATCTAGTTTGTCTGAAAAATGACATTA  | AGGAAGTTGCTGTGTTTTAGCAAAAGCG   | 3660             |                 |      |
| OY | 3661 | TCCAGAAAGAGAGCTTAGCAGAGTCTC     | TAGCCCTTACCCATACACATTTGGCTCAG  | 3720             |                 |      |
| Db | 3661 | TCCAGAAAGAGAGCTTAGCAGAGTCTC     | TAGCCCTTACCCATACACATTTGGCTCAG  | 3720             |                 |      |
| OY | 3721 | GTTACCGGAAGAGGGGCCAAAGAAATTA    | AGAGTCTCTCAAGAGAACTTATCTAGTAG  | 3780             |                 |      |
| Db | 3721 | GTTACCGGAAGAGGGGCCAAAGAAATTA    | AGAGTCTCTCAAGAGAACTTATCTAGTAG  | 3780             |                 |      |
| OY | 3781 | AAGAGCTTCCCGTCTCCAAACCTGTTAT    | TGTAATGTAACAAATATACCTCTCAGT    | 3840             |                 |      |
| Db | 3781 | AAGAGCTTCCCGTCTCCAAACCTGTTAT    | TGTAATGTAACAAATATACCTCTCAGT    | 3840             |                 |      |
| OY | 3841 | CTACTAGGCATAGCAACCGTTGCTACCG    | AGTGTCTGTCTAAGAACACAGAGAGAA    | TTTAT 3900       |                 |      |
| Db | 3841 | CTACTAGGCATAGCAACCGTTGCTACCG    | AGTGTCTGTCTAAGAACACAGAGAGAA    | TTTAT 3900       |                 |      |
| OY | 3901 | TATCATTTAGAAGATGCTTAAATGCTGCA   | AGTAACACAGTAATATGGCAAAAGCATCTC | 3960             |                 |      |
| Db | 3901 | TATCATTTAGAAGATGCTTAAATGCTGCA   | AGTAACACAGTAATATGGCAAAAGCATCTC | 3960             |                 |      |
| OY | 3961 | AGGAACATCACCTTAGTAGAGAAACAA     | ATGTTGCTGAGGTTGTTTTCTTCAAGTGCA | 4020             |                 |      |
| Db | 3961 | AGGAACATCACCTTAGTAGAGAAACAA     | ATGTTGCTGAGGTTGTTTTCTTCAAGTGCA | 4020             |                 |      |
| OY | 4021 | GTGAATTTGAAGACTTGACTCAATACAA    | ACACCCAGAGTCTTTCTTGATTTGGTCTT  | 4080             |                 |      |
| Db | 4021 | GTGAATTTGAAGACTTGACTCAATACAA    | ACACCCAGAGTCTTTCTTGATTTGGTCTT  | 4080             |                 |      |
| OY | 4081 | CCAAACAAATAGAGCATAGTCTGAAAG     | CCAGGAGTTGTTCTGATGACAAAGAA     | TTGG 4140        |                 |      |

|    |      |  |      |
|----|------|--|------|
| D  | 4081 | CCAAACCAATGAGCATCAGTCTGAAAGCCAGGGAGTTGGTGTGAGTCACAAAGAAATTGG   | 4144 |
| OY | 4141 | TTTCAGATGATGAAAGAAAGGAAACGGGCTTGGAAAGAAATATCTAAGAAAGCAAAACA    | 4200 |
| D  | 4141 | TTTCAGATGATGAAAGAAAGGAAACGGGCTTGGAAAGAAATATCTAAGAAAGCAAAACA    | 4200 |
| OY | 4201 | TGGATTCAAACCTTAGTGTAAGAGCATCTGGGTGTGACAGTGAACCAAGCCCTCTGAAAG   | 4266 |
| D  | 4201 | TGGATTCAAACCTTAGTGTAAGAGCATCTGGGTGTGACAGTGAACCAAGCCCTCTGAAAG   | 4266 |
| OY | 4261 | ACTGCTCAGGGGCTATCCTCTCAGAGTGACATTTTAACCACTGACAGAGGATACCATGC    | 4322 |
| D  | 4261 | ACTGCTCAGGGGCTATCCTCTCAGAGTGACATTTTAACCACTGACAGAGGATACCATGC    | 4322 |
| OY | 4321 | AAACATTAACCTGATTAAGCTCCAGCAGAAATGGCTGAACTAGAACTGTGTAGAACACG    | 4380 |
| D  | 4321 | AAACATTAACCTGATTAAGCTCCAGCAGAAATGGCTGAACTAGAACTGTGTAGAACACG    | 4380 |
| OY | 4381 | ATGGAGAGCCAGGCTTCTTAACAGCTACCTTCATATAGTGACTCTTCTGCGCTTTGAGG    | 4440 |
| D  | 4381 | ATGGAGAGCCAGGCTTCTTAACAGCTACCTTCATATAGTGACTCTTCTGCGCTTTGAGG    | 4440 |
| OY | 4441 | ACCTGCGAAATCCAGAACAAAGCAATCAGAAAAAGAGTATTAACCTTCAAGAAAAAGTA    | 4500 |
| D  | 4441 | ACCTGCGAAATCCAGAACAAAGCAATCAGAAAAAGAGTATTAACCTTCAAGAAAAAGTA    | 4500 |
| OY | 4501 | GTGAATACCTTATTAAGCCAGAAATCCAGAGGCTTTCTGCTGACAAAGTTTGAGGTGCTG   | 4560 |
| D  | 4501 | GTGAATACCTTATTAAGCCAGAAATCCAGAGGCTTTCTGCTGACAAAGTTTGAGGTGCTG   | 4560 |
| OY | 4561 | CAGATAGTTCTACGAGTAAATAAAGAACCAAGAGTGGAAAGTCATCCCTCTTAAT        | 4620 |
| D  | 4561 | CAGATAGTTCTACGAGTAAATAAAGAACCAAGAGTGGAAAGTCATCCCTCTTAAT        | 4620 |
| OY | 4621 | GCCCATCAATTGATATAGTGGTGCATAGCAAGTGGCTGCGGAGCTTCAGAAATAGAA      | 4680 |
| D  | 4621 | GCCCATCAATTGATATAGTGGTGCATAGCAAGTGGCTGCGGAGCTTCAGAAATAGAA      | 4680 |
| OY | 4681 | ACTACCCATCTCAAGAGAGGCTCATTAAGTGTGTGATGTGAGAGCAACAGCTGGAAG      | 4740 |
| D  | 4681 | ACTACCCATCTCAAGAGAGGCTCATTAAGTGTGTGATGTGAGAGCAACAGCTGGAAG      | 4740 |
| OY | 4741 | AGTGTGGGCGACAGATTTGAACGGAACATCTTACTTCCAAAGCAGATTTAGAGGAA       | 4800 |
| D  | 4741 | AGTGTGGGCGACAGATTTGAACGGAACATCTTACTTCCAAAGCAGATTTAGAGGAA       | 4800 |
| OY | 4801 | CCCCCTTACCTGGAATCTGGGAATCAGCCCTTCTCTGATGAGCCCTGAATCTGATCCTTCTG | 4860 |
| D  | 4801 | CCCCCTTACCTGGAATCTGGGAATCAGCCCTTCTCTGATGAGCCCTGAATCTGATCCTTCTG | 4860 |
| OY | 4861 | AAGACAGAGCCCCAGAGTCAGCTGGTGTGGCAATACATCACTTTCAACCTCTGCATTTGA   | 4920 |
| D  | 4861 | AAGACAGAGCCCCAGAGTCAGCTGGTGTGGCAATACATCACTTTCAACCTCTGCATTTGA   | 4920 |
| OY | 4921 | AAAGTCCCAATTGAAAGTTGACAGATCTGCCAGAGTCAGCTGCTCTCATACTG          | 4980 |
| D  | 4921 | AAAGTCCCAATTGAAAGTTGACAGATCTGCCAGAGTCAGCTGCTCTCATACTG          | 4980 |
| OY | 4981 | ATACTGCTGGGATTAATGCAATGGAAGAAATGTGAGCAGAGGAGAAAGCACAATTTGACAG  | 5040 |
| D  | 4981 | ATACTGCTGGGATTAATGCAATGGAAGAAATGTGAGCAGAGGAGAAAGCACAATTTGACAG  | 5040 |
| OY | 5041 | CTTCAACAGAAAGGCTCAACAAAGAAATGTGCATGAGTGGTGTGCGGCTGACCCCAAG     | 5100 |
| D  | 5041 | CTTCAACAGAAAGGCTCAACAAAGAAATGTGCATGAGTGGTGTGCGGCTGACCCCAAG     | 5100 |
| OY | 5101 | AATTATGCTGCTGTAACAAGTTTGCAGAAAAACAACATCACTTTAACTAATCTAAATTA    | 5160 |
| D  | 5101 | AATTATGCTGCTGTAACAAGTTTGCAGAAAAACAACATCACTTTAACTAATCTAAATTA    | 5160 |
| OY | 5161 | CTGAAGAGACTACATGTTGTTATGAAAACAGATGCTGAAGTTGTGTGAAACGACAC       | 5220 |
| D  | 5161 | CTGAAGAGACTACATGTTGTTATGAAAACAGATGCTGAAGTTGTGTGAAACGACAC       | 5220 |

Db 781 CAAAAAGGCTGCTGTGAAATTTCTGAGCGAGTGAACAATACTGAAACATCATCAAC 840  
Qy 841 CCGATTAATATGTTTGAACACACTGAGAGCGTGCACTGAGAGCATCCGAAAAAGT 900  
Db 841 CCGATTAATATGTTTGAACACACTGAGAGCGTGCACTGAGAGCATCCGAAAAAGT 900  
Qy 901 ATGAGGATGTTCTGTTTCAAACTGTGATGAGGCACTGGCACAAAATACCTCATGCC 960  
Db 901 ATGAGGATGTTCTGTTTCAAACTGTGATGAGGCACTGGCACAAAATACCTCATGCC 960  
Qy 961 GCTCATTAACAGCATGAGAACAGCAGTTTATTACTCACTAAAGA CAGATGATGTAGAAA 1020  
Db 961 GCTCATTAACAGCATGAGAACAGCAGTTTATTACTCACTAAAGA CAGATGATGTAGAAA 1020  
Qy 1021 AGGCTGAATTTCTGTAATAAAGCAACAGCTGGCTTAGCAAGAGCCAACTAACAGAT 1080  
Db 1021 AGGCTGAATTTCTGTAATAAAGCAACAGCTGGCTTAGCAAGAGCCAACTAACAGAT 1080  
Qy 1081 GGGCTGGAAGTAAAGAAACATGTAATGATAGCGGAGCTCCAGCACAGAAAAAGGTAG 1140  
Db 1081 GGGCTGGAAGTAAAGAAACATGTAATGATAGCGGAGCTCCAGCACAGAAAAAGGTAG 1140  
Qy 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAGATGGAATGAAGCAAGAACTGCAATGCT 1200  
Db 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAGATGGAATGAAGCAAGAACTGCAATGCT 1200  
Qy 1201 CAGAGAACTCTAAGATACTGAAAGATGTTCTTGATTAACACTAAATAGACATTCAGA 1260  
Db 1201 CAGAGAACTCTAAGATACTGAAAGATGTTCTTGATTAACACTAAATAGACATTCAGA 1260  
Qy 1261 AAGTTATGAGTGGTGTTCAGAGAGTGAACGTGATAGTCTGATGACTCATGATGATG 1320  
Db 1261 AAGTTATGAGTGGTGTTCAGAGAGTGAACGTGATAGTCTGATGACTCATGATGATG 1320  
Qy 1321 GGGAGTCTGAATCAAAATGCCAAAGTACGTATGTAAGCGTTCTAAATGAGTGAATG 1380  
Db 1321 GGGAGTCTGAATCAAAATGCCAAAGTACGTATGTAAGCGTTCTAAATGAGTGAATG 1380  
Qy 1381 AATATTTCTGTTCTTTCAGAGAAATAGACTTACTGCGCAAGTATCTCATGAGGCTTTAA 1440  
Db 1381 AATATTTCTGTTCTTTCAGAGAAATAGACTTACTGCGCAAGTATCTCATGAGGCTTTAA 1440  
Qy 1441 TATGTAAGTGAAGAGTCACTCCAAATCAGTAGAGTAATATTGAAGCAAAATAT 1500  
Db 1441 TATGTAAGTGAAGAGTCACTCCAAATCAGTAGAGTAATATTGAAGCAAAATAT 1500  
Qy 1501 TTGGGAAAACTTATCGGAAAGAGCAAGCTCCCAACTTAAGCCATGTAACTGAAATC 1560  
Db 1501 TTGGGAAAACTTATCGGAAAGAGCAAGCTCCCAACTTAAGCCATGTAACTGAAATC 1560  
Qy 1561 TAATTTATAGAGCAATTTGTTACTGAGCACAGATAAACAAGAGCGTCCCTCAAAATA 1620  
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Qy 1921 ACAATTTCAAAGACCTTAATAAAGATAGGCTGAGAGAGTCTTCTACAGGCATATTC 1980  
Db 1921 ACAATTTCAAAGACCTTAATAAAGATAGGCTGAGAGAGTCTTCTACAGGCATATTC 1980  
Qy 1981 ATGCGCTTGAATAGTATGATGATGAAATCTAAGCCACTAATTTGATCTGATTTGCAAA 2040  
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Qy 2101 GGCACAGCAGAAACCTACACACTCATGGAAGTAAAGAACTGCAACTGAGGCCAAGAGA 2160  
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DB 5521 GCACAGGTGTCACCAATTTGTTGTGACCAATCCCTGACAGAGCAATGGCT 5580  
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DB 5581 TCCATGCAATTTGAGAGATGTGTGAGGACCTGTGTGACCCGAGAGTGGTGTGACA 5640  
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DB 5641 GTGTGACACTTACCAAGTGCAGAGCTGAGACACTTACTGATACCCAGATCCCCACA 5700  
QY 5701 GCCACTACTGA 5711  
DB 5701 GCCACTACTGA 5711

RESULT 13

AAT32601 standard: cDNA, 5914 BP.

AC AAT32601;  
DT 19-NOV-1996 (first entry)  
DE BRCA1, breast and ovarian cancer susceptibility gene.  
XX BRCA1, breast cancer; ovarian cancer; predisposing gene; diagnosis;  
KM susceptibility gene; prognosis; gene therapy; ds.  
XX Homo sapiens.

XX Key Location/Qualifiers  
FT CDS 120..5711  
FT /tag= a  
FT /product= BRCA1 protein

XX W09605308-A1.

XX 22-FEB-1996.

XX 11-AUG-1995; 95WO-US10220.

XX 07-JUN-1995; 95US-0488011.  
XX 12-AUG-1994; 94US-0289221.  
XX 02-SEP-1994; 94US-0300266.  
XX 16-SEP-1994; 94US-0308104.  
XX 29-NOV-1994; 94US-0348824.  
XX 24-MAR-1995; 95US-0409305.  
XX 07-JUN-1995; 95US-0483554.  
XX 07-JUN-1995; 95US-0487002.

XX (MYRI-) MYRIAD GENETICS INC.  
XX (UTAH) UNIV UTAH RES FOUND.  
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Futreal PA, Goldgar DE, Harshman KD, Kamb A, Miki Y;  
XX Shattuck-Eidens DM, Skolnick MH, Swenson J, Tavtigian SV;  
XX Wiseman RW;

XX WPI; 1996-139704/14.

XX P-PSDB; AAR97128.

XX New method for diagnosing a predisposition to breast and ovarian  
XX cancer - by detecting a germline alteration in the BRCA1 gene or  
XX PT gene regulatory sequence; for gene therapy and to screen for drugs

XX Claim 4; Page 108-117; 200pp; English.

CC This is the nucleotide sequence of the breast and ovarian cancer  
CC susceptibility gene, BRCA1. Four kindred families provided genetic  
CC evidence for localization of BRCA1 to a sufficiently small region for  
CC the application of positional cloning strategies. A detailed map of  
CC transcripts was developed for the region of 17q21 between D17S1321 and  
CC D17S1324. A combination of sequences obtained from cDNA clones,  
CC hybrid-selected sequences and PCR products, allowed construction of a  
CC composite full-length BRCA1 cDNA (see AAT32612 for genomic sequence).  
CC The isolated cDNA is used in methods for either diagnosis of the  
CC predisposition to cancer (partic. breast and ovarian cancer), or for the  
CC diagnosis or prognosis of cancer, and also in gene-based therapies  
CC directed at cancer cells.

XX Sequence 5914 BP; 2006 A; 1156 C; 1316 G; 1436 T; 0 other;

Query Match 100.0%; Score 5709.4; DB 17; Length 5914;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 5710; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AGCTGCTGAGACTTCTGGAACCCGACAGAGCTGTGGGTTTCTGATTAACCTGGGCC 60  
DB 1 AGCTGCTGAGACTTCTGGAACCCGACAGAGCTGTGGGTTTCTGATTAACCTGGGCC 60  
QY 61 CTTGGGCTCAGAGAGGCTTCACTCTGTCTGTGGTTAAAGTTCAATGGAACAGAAAGAA 120  
DB 61 CTTGGGCTCAGAGAGGCTTCACTCTGTCTGTGGTTAAAGTTCAATGGAACAGAAAGAA 120  
QY 121 TGGATTTATCTGCTCTTGGGTTGAAGAAGTAAATGATTAATGATTAATGATTAATG 180  
DB 121 TGGATTTATCTGCTCTTGGGTTGAAGAAGTAAATGATTAATGATTAATGATTAATG 180  
QY 181 TCTTAGAGTGTCCCATCTGTCTGTGAGTTGATCAAGAACCTGTCTCCCAAAAGTGTACC 240  
DB 181 TCTTAGAGTGTCCCATCTGTCTGTGAGTTGATCAAGAACCTGTCTCCCAAAAGTGTACC 240  
QY 241 ACATATTTTGGAAATTTTGCATGCTGAACCTTCTCAACAGAAAGAGGCTTCAACAGT 300  
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DB 361 AACTGTGTAAGAGCTATTTGAATCATTTGTGCTTTACAGTGAACAGTTTGGAGT 420  
QY 421 ATGCAAAACAGCTAATTTTGCAGAAAGAAATTAATCTCTGTAACATTAAGATG 480  
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DB 481 AAGTTTCATCATCAAGATTAAGGCTTCAAGAAAGGCTTCAAGAAAGCTTCAAGATG 540  
QY 541 AACCGAAATTCCTTCTCTGAGAAACAGCTCTCACTCTCAACTCTTAACCTTGA 600  
DB 541 AACCGAAATTCCTTCTCTGAGAAACAGCTCTCACTCTCAACTCTTAACCTTGA 600  
QY 601 CTGTGAGAACTCTGAGAGCAAGAGGATTAACCTCAAAAGAGCTGTCTACATG 660  
DB 601 CTGTGAGAACTCTGAGAGCAAGAGGATTAACCTCAAAAGAGCTGTCTACATG 660  
QY 661 AATTGGATCTGATTTCTTGAAGATTAAGTAAAGGCACTTAATGAGAGTGTGAG 720  
DB 661 AATTGGATCTGATTTCTTGAAGATTAAGTAAAGGCACTTAATGAGAGTGTGAG 720  
QY 721 ATCAAGATTTGTAACAAATCAACCTCAAGAGCAAGAGTAAATCAAGTTGGATTG 780  
DB 721 ATCAAGATTTGTAACAAATCAACCTCAAGAGCAAGAGTAAATCAAGTTGGATTG 780  
QY 781 CAAAAAGGCTGTGTGAATTTTCTGAGAGCGAGTGAACAAATAGTGAACATCAAC 840  
DB 781 CAAAAAGGCTGTGTGAATTTTCTGAGAGCGAGTGAACAAATAGTGAACATCAAC 840

Db 3241 CAAGCAATATTAATGAGTAGTTCACAGTACTAATGAGTGGGCTCCAGATTATTAAGAA 3300  
QY 3301 TAGGTTCCAGTGTATGAAAAATTCAAGCAGAACTAGTAGAAAACAGAGGGCCAAATTTGA 3360  
Db 3301 TAGGTTCCAGTGTATGAAAAATTCAAGCAGAACTAGTAGAAAACAGAGGGCCAAATTTGA 3360  
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QY 3421 GTAATTGTAAAGCATCTGTAATAAAGAGCAAGATATGAAAGTAGTTCAAGCTGTA 3480  
Db 3421 GTAATTGTAAAGCATCTGTAATAAAGAGCAAGATATGAAAGTAGTTCAAGCTGTA 3480  
QY 3481 ATACCAATTTCTCCATATCTGATTTTCAGATACTTAGAACGCTTAGAGGAAGTAGTC 3540  
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QY 3601 AAGATATCTAGTTTGTCTGTAATAAGATTAAGAAAGTTCTGCTGTTTTAGCAAAAGCG 3660  
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Db 3901 TATCATTTGAAGATTAAGTAAATGATGACGTACAGTAACAGTAATTTGGCAAGGATCTC 3960  
QY 3961 AGGAACATCACTTAACTGAGGAAACAAATGTTCTGCTAGCTGTTTTCTTCAAGTGA 4020  
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QY 5401 TCAAGGGGCTAAGATCTGTTCTATGGGCTTCAACCAATGCCCAAGATCAATCG 5460  
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 PI Robinson-Benton CL, Szabo CI, Thompson ME;  
 XX  
 XX WPI: 1997-434733/40.  
 DR P-PSDB: AAW23286.  
 DR  
 PT BRCA1 and BRCA2 tumour suppressor gene products - useful to inhibit  
 PT breast and ovarian cancer cell growth and tumourigenesis, or treat  
 PT gene linked hereditary or sporadic ovarian or breast cancer  
 XX  
 PS Claim 13; Page 54-63; 148bp; English.  
 XX  
 CC This sequence comprises a full-length BRCA1 cDNA. Genetic analysis  
 CC of familial and ovarian cancer indicates that BRCA1 is a tumour  
 CC suppressor gene. It encodes a 190 kDa protein (see AAW23286) that is  
 CC an inhibitor of the growth and proliferation of human breast and  
 CC ovarian cancer cells. DNA encoding the BRCA1 protein can thus be  
 CC used in gene therapy methods for the treatment of breast and  
 CC ovarian cancers. A purified BRCA1 protein can also be used to treat  
 CC these cancers and, since it is secreted, can be used to identify  
 CC the BRCA1 receptor and hence to identify BRCA1 protein-mimetic  
 CC agents which act on the receptor for use in breast and ovarian  
 CC cancer treatment. The BRCA2 gene (see AAT84841) and BRCA2 protein  
 CC (see AAW2287) have also been characterised. Methods are claimed for  
 CC the isolation of BRCA1 or BRCA2 receptors, and for treating or  
 CC preventing breast and (gene-linked hereditary or sporadic) ovarian  
 CC cancers using BRCA1 and BRCA2 proteins and genes.  
 CC  
 XX  
 XX  
 SO Sequence 5712 BP; 1956 A; 1099 C; 1274 G; 1383 T; 0 other;  
 Query Match 100.0%; Score 5709.4; DB 18; Length 5712;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 5710; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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 841 CCAATTAATGATTTGAAACCACTGAGAAAGCTGAGCTGAGAGGATCCAGAAAGT 900  
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 961 GCTATTACAGCAATGAGAAACAGAGCTTATTAATCACTAAAGCAGAAATGATGAA 1020  
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 QY  
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 DB  
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 DB  
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 QY  
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 DB  
 1321 GGGAGCTGATCAATGCAAAAGTATGATATATGAGAGCTTAAATGAGAGTATG 1380  
 QY  
 1381 AATATCTGATTTCTCAGAGAAATGATGATGATGATGATGATGATGATGATGATG 1440



QY 1801 CTATTGAGATGAGAAAAATCTTAACCCAAATAGAACTCACTCGAAAAAGAAATCTGCTTCA 1860  
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Db 1861 AAAGCAAAAGCTGAACTTAATACAGACAGATTAAGCAATTTGGAATCTCGAAATTAATATCC 1920  
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Db 1921 ACAATTCAAAAGCACCCTTAAGAAATAGGCTGAGAGAAAGTCTTCTACAGAGCAATATTC 1980  
QY 1981 ATGGGCTTGAACCTAGTAGCAAGAAATCTAAGCCCACTAATTTGTAATTCGAAA 2040  
Db 1981 ATGGGCTTGAACCTAGTAGCAAGAAATCTAAGCCCACTAATTTGTAATTCGAAA 2040  
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Db 3481 ATACAGATTTTCTCCCATATCTGATTTCAATTAATTTAGAAACAGCTTATGGGAAGTATG 3540  
QY 3541 ATGCATCTCAGGTTGTTCTGAGACACCTGATGACCTGTAGATGATGGAATTAAG 3600  
Db 3541 ATGCATCTCAGGTTGTTCTGAGACACCTGATGACCTGTAGATGATGGAATTAAG 3600  
QY 3601 AAGATTAAGTGTGCTGAAATGAACATTAAGAAAGTTCGCTGTTTAAAGCAAGG 3660  
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QY 3721 GTTACGAGAGGAGGCGCAAGAAATTAAGAGCTCAGAGAGAACTATCTAGAGAGAG 3780  
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QY 3901 TATCATTAAGAAATATGCTTAATGATGACGAGTAAACAGAGTAATTTGCAAGGCACTTC 3960  
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QY 3961 AGGAACATCACTTAGTAGAGAAACAAATGTTCTGCTAGCTTGTCTTCTCAAGTGA 4020



PT BRCA1 om1 gene coding sequences - useful for distinguishing between  
PT polymorphisms and mutation(s) in the screening for disposition to  
breast or ovarian cancer

XX Claim 2e; Page -; 54dp; English.

CC This sequence encodes a human BRCA1 (breast and ovarian cancer  
CC predisposing gene) om12 gene in which a polymorphic variation occurs at  
CC nucleotide 3687. This sequence and other polymorphic variations of this  
CC sequence are useful for the identification of an individual who may or  
CC may not have an increased susceptibility to breast or ovarian cancer.  
CC The sequences used identify gene changes which are due to polymorphisms,  
CC rather than cancer causing mutations. BRCA1 is an anti-oncogene (tumour  
CC suppressor) which is involved in genetic inheritance of cancers,  
CC especially breast and ovarian cancer. It is found at human chromosome  
CC 17q which is known to be linked to cancer susceptibility, especially  
CC breast cancer. Cells containing a mutation in this gene lose the  
CC wild-type function of BRCA1 and are more susceptible to cancers.  
CC NOTE: This sequence does not appear in the specification but has been  
CC created from the wild type BRCA1 om12 gene represented in AAV46449.

XX Sequence 5711 BP, 1955 A, 1098 C, 1274 G, 1383 T, 1 other;

Query Match 100.0%; Score 5710.6; DB 19; Length 5711;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 5710; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 61 CCTGGCGTGAAGAGGCGCTTACCCCTGCTGCTGGGTAAAGTTGATGGAACAGAAAGAA 120
DB 61 CTGCGCTGAGAGGCGCTTACCCCTGCTGCTGGGTAAAGTTGATGGAACAGAAAGAA 120
QY 121 TGGATTATCTGCTCTTCCGCTTGAAGAAAGTACAAATGTCATTAATGCTATGACAGAAA 180
DB 121 TGGATTATCTGCTCTTCCGCTTGAAGAAAGTACAAATGTCATTAATGCTATGACAGAAA 180
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DB 421 ATGCAAAACAGCTATTAATTTTGAAGAAAGAAATTAATCTCTGAAACATTAAGAGATG 480
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QY 541 AACCCGAAATCTCTTCTTGCAGAGAAACAGCTCAAGTGTCCAAAGCTTCTACAGAGT 600
DB 541 AACCCGAAATCTCTTCTTGCAGAGAAACAGCTCAAGTGTCCAAAGCTTCTACAGAGT 600
QY 601 CTGTGGAAGTCTGAGAGCAAGAGGAGATACACCTCAAAAGAGAGTGTCTACATG 660
DB 601 CTGTGGAAGTCTGAGAGCAAGAGGAGATACACCTCAAAAGAGAGTGTCTACATG 660
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RESULT 10  
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 XX  
 DE Human BRCA1 omi2 polymorphism #5 cDNA.  
 XX  
 KW BRCA1; omi2; human; breast and ovarian cancer predisposing gene;  
 KW polymorphism; susceptibility; anti-oncogene; tumour suppressor;  
 KW chromosome 17q; ss.  
 XX  
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 XX  
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 FT FT variation  
 FT FT 3667  
 FT FT /\*tag= b  
 FT FT /note= "This polymorphic variation can be an A or G  
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 XX  
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 XX PF 12-FEB-1997; 97US-0798691.  
 XX  
 XX PR 12-FEB-1996; 96US-0598591.  
 XX PR 12-FEB-1997; 97US-0798691.  
 XX  
 XX PA (ONCO-) ONCOMED INC.  
 XX  
 XX PI Allen AC, Alvares CP, Critz BS, Murphy PD, Olson SJ;  
 XX PI Scheller DB, Zeng B;  
 XX  
 XX WP1; 1998-296774/26.

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Db 2101 GGCACGCGAAGAACCTTACAACTCATGGAAGGTAAAGAACCTGCACTGGAGCCCAAGT 2160  
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Db 2401 AAGATCTGTGAAGAGTACGATATTTCTGTTGCTGCTGCTGCTGCTGCTGCTGCTG 2460  
QY 2461 AAAGTATCTGCTGAAGAGTACGATATTTCTGTTGCTGCTGCTGCTGCTGCTGCTGCTG 2520  
Db 2461 AAAGTATCTGCTGAAGAGTACGATATTTCTGTTGCTGCTGCTGCTGCTGCTGCTGCTG 2520  
QY 2521 GTGTGAGTCACTGCTGAGATTTGAAACCCCAAGGAGCTAATTTCTGTTTCCAAAG 2580  
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QY 2581 ATTAATGGAATGACAGAAAGGCTTTAAGTATCTGGAATGGAATGGAATGGAATGGA 2640  
Db 2581 ATTAATGGAATGACAGAAAGGCTTTAAGTATCTGGAATGGAATGGAATGGAATGGA 2640  
QY 2641 GGGAAACAGCAGTGAAGAAATGGAAGAAAGTGAATGGAATGGAATGGAATGGAATGGA 2700  
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Db 2761 AATGTGCAATCTCTGCGCACTCTGCGGCTCTTAAAGAAAGTCCAAAGTCACTT 2820  
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Db 2821 TTGAATGTGAACAAAGAGAAAGAAATCAAGAAAGTGAATGGAATGGAATGGAATGGA 2880  
QY 2881 AGACAGTTAATCACTGAGGCTTCTGCTGTTGCTGCAAGAAATGCAAGAGTGA 2940  
Db 2881 AGACAGTTAATCACTGAGGCTTCTGCTGTTGCTGCAAGAAATGCAAGAGTGA 2940  
QY 2941 ATGCCAAATGATATCAAGAGAGGCTCTGAGTTTGTCTAATCTCACTGCAAGAGG 3000  
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Db 3001 ACCAAACTGAGCTCATCTCAAAATTAACATGAGCTTTTACAAAGCCATATCTGATAC 3060  
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Db 3061 CACCACTTTTCCATCAAGTCACTTTGTTAAATTAATTAAGAAATCTGCTAGAGG 3120

QY 3121 AAAAATTGAGAGACATTTCAATGCACTGAAAGAAATGGAATGGAATGGAATGGAATGGA 3180  
Db 3121 AAAAATTGAGAGACATTTCAATGCACTGAAAGAAATGGAATGGAATGGAATGGAATGGA 3180  
QY 3181 GTACAGTGAAGCAATTTAGCCGTAATTAACATTAAGAAATGTTTAAAGAACCCAGCT 3240  
Db 3181 GTACAGTGAAGCAATTTAGCCGTAATTAACATTAAGAAATGTTTAAAGAACCCAGCT 3240  
QY 3241 CAAGCAATTAATGAAGTGGTTCAGTACATTAAGAGTGGGCTCAGTATTAATGA 3300  
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Db 3301 TAGGTTCCAGTATGAAACATTTCAAGCAAGCTAGTGAAGAAAGAGGAGCCAAATTTGA 3360  
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Db 3601 AAGATCTAGTTTGTCTGAGAAATGACATTAAGAAAGTCTGCTGTTTACCAAGG 3660  
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Db 3781 AAGAGCTTCCCTGCTTCAACACTTGTATTTTGTGAAGTAAAGTAAATTAATCTTCACT 3840  
QY 3841 CTACTAGGATGACACCGTGTACAGAGGCTGCTGCTAAGAAACAGAGAGATTTAT 3900  
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QY 3901 TATCATTTGAAGATTAAGCTTAAATGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 3960  
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QY 4081 CCAAACTGAAGCATCACTGAAAGCAGGAGTGGTCTGAGTGAAGTGAAGTGAAGTGA 4140  
Db 4081 CCAAACTGAAGCATCACTGAAAGCAGGAGTGGTCTGAGTGAAGTGAAGTGAAGTGAAGTGA 4140  
QY 4141 TTTCAATGATGAAGAAAGAGGAGGCTTGAAGAAATTAATCAAGAAAGTGAAGTGAAGTGA 4200  
Db 4141 TTTCAATGATGAAGAAAGAGGAGGCTTGAAGAAATTAATCAAGAAAGTGAAGTGAAGTGA 4200

CC 17q which is known to be linked to cancer susceptibility, especially  
CC breast cancer. Cells containing a mutation in this gene lose the  
CC wild-type function of BRCA1 and are more susceptible to cancers.  
CC NOTE: This sequence does not appear in the specification but has been  
CC created from the wild type BRCA1 omi2 gene represented in AAIV46449.

XX Sequence 5711 BP, 1955 A; 1098 C; 1274 G; 1383 T; 1 other;

Query Match 100.0%; Score 5710.6; DB 19; Length 5711;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 5710; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGCTGAGACTTCTGAGACCCGACACAGCTGTGGGTTTCTCAGATACTGGGCC 60  
DB 1 AGCTGCTGAGACTTCTGAGACCCGACACAGCTGTGGGTTTCTCAGATACTGGGCC 60  
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DB 61 CCTGCGCTCAGAGAGCCCTTCAACCTCTGCTGTGGGTTAAAGTTGAAACGAAAGAA 120  
QY 121 TGAATTTATCTGCTCTGCGGTTGAAGAACTCAATTAATGCTATGCAAGAAA 180  
DB 121 TGAATTTATCTGCTCTGCGGTTGAAGAACTCAATTAATGCTATGCAAGAAA 180  
QY 181 TCTTAGAGTGTCCCATCTGTCTGAGTTGATCAAGAAACCTGTCTCCAAAGTGTGACC 240  
DB 181 TCTTAGAGTGTCCCATCTGTCTGAGTTGATCAAGAAACCTGTCTCCAAAGTGTGACC 240  
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DB 241 ACATATTTTGAATAATTTTGCATGCTGAACTTCTCAACGAGAAAGGCGCTTCAACT 300  
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DB 301 GTCCCTTTATGTAAGATATATAACCAAAAGAGCCCTACAAAGAAAGTACGATTTAGTC 360  
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QY 421 ATGCAACAGCTATTAATTTTGCAGAAAGAAATTAACCTCTCTGAACATCTTAAAGATG 480  
DB 421 ATGCAACAGCTATTAATTTTGCAGAAAGAAATTAACCTCTCTGAACATCTTAAAGATG 480  
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DB 601 CTGTGAGAACTCTGAGGCAAAAGCAGCGGATCAACCTCAAAAGACGCTGTCTACATTTG 660  
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QY 781 CAAAAAAGGCTGCTTGTGAATTTTCTGAGAGGATGAACAAATCTGAAACATCTCAAC 840  
DB 781 CAAAAAAGGCTGCTTGTGAATTTTCTGAGAGGATGAACAAATCTGAAACATCTCAAC 840  
QY 841 CCAGTAAATTAATGATTTGAAACCACTGAGAGCGTGAGGAGGATCCAGAAAGT 900  
DB 841 CCAGTAAATTAATGATTTGAAACCACTGAGAGCGTGAGGAGGATCCAGAAAGT 900  
QY 901 ATCAGGGTAGTTCGTTCMAAATTGATGAGACCATGTGGCACAATAACTCATGCA 960

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QY 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAGATGAATTAACACAAACCTGCATGCT 1200  
DB 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAGATGAATTAACACAAACCTGCATGCT 1200  
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QY 1681 CAGATTTGGCAGTTCAAAAGCTCTGTAATGATTAATCAAGGAACTTAACCAAGAGG 1740  
DB 1681 CAGATTTGGCAGTTCAAAAGCTCTGTAATGATTAATCAAGGAACTTAACCAAGAGG 1740  
QY 1741 AGAATGCTCAAGTATGAATTTTACTAATAGTGTCTAGGAATTAACCAAGAGGAT 1800  
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QY 1801 CTATTCAGATGAGAAATATCTTAACCAATTAAGATCACTCGAAAGAAATTCGCTTCA 1860  
DB 1801 CTATTCAGATGAGAAATATCTTAACCAATTAAGATCACTCGAAAGAAATTCGCTTCA 1860  
QY 1861 AAAGGAAAGCTGAACCTTAAGAGAGGATTAAGCAATTAAGCAATTAAGCAATTAAG 1920  
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QY 1921 ACAATTCAAAAGCACTTAAAGAAATAGCTGAGAGAGAGTCTTCTCAACGAGCATATTC 1980  
DB 1921 ACAATTCAAAAGCACTTAAAGAAATAGCTGAGAGAGAGTCTTCTCAACGAGCATATTC 1980  
QY 1981 ATGCGCTTGAATAGTAGTGAAGAAATTAAGCCCACTTAATGTACTGAATTCGAA 2040

ORGANISM: Homo sapiens  
STRAIN: BRCA1  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: 17  
MAP POSITION: 17q21  
US-08-798-691-1

Query Match 100.0%; Score 5711; DB 1; Length 5711;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 5711; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 AGCTCGCTGAGACTTCTCTGAGACCCCGACACGAGCTGAGGCTTTCTCAGATACTGGGCC 60
QY 61 CTTGCGCTCAGAGAGGCTTCAACCTCTGCTGGGTAAATTCATTGGAAACAGAAAGAA 120
DB 61 CTTGCGCTCAGAGAGGCTTCAACCTCTGCTGGGTAAATTCATTGGAAACAGAAAGAA 120
QY 121 TGGATTATCTGCTCTTCCGCTTGAAGAGTAACAAATGTCATTAAATGCTATGACAGAAA 180
DB 121 TGGATTATCTGCTCTTCCGCTTGAAGAGTAACAAATGTCATTAAATGCTATGACAGAAA 180
QY 181 TCTTGAAGTGTCCCATCTGTCTGAGATTGATCAAGAACTGTCTCCAAAGTGTGACC 240
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QY 421 ATGCAAAACAGCTAATTTTGGCAAAAAGAAATACTCTGTAACCTTAAGAGATG 480
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DB 601 CTGTGGAATCTGAGAGACAAAGCAGGATACAACTCAAGAGAGCTGTCTTAATTTG 660
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DB 841 CAGATATATATGATTTGAACACCACTGAGAAAGGCTCAGCTGAGAGCAATTCAGAAAAT 900
QY 901 ATGAGGTAGTTCTGTTTCAAACTTGATGTGAGCAATGTGACAAATATCTCATGCCA 960
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DB 1621 AATTAAAGGTAAAGAGACCTACATGAGGCTTCACTGAGGATTTTATCAAGAAAG 1680
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QY 1861 AAAAGAAAGCTGAACCTTAAGAGCAGATTAAGCAATATGGAATCTGAATTAATATCC 1920
DB 1861 AAAAGAAAGCTGAACCTTAAGAGCAGATTAAGCAATATGGAATCTGAATTAATATCC 1920
QY 1921 ACAATTCAAAAAGCACTTAAGAAATAGCTGAGAGAGAGTCTTCTACAGAGATATTC 1980
DB 1921 ACAATTCAAAAAGCACTTAAGAAATAGCTGAGAGAGAGTCTTCTACAGAGATATTC 1980
QY 1981 ATGCGCTTGAATAGTATGCTAGTGAATCTTAAGCCCACTTAATTTGATCTGATTTGCAA 2040
DB 1981 ATGCGCTTGAATAGTATGCTAGTGAATCTTAAGCCCACTTAATTTGATCTGATTTGCAA 2040
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5641 GTGAGCACTTACCAAGTCCAGAGCTGGAACCTTACTGATATCCCAAGATCCCGACA 5700  
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5701 GCCACTACTGA 5711  
5701 GCCACTACTGA 5711

RESULT 3  
US-08-825-487A-1  
Sequence 1, Application US/08825487A  
Patent No. 6048689  
GENERAL INFORMATION:  
APPLICANT: Murphy, Patricia D.  
APPLICANT: White, Margie B.  
TITLE OF INVENTION: METHODS FOR IDENTIFYING VARIATIONS IN POLYNUCLEOTIDE SEQUENC  
NUMBER OF SEQUENCES: 110  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Howrey & Simon  
STREET: 1299 Pennsylvania Avenue., N.W.  
CITY: Washington,  
STATE: DC  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/825,487A  
FILING DATE: 28-MAR-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US98/060002  
FILING DATE: 26-MAR-1998  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Albert P. Halluin  
REGISTRATION NUMBER: 25,227  
REFERENCE/DOCKET NUMBER: 05371, 0012, 999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-463-8100  
TELEFAX: 650-463-8400  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5711 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear

MOLECULE TYPE: cDNA  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
STRAIN: BRCAL  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: 17  
MAP POSITION: 17q21  
US-08-825-487A-1

Query Match 100.0%; Score 5711; DB 3; Length 5711;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 5711; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 601 CTGTGAGAACTCTGAGCAAAAGCAGCGGATACAACTCAAAAGAGTCTGTCTACATG 660
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DB 661 AATTGGGATCTGATCTTCTGAGAAATCCGTTAATAGGCACTTAATTCAGAGTGGAG 720
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DB 721 ATCAAGAATTTGTAACAAATCACTCTCAAGAAACAGGATGAATCAAGTTTGGATTCTG 780
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DB 781 CAAAAAGGCTGCTTGTGAATTTTCTGAGACGAGATGAACAAATACATCAATCAAC 840
QY 841 CCAGTAATTAATTAATTTGAACACCACTGAGAGAGCTGACAGTGAAGGCAATCCAGAAAGT 900
DB 841 CCAGTAATTAATTAATTTGAACACCACTGAGAGAGCTGACAGTGAAGGCAATCCAGAAAGT 900
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QY 1261 AAGTTAATGAGTGTCTTCCAGAAAGTGAATGTTAGTTCTGATGACTCAATGATG 1320
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DB 1321 GGGAGTCTGAATCAAAATGCCAAAGTGTGATGTTTGGACCTTAAATAGGTAGATG 1380
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DB 1801 CTATTCAAGATGAGAAATCTTAAACCAATTAAGATCACTGAAAGAAATCTGCTTTCA 1860
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 QY 5701 GCCACTACTGA 5711  
 DB GCCACTACTGA 5711

RESULT 4  
 US-09-074-476-1  
 ; Sequence 1, Application US/09074476  
 ; Patent No. 6130322  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Murphy, Patricia D.  
 ; APPLICANT: Allen, Antoinette C.  
 ; APPLICANT: Alvarado, Christopher P.  
 ; APPLICANT: Critz, Brenda S.  
 ; APPLICANT: Olson, Sheri J.  
 ; APPLICANT: Thunder, Denise  
 ; APPLICANT: Zeng, Bin  
 ; TITLE OF INVENTION: Coding Sequences of the Human  
 ; TITLE OF INVENTION: BRCA1 Gene  
 ; NUMBER OF SEQUENCES: 72  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Howrey & Simon  
 ; STREET: 1299 Pennsylvania Avenue N. W.  
 ; CITY: Washington  
 ; STATE: DC  
 ; COUNTRY: USA  
 ; ZIP: 20004  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/074.476  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 09/074.453  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Albert P. Halluin  
 ; REGISTRATION NUMBER: 25,227  
 ; REFERENCE/DOCKET NUMBER: 5371.34.US01  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 650-463-8109

TELEFAX: 650-463-8400  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5711 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
STRAIN: BRCA1 (om11)  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: 17  
MAP POSITION: 17q21  
US-09-074-476-1

Query Match 100.0%; Score 5711; DB 3; Length 5711;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 5711; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGCTGCGTGAAGTCTTCTGGAACCCGACACGAGCTGAGGGTTCTCAGATACCTGGGC 60  
DB 1 AGCTGCGTGAAGTCTTCTGGAACCCGACACGAGCTGAGGGTTCTCAGATACCTGGGC 60  
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DB 121 TGGATTATCTGCTCTTCCGCTTGAAGAAAGTACAAATGTCATTAATGCTATGACAGAAA 180  
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DB 181 TCTTAAGTGTCCCATCTGCTGGAAGTGTATCAAGAACCTGCTCACAAAAGTGTGACC 240  
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REGISTRATION NUMBER: 32,692  
REFERENCE/DOCKET NUMBER: PA-0054CIP  
TELEPHONE: 301-527-2051  
TELEFAX: 301-208-6997  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5711 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
STRAIN: BRCAL  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: 17  
MAP POSITION: 17q21  
US-08-798-691-5

Query Match 100.0%; Score: 5709.4; DB 1; Length 5711;  
Best Local Similarity 100.0%; Pred. No. 0; Mismatches 1; Indels 0; Gaps 0;

Matches 5710; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Sequence 5, Application US/08825487A  
Patent No. 6048689  
GENERAL INFORMATION:  
APPLICANT: Murphy, Patricia D.  
APPLICANT: White, Marga B.  
TITLE OF INVENTION: METHODS FOR IDENTIFYING VARIATIONS IN POLYNUCLEOTIDE SEQUENC.  
NUMBER OF SEQUENCES: 110  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Howrey & Simon  
STREET: 1299 Pennsylvania Avenue., N.W.  
CITY: Washington,  
STATE: DC  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/825,487A  
FILING DATE: 28-MAR-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US98/060002  
FILING DATE: 26-Mar-1998  
CLASSIFICATION: 435

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 INFORMATION FOR SEQ ID NO: 5:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 5711 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: not relevant  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 ORIGINAL SOURCE:  
 ORGANISM: Homo sapiens  
 STRAIN: BRCAL  
 POSITION IN GENOME:  
 CHROMOSOME/SEGMENT: 17  
 MAP POSITION: 17q21  
 US-08-825-487A-5

Query Match 100.0%; Score 5709.4; DB 3; Length 5711;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 5710; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 3661 TCCAGAGAGAGAGTTGACAGAGTCTTACCCCTTACACCATTAATTTGCTCAGG 3720  
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QY 3781 AAGAGCTTCCGCTTCCAACTTGTATTTGTAAGTAAACATATACCTTCTCAGT 3840  
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Db 3841 CTACAGGATGACACCGTTGTCACCGAGTCTGTCTTAAGAACACAGAGAGAAATTAAT 3900  
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Db 3901 TATCATTTGAAGATGCTTAAATGATGCTCAAGTAAACAGGTAATTTGCAAGGCACTTC 3960  
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Db 5341 TCAATGAGAAAGAACCAAGGCTCCAAAGCGAGAGAGAAATCCAGAGACAGAAAGATCT 5400  
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Db 5701 GCCACTACTGA 5711

RESULT 7  
US-09-074-476-3  
; Sequence 3, Application US/09074476  
; Patent No. 6130322  
; GENERAL INFORMATION:  
; APPLICANT: Murphy, Patricia D.  
; APPLICANT: Allen, Antonette C.  
; APPLICANT: Alvares, Christopher P.  
; APPLICANT: Critz, Brenda S.  
; APPLICANT: Olson, Sheri J.  
; APPLICANT: Thumber, Denise  
; APPLICANT: Zeng, Bin  
; TITLE OF INVENTION: Coding Sequences of the Human  
; NUMBER OF INVENTION: BRCA1 Gene  
; NUMBER OF SEQUENCES: 72  
; CORRESPONDENCE ADDRESS:  
; ADDRESSER: Howrey & Simon  
; STREET: 1299 Pennsylvania Avenue N. W.  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30



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COUNTRY: USA  
ZIP: 20877  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/798,691  
FILING DATE: 12-Feb-97  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Thomas Gallegos  
REGISTRATION NUMBER: 32,692  
REFERENCE/DOCKET NUMBER: PA-0054CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 301-527-2051  
TELEFAX: 301-208-6997  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5711 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
STRAIN: BRCA1  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: 17  
MAP POSITION: 17q21  
US-08-798-691-3

Query Match 99.8%; Score 5701.4; DB 1; Length 5711;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 5705; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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DB 1 AGCTGCTGAGACTTCTGAGACCCGACACGAGCTGTGGGCTTTCAGATTAATCTGGCC 60

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DB 61 CCTGCGCTCAGAGAGGCGCTTCACTCTGCTCTGGGTAAGTTGATGGAACAGAAAGAA 120

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DB 121 TGAATTTATCTGCTCTTCCGCTTGAAGAGTACAAATGTCATTATGCTATGCAAGAAA 180

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Qy 1861 AAAGGAAAGCTGAAGCTTAATAGCAGCAGATTAAGCAATATGGAATTCGAAATTAATATCC 1920  
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 Db 5041 CTTCACAG 5100  
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 Db 5701 GCCACTACTGA 5711

RESULT 9  
 US-08-825-487A-3  
 ; Sequence 3, Application us/08825487A  
 ; Patent No. 6048689  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Murphy, Patricia D.  
 ; APPLICANT: white, Marga B.  
 ; TITLE OF INVENTION: METHODS FOR IDENTIFYING VARIATIONS IN POLYNUCLEOTIDE SEQUENC  
 ; NUMBER OF SEQUENCES: 110  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Howrey & Simon  
 ; STREET: 1299 Pennsylvania Avenue., N.W.  
 ; CITY: Washington,  
 ; STATE: DC  
 ; COUNTRY: USA  
 ; ZIP: 20004

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COMPUTER READABLE FORM:
MEDUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/825,487A
FILING DATE: 28-MAR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US98/060002
FILING DATE: 26-Mar-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Albert P. Halluin
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 05371, 0012, 999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-463-8100
TELEFAX: 650-463-8400
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 5711 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: cdna
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
STRAIN: BRCA1
POSITION IN GENOME:
CHROMOSOME/SEGMENT: 17
MAP POSITION: 17q21
US-08-825-487A-3

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Query Match 99.8%; Score 5701.4; DB 3; Length 5711;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 5705; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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| OY |  | 1621 | AATTAAACGGTAAAGGAGCACTTAATACAGCGCTTCATCCTGAGATTTTATCAAAGAAG      | 1680 |
| Dd |  | 1621 | AATTAAAGCGTAAAGAGAACCTTACATCAGGCTTCATCCTGAGATTTTATCAAAGAAG       | 1680 |
| OY |  | 1681 | CAGATTTTGCGAGTTCAAAAAGACTCCCTGAATATGATTAATCAGGGAACCTAACCAACGAGAC | 1740 |
| Dd |  | 1681 | CAGATTTTGCGAGTTCAAAAAGACTCCCTGAATATGATTAATCAGGGAACCTAACCAACGAGAC | 1740 |
| OY |  | 1741 | AGAATGCTCAAGTGTATGAATATTACTTAATAGTGGTCATGAGATTTAAACAAAAGGTGATT   | 1800 |
| Dd |  | 1741 | AGAATGCTCAAGTGTATGAATATTACTTAATAGTGGTCATGAGATTTAAACAAAAGGTGATT   | 1800 |
| OY |  | 1801 | CTATTCCAGATTAGAAAAATCCTTAACCCCAATGATTCATCTGAAAAAGAAATCTGCTTTCA   | 1860 |
| Dd |  | 1801 | CTATTCCAGATTAGAAAAATCCTTAACCCCAATGATTCATCTGAAAAAGAAATCTGCTTTCA   | 1860 |
| OY |  | 1861 | AAACGAAAGCTGGAACCTTAATAGCACAGATTAAGCAATATGGAATCTGAAATTAATATCC    | 1920 |
| Dd |  | 1861 | AAACGAAAGCTGGAACCTTAATAGCACAGATTAAGCAATATGGAATCTGAAATTAATATCC    | 1920 |
| OY |  | 1921 | ACAATTCAAAAGCACCTTAATAAGATAGAGGAGGAGGAAAGTTCTCTACAGGCATATTC      | 1980 |
| Dd |  | 1921 | ACAATTCAAAAGCACCTTAATAAGATAGAGGAGGAGGAAAGTTCTCTACAGGCATATTC      | 1980 |
| OY |  | 1981 | ATGCCCTTGAACCTAAGTACAGTAAATACTTAAGCCCACTTAATTTGTACTGAATTTGCMAA   | 2040 |
| Dd |  | 1981 | ATGCCCTTGAACCTAAGTACAGTAAATACTTAAGCCCACTTAATTTGTACTGAATTTGCMAA   | 2040 |
| OY |  | 2041 | TTGATATGTTGTTCTACAGCTGAGAGATTAAGAAAAAAGTACACCMAATGCCAGTCA        | 2100 |
| Dd |  | 2041 | TTGATATGTTGTTCTACAGCTGAGAGATTAAGAAAAAAGTACACCMAATGCCAGTCA        | 2100 |
| OY |  | 2101 | GGCACAGCAGAAAACTTACAACTCAATGAAGGTAAAGAACTCTGCAACTGAGACCAAGAAGA   | 2160 |
| Dd |  | 2101 | GGCACAGCAGAAAACTTACAACTCAATGAAGGTAAAGAACTCTGCAACTGAGACCAAGAAGA   | 2160 |
| OY |  | 2161 | GTAACAAAGCCAAATGACAGACAACTAAGAAACATGACAGTGATCTTTCCAGAGCTGA       | 2220 |
| Dd |  | 2161 | GTAACAAAGCCAAATGACAGACAACTAAGAAACATGACAGTGATCTTTCCAGAGCTGA       | 2220 |
| OY |  | 2221 | AGTTAACAAATGSCACCTGGTCTTTTACTAAGTGTCAAAATACAGAGAACCTTAAAGAT      | 2280 |
| Dd |  | 2221 | AGTTAACAAATGSCACCTGGTCTTTTACTAAGTGTCAAAATACAGAGAACCTTAAAGAT      | 2280 |
| OY |  | 2281 | TTGTCAATCTAGACCTTCCAAGAGAGAAAAAGAAAGAAACAGTTAAAGTGT              | 2340 |
| Dd |  | 2281 | TTGTCAATCTAGACCTTCCAAGAGAGAAAAAGAAAGAAACAGTTAAAGTGT              | 2340 |
| OY |  | 2341 | CTAATATATGCTGAAGAACCCCAAAGATCTCATGTTTAATGAGAAAGGGTTTTGCAAACTG    | 2400 |
| Dd |  | 2341 | CTAATATATGCTGAAGAACCCCAAAGATCTCATGTTTAATGAGAAAGGGTTTTGCAAACTG    | 2400 |
| OY |  | 2401 | AAAGATCTGTAGAAGTAGCAGTATTTTCACTGGTACCTGAGATACGATTATAGGCACTCAGG   | 2460 |
| Dd |  | 2401 | AAAGATCTGTAGAAGTAGCAGTATTTTCACTGGTACCTGAGATACGATTATAGGCACTCAGG   | 2460 |
| OY |  | 2461 | AAAGATCTGCTTACTGGAAGTTAGCACTTAGGGAAGGCAAAAAACAGAACCAATTAAT       | 2520 |
| Dd |  | 2461 | AAAGATCTGCTTACTGGAAGTTAGCACTTAGGGAAGGCAAAAAACAGAACCAATTAAT       | 2520 |
| OY |  | 2521 | GTGTGAGTCAGTGGCGACATTTTGAAAAACCCCAAGGACCTAAATTCATGSGTTGTTCCAAAG  | 2580 |
| Dd |  | 2521 | GTGTGAGTCAGTGGCGACATTTTGAAAAACCCCAAGGACCTAAATTCATGSGTTGTTCCAAAG  | 2580 |
| OY |  | 2581 | ATATATAGAAATGACACAGAAAGGCTTTAATGATTCATTGAGCATGAGATTAACAACAGTCC   | 2640 |
| Dd |  | 2581 | ATATATAGAAATGACACAGAAAGGCTTTAATGATTCATTGAGCATGAGATTAACAACAGTCC   | 2640 |
| OY |  | 2641 | GGGAAACAAAGCATATGAATTGAAGAAATGTAATGCTCAGTATTTTGCAGAAATACAT       | 2700 |
| Dd |  | 2641 | GGGAAACAAAGCATATGAATTGAAGAAATGTAATGTAATGCTCAGTATTTTGCAGAAATACAT  | 2700 |

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| Db | 2701 | TCAGAGTTCAAAGGCCAGCACTTGGCTGTTTCAAAATCCAGGAAATGCCAAGAG         | 2760 |
| QY | 2761 | AATGCGCAACATTCCTGTCGCCACTCTGGGTCCTTAAAGAAACAAGTCCAAAGTCACCTT   | 2830 |
| Db | 2761 | AATGCGCAACATTCCTGTCGCCACTCTGGGTCCTTAAAGAAACAAGTCCAAAGTCACCTT   | 2830 |
| QY | 2821 | TTGAATGTGAACAAAGGAGAAAATCAAGGAAGAATGAGTCTTAATATCAAGCTGTAC      | 2880 |
| Db | 2821 | TTGAATGTGAACAAAGGAGAAAATCAAGGAAGAATGAGTCTTAATATCAAGCTGTAC      | 2880 |
| QY | 2881 | AGACAGTTAAATATCACTGCAAGGCTTTCCTGTGTGTTGGTCAGAAAGATPAAGCACTGATA | 2940 |
| Db | 2881 | AGACAGTTAAATATCACTGCAAGGCTTTCCTGTGTGTTGGTCAGAAAGATPAAGCACTGATA | 2940 |
| QY | 2941 | ATGCCAAATGTAGATCAAAAGSAGCTCTAGCTTTTGCTATCATCTCAGTTCAGAGCA      | 3000 |
| Db | 2941 | ATGCCAAATGTAGATCAAAAGSAGCTCTAGCTTTTGCTATCATCTCAGTTCAGAGCA      | 3000 |
| QY | 3001 | ACGAAATCGAGCTCATTACTCCAAATAAACATGAGACTTTTAAACAAACCCATATGATAC   | 3060 |
| Db | 3001 | ACGAAATCGAGCTCATTACTCCAAATAAACATGAGACTTTTAAACAAACCCATATGATAC   | 3060 |
| QY | 3061 | CACCACTTTTCCCATCAAGTCATTTGTTAAACTTAATGTAGAAAAATCTGCTAAGG       | 3120 |
| Db | 3061 | CACCACTTTTCCCATCAAGTCATTTGTTAAACTTAATGTAGAAAAATCTGCTAAGG       | 3120 |
| QY | 3121 | AAAACCTTGAAGAACATTCATATGTCACCTGTAAGAGAAATGGGAAATGAGAACATTC     | 3180 |
| Db | 3121 | AAAACCTTGAAGAACATTCATATGTCACCTGTAAGAGAAATGGGAAATGAGAACATTC     | 3180 |
| QY | 3181 | GTCACGTAGACACATTAAGCCGTATTAACATTAAGAGAAATGTTTTTAAAGSAGCCAGCT   | 3240 |
| Db | 3181 | GTCACGTAGACACATTAAGCCGTATTAACATTAAGAGAAATGTTTTTAAAGSAGCCAGCT   | 3240 |
| QY | 3241 | CAAGCAATATTAATGAAGTAGTTCACGATCTAATGAAAGTGCGCTCCAGTATTAATGAAA   | 3300 |
| Db | 3241 | CAAGCAATATTAATGAAGTAGTTCACGATCTAATGAAAGTGCGCTCCAGTATTAATGAAA   | 3300 |
| QY | 3301 | TAGGTTCCAGATGAGAAAACATTCACAGAGAACTAGGTATGAAGAGAGGCGCAAAATTTGA  | 3360 |
| Db | 3301 | TAGGTTCCAGATGAGAAAACATTCACAGAGAACTAGGTATGAAGAGAGGCGCAAAATTTGA  | 3360 |
| QY | 3361 | ATGCTATGCTTAAATTAAGGGGTTTTTGCAACCTGAGGCTCTATTAACAAAGTCTTCTGGAA | 3420 |
| Db | 3361 | ATGCTATGCTTAAATTAAGGGGTTTTTGCAACCTGAGGCTCTATTAACAAAGTCTTCTGGAA | 3420 |
| QY | 3421 | GTAATTTGTAAGCATCTGAAAATAAAAAAGCAAGATATGAAGAAATGAGTTCAGACTGTA   | 3480 |
| Db | 3421 | GTAATTTGTAAGCATCTGAAAATAAAAAAGCAAGATATGAAGAAATGAGTTCAGACTGTA   | 3480 |
| QY | 3481 | ATAACGATTTCTTCACATATCTGATTTTCAAGTAACTTAGAACAGCCTTAGGGAATGATC   | 3540 |
| Db | 3481 | ATAACGATTTCTTCACATATCTGATTTTCAAGTAACTTAGAACAGCCTTAGGGAATGATC   | 3540 |
| QY | 3541 | ATGCAATCAGGTTGGTTCTGAGACACCTGATGACCTGTTAGATGATGGTGAATAAAGG     | 3600 |
| Db | 3541 | ATGCAATCAGGTTGGTTCTGAGACACCTGATGACCTGTTAGATGATGGTGAATAAAGG     | 3600 |
| QY | 3601 | AAGATACTAGTTTGTCTGAAAATATACATTAAGAAAGTTCTGCTGTTTTTAAAGCAAGCG   | 3660 |
| Db | 3601 | AAGATACTAGTTTGTCTGAAAATATACATTAAGAAAGTTCTGCTGTTTTTAAAGCAAGCG   | 3660 |
| QY | 3661 | TCGAGAGAGAGAGCTTAGCAGAGTCTTAGCCCTTTCAACCATACACATTTGGCTCAGG     | 3720 |
| Db | 3661 | TCGAGAGAGAGAGAGCTTAGCAGAGTCTTAGCCCTTTCAACCATACACATTTGGCTCAGG   | 3720 |
| QY | 3721 | GTTACCGAAGAGGGGCCAAGAAATTAAGTCTCAGAAAGAACTTATCTAGTAGGAGATG     | 3780 |
| Db | 3721 | GTTACCGAAGAGGGGCCAAGAAATTAAGTCTCAGAAAGAACTTATCTAGTAGGAGATG     | 3780 |
| QY | 3781 | AAGGCTTCCCTGCTTCCAACTCTTGTATTTTGGTAAAGTAAACAATATACCTTCTCAGT    | 3840 |

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Qy 3841 CTACTAGGCATAGACCCGTTGCTACCGAGTGTCTGTCTAAGAACACAGAGGAAATTTAT 3900  
Db 3841 CTACTAGGCATAGACCCGTTGCTACCGAGTGTCTGTCTAAGAACACAGAGGAAATTTAT 3900  
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Db 3901 TATCATTAAGAAATAGCTTAATTAAGCTGAGTAACAGGTAATATTTGGCAAGGCAATTC 3960  
Qy 3961 AGGAACATCACCTTAGTGAGGAAACAAATGTTCTAGCTGTTGTTTCTTCAAGTGCA 4020  
Db 3961 AGGAACATCACCTTAGTGAGGAAACAAATGTTCTAGCTGTTGTTTCTTCAAGTGCA 4020  
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Db 4081 CCAACAAATGAGGATGATGTAAGGCTGAGGAGTGTCTGAGTGAACAAGAAATGG 4140  
Qy 4141 TTTGAGATGATGAGAAAGAGAACGGCTTGGAAAGAAATATCAAGAGACAAAGCA 4200  
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Db 4321 AACATTAACCTGATTAAGCTCCAGCAGAAATGGCTGAACTAGAAAGCTGTGTTAGAACAC 4380  
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Qy 4621 GCCCATCATTAAGATAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 4680  
Db 4621 GCCCATCATTAAGATAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 4680  
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Qy 4741 AGTCGGGGCCACAGATTTGAGGAAACATCTTACTGCGAAGGCAAGATCTAGAGGGAA 4800  
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Db 4801 CCCCTTACCTGGAATCTGGAATCAGCTCTTCTGTGATGATGATGATGATGATGATGATGATGAT 4860  
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Db 4861 AAGACAGAGCCCAAGTCAAGTCTGTTGGCAACATCACTTCAACCTCTGCAATGA 4920  
Qy 4921 AAGTCCCCCAATGGAAGTTGAGATCTGCCAGGGGTCAGCTGCTCATCTACTG 4980  
Db 4921 AAGTCCCCCAATGGAAGTTGAGATCTGCCAGGGGTCAGCTGCTCATCTACTG 4980  
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Qy 5521 GCACAGGTGTCCACCAATGCTGTTGCTGAGCAGATGCTCTGAGAGAGACATGCT 5580  
Db 5521 GCACAGGTGTCCACCAATGCTGTTGCTGAGCAGATGCTCTGAGAGAGACATGCT 5580  
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Db 5581 TCCATGCAATTTGGGAGATGTTGAGGCACTGTTGTTGAGCA 5640  
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Db 5701 GCCACTACTGA 5711

RESULT 10  
US-09-074-476-5  
; Sequence 5, Application US/09074476  
; Patent No. 6130322  
GENERAL INFORMATION:  
; APPLICANT: Murphy, Patricia D.  
; APPLICANT: Allen, Antoinette C.  
; APPLICANT: Alvares, Christopher P.  
; APPLICANT: Citez, Brenda S.  
; APPLICANT: Olson, Sheri J.  
; APPLICANT: Thunder, Denise  
; APPLICANT: Zeng, Bin  
; TITLE OF INVENTION: Coding Sequences of the Human  
; TITLE OF INVENTION: BRCA1 Gene

NUMBER OF SEQUENCES: 72  
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 ADDRESSEE: Howrey & Simon  
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 STATE: DC  
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 ZIP: 20004  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/074,476  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 09/074,453  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Albert P. Halluin  
 REGISTRATION NUMBER: 25,227  
 REFERENCE/DOCKET NUMBER: 5371.34.US01  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 650-463-8109  
 TELEFAX: 650-463-8400  
 INFORMATION FOR SEO ID NO: 5:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 5711 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: not relevant  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 ORIGINAL SOURCE:  
 ORGANISM: Homo sapiens  
 STRAIN: BRCA1 (om13)  
 POSITION IN GENOME:  
 CHROMOSOME/SEGMENT: 17  
 MAP POSITION: 17q21  
 US-09-074-476-5

Query Match 99.8%; Score 5701.4; DB 3; Length 5711;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 5705; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 AGCTCGCTGAGACTTCTCTGSAACCCGACACGAGCTGTGGGTTTCTCAAGTAATCTGGCC 60  
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 QY 61 CCTGGCTGAGAGGCTTCACTCTGCTGTGGGTAAGTTGATTTGAAACGAAAGAA 120  
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 DB 121 TGGATTATCTGCTCTTCCGCTTGAAGAGTACAAATGTCATTAATGCTATGCAAGAA 180  
 QY 181 TCTTAAGAGTCCCACTGTCTGGAAGTTGATCAAGAACTGTCTCCAAAGTGTGACC 240  
 DB 181 TCTTAAGAGTCCCACTGTCTGGAAGTTGATCAAGAACTGTCTCCAAAGTGTGACC 240  
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 QY 361 AACTTGTGAAGAGCTATTTGAAATATTTTGTCTTTTCACTTGAACACAGGTTTGGAGT 420  
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2701 TCAAGGTTTCAAGAGGAG 2760  
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2761 AATGCAACATCTCTGAG 2820  
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Db 3721 GTTACCGAGAGGGGCCAAGAAATTAGATCCTCAGAGAGAACTTATAGTGGAGATG 3780  
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Qy 4081 CCAAAACAAATGAGGCACTGCTGAAGAGGAGTGTGCTGAGTGAACAGAAATTTG 4140  
Db 4081 CCAAAACAAATGAGGCACTGCTGAAGAGGAGTGTGCTGAGTGAACAGAAATTTG 4140  
Qy 4141 TTTCAATGATGAAGAAAGAGAAACGGGCTTTGGAAGAAATTAATCAAGAAAGCAAGCA 4200  
Db 4141 TTTCAATGATGAAGAAAGAGAAACGGGCTTTGGAAGAAATTAATCAAGAAAGCAAGCA 4200  
Qy 4201 TGGATTTCAAACTTATAGTGAAGAGCACTGTGGGTGTGAGTGAACAGAGCTTCTGAG 4260  
Db 4201 TGGATTTCAAACTTATAGTGAAGAGCACTGTGGGTGTGAGTGAACAGAGCTTCTGAG 4260  
Qy 4261 ACTGCTCAGGGGCTATCCTCTCAGAGTGAATTTTAACACTCAGCAGAGGAGTATCCATGC 4320  
Db 4261 ACTGCTCAGGGGCTATCCTCTCAGAGTGAATTTTAACACTCAGCAGAGGAGTATCCATGC 4320  
Qy 4321 AACATAACCTGATTAAGAGCTCCAGAGAGAAATGGCTGAATAGAGCTGTGTTGAACAGC 4380  
Db 4321 AACATAACCTGATTAAGAGCTCCAGAGAGAAATGGCTGAATAGAGCTGTGTTGAACAGC 4380  
Qy 4381 ATGGAGAGCCAGCCTTCTTACAGCTACCTTCCATCATATAGTGACTCCTCTGCTTGAAG 4440  
Db 4381 ATGGAGAGCCAGCCTTCTTACAGCTACCTTCCATCATATAGTGACTCCTCTGCTTGAAG 4440  
Qy 4441 ACCTGGAGAAATCGAGAACAAAGCAATCAGAAAAGAGTATTAATCTTCAAGAAAAGTA 4500  
Db 4441 ACCTGGAGAAATCGAGAACAAAGCAATCAGAAAAGAGTATTAATCTTCAAGAAAAGTA 4500  
Qy 4501 GTGAATACCTTATAGCCAGAAATCCAGAAAGGCTTTCTGCTGAACAAGTTGAGTGTCTG 4560  
Db 4501 GTGAATACCTTATAGCCAGAAATCCAGAAAGGCTTTCTGCTGAACAAGTTGAGTGTCTG 4560  
Qy 4561 CAATATGTTCTTACCACTTAATAAAGAACACAGAGTGAAGAGTCAATCCCTCTTCTTAAT 4620  
Db 4561 CAATATGTTCTTACCACTTAATAAAGAACACAGAGTGAAGAGTCAATCCCTCTTCTTAAT 4620  
Qy 4621 GCCCATCATTAAGTATAGTGTGATACATGACAGTGTCTGTGGAGCTTTCAGAAATAGAA 4680  
Db 4621 GCCCATCATTAAGTATAGTGTGATACATGACAGTGTCTGTGGAGCTTTCAGAAATAGAA 4680  
Qy 4681 ACTATCCATCTCAAGAGAGCTCATTAAGTGTGTGATGTGAGAGCAACAGCTGGAAG 4740  
Db 4681 ACTATCCATCTCAAGAGAGCTCATTAAGTGTGTGATGTGAGAGCAACAGCTGGAAG 4740  
Qy 4741 AGTCTGGGCGCACGATTTGACGGAACATCTTACTTCCAGAGCAAGATCTAGAGGAA 4800  
Db 4741 AGTCTGGGCGCACGATTTGACGGAACATCTTACTTCCAGAGCAAGATCTAGAGGAA 4800

Qy 4801 CCCCTTACCTGGAATCTGGAATCAGCCTCTTCTGATGACCTGATCTGATCTTCTG 4860  
Db 4801 CCCCTTACCTGGAATCTGGAATCAGCCTCTTCTGATGACCTGATCTGATCTTCTG 4860  
Qy 4861 AAGACAGAGCCCGAGAGTCAAGTCTGTGTGGCAACATACATCTTCAACCTCTGATTTGA 4920  
Db 4861 AAGACAGAGCCCGAGAGTCAAGTCTGTGTGGCAACATACATCTTCAACCTCTGATTTGA 4920  
Qy 4921 AAGTTCCTCAATTTGAAGTTGCAAGATCTGCCAGAGTCCAGTCTGCTCATATCTG 4980  
Db 4921 AAGTTCCTCAATTTGAAGTTGCAAGATCTGCCAGAGTCCAGTCTGCTCATATCTG 4980  
Qy 4981 ATACTCTGGGTATTAATGCAATGGAAGAAAGTGTGACGAGGAGGAGCCGAATTTGACAG 5040  
Db 4981 ATACTCTGGGTATTAATGCAATGGAAGAAAGTGTGACGAGGAGGAGCCGAATTTGACAG 5040  
Qy 5041 CTTCAACAGAAAGGCTCAACAAAGAAATGTCATGAGTGTGTGCTGACCTGACCCAGAAAG 5100  
Db 5041 CTTCAACAGAAAGGCTCAACAAAGAAATGTCATGAGTGTGTGCTGACCTGACCCAGAAAG 5100  
Qy 5101 AATTTATGCTCGTGTCAAGTTTGGCAAGAAACCAACATCACTTAACTTAATCTAATTA 5160  
Db 5101 AATTTATGCTCGTGTCAAGTTTGGCAAGAAACCAACATCACTTAACTTAATCTAATTA 5160  
Qy 5161 CTGAAGAGCTACTCATGTTGTTATGAAAACAGATGCTGAGTTGTGTGAAACGAGACAC 5220  
Db 5161 CTGAAGAGCTACTCATGTTGTTATGAAAACAGATGCTGAGTTGTGTGAAACGAGACAC 5220  
Qy 5221 TGAATATTTTCTAGGAATTTGGGAGAGAAATGGGTAGTTAGCTATTTCTGGGTGACCC 5280  
Db 5221 TGAATATTTTCTAGGAATTTGGGAGAGAAATGGGTAGTTAGCTATTTCTGGGTGACCC 5280  
Qy 5281 AGTCTATTTAAAGAAAGAAATGCTGAATGAGCATATTTTGAAGTCAAGAGAGATGTGG 5340  
Db 5281 AGTCTATTTAAAGAAAGAAATGCTGAATGAGCATATTTTGAAGTCAAGAGAGATGTGG 5340  
Qy 5341 TCAATGGAAGAAACCAAGGCTCCAAAGGAGCAAGAGAAATCCAGAGCAGAGAAATCT 5400  
Db 5341 TCAATGGAAGAAACCAAGGCTCCAAAGGAGCAAGAGAAATCCAGAGCAGAGAAATCT 5400  
Qy 5401 TCAGGGGCTAGAAATCTGTGTGATGAGCCTTCTCAACAAATGCCCCAGATCAACTGG 5460  
Db 5401 TCAGGGGCTAGAAATCTGTGTGATGAGCCTTCTCAACAAATGCCCCAGATCAACTGG 5460  
Qy 5461 AATGATGATCAAGCTGTGTGCTTCTGTGTGAAGAGCTTTATCATTCACCTTGG 5520  
Db 5461 AATGATGATCAAGCTGTGTGCTTCTGTGTGAAGAGCTTTATCATTCACCTTGG 5520  
Qy 5521 GCACAGGCTGTCACCCCAATTTGGTTGTGACAGCATGCTGAGACAGAGCAATAGGCT 5580  
Db 5521 GCACAGGCTGTCACCCCAATTTGGTTGTGACAGCATGCTGAGACAGAGCAATAGGCT 5580  
Qy 5581 TCCATGCAATTTGGGAGATGTGAGGCACTGTGTGACCCGAGAGTGGGTGTGGACA 5640  
Db 5581 TCCATGCAATTTGGGAGATGTGAGGCACTGTGTGACCCGAGAGTGGGTGTGGACA 5640  
Qy 5641 GTGTAGCACTTACCACTGTCAGAGCTGCAAGACTGGAACCTGATATCCCAATCCCAACA 5700  
Db 5641 GTGTAGCACTTACCACTGTCAGAGCTGCAAGACTGGAACCTGATATCCCAATCCCAACA 5700  
Qy 5701 GGCACACTGA 5711  
Db 5701 GGCACACTGA 5711

RESULT 11  
US-08-658-322-1  
; Sequence 1, Application US/08658322  
; Patent No. 5869245  
; GENERAL INFORMATION:  
; APPLICANT: Yeung, Anthony T.  
; TITLE OF INVENTION: Mismatch Endonuclease And Its Use in



|    |      |  |      |
|----|------|--|------|
| QY | 1631 | AATTAAAGCGTAAAGAGGACCTCATCATGAGGCTTCACTCGAGATTTTTCAGAAAG       | 1680 |
| Db | 1621 | AATTAAAGCGTAAAGAGGACCTCATCATGAGGCTTCACTCGAGATTTTTCAGAAAG       | 1680 |
| QY | 1681 | CAGATTTGGCGAGTTCAAAAAGACTCCTGAATATGATTAATCAGGGAATTAACCAAGC     | 1740 |
| Db | 1681 | CAGATTTGGCGAGTTCAAAAAGACTCCTGAATATGATTAATCAGGGAATTAACCAAGC     | 1740 |
| QY | 1741 | AGAAATGTCAGAGTGTGTAATATTAATTAATGTCATGAGATTAATTAACCAAGTAT       | 1800 |
| Db | 1741 | AGAAATGTCAGAGTGTGTAATATTAATTAATGTCATGAGATTAATTAACCAAGTAT       | 1800 |
| QY | 1801 | CTATTACAGATAGAGAAAAATCCTTAATCCCAATAGATCACTCGAAAAAGAAATCTGTTCA  | 1860 |
| Db | 1801 | CTATTACAGATAGAGAAAAATCCTTAATCCCAATAGATCACTCGAAAAAGAAATCTGTTCA  | 1860 |
| QY | 1861 | AAACGAAGCTGGAACCTTAATTAAGCAGAGTATTAAGCATATGGAATCTGAAATTAATATCC | 1920 |
| Db | 1861 | AAACGAAGCTGGAACCTTAATTAAGCAGAGTATTAAGCATATGGAATCTGAAATTAATATCC | 1920 |
| QY | 1921 | ACAAATTCAAAAGCACTTAATTAAGGATAGGAGGAAATCTTATACCGAGGATATTC       | 1980 |
| Db | 1921 | ACAAATTCAAAAGCACTTAATTAAGGATAGGAGGAAATCTTATACCGAGGATATTC       | 1980 |
| QY | 1981 | ATGCGCTTGAACCTAGTAGTCTAGTAAATCTTAAGCCCACTAATTTGATCTGAATTCGAAA  | 2040 |
| Db | 1981 | ATGCGCTTGAACCTAGTAGTCTAGTAAATCTTAAGCCCACTAATTTGATCTGAATTCGAAA  | 2040 |
| QY | 2041 | TTGATATGTTGTTCTTAAGCAGTGAAGATTAAGAAAAAAGTACACCAATTCGCAGTCA     | 2100 |
| Db | 2041 | TTGATATGTTGTTCTTAAGCAGTGAAGATTAAGAAAAAAGTACACCAATTCGCAGTCA     | 2100 |
| QY | 2101 | GGCAGCAGCAAAACCTTAACAATCAATGAGAGGTAAAGAACTGCAACTGAGCCCAAGAGA   | 2160 |
| Db | 2101 | GGCAGCAGCAAAACCTTAACAATCAATGAGAGGTAAAGAACTGCAACTGAGCCCAAGAGA   | 2160 |
| QY | 2161 | GTAACAGACCAATATGAACAGACAGTAAGAAAGATGATATCTTTCCAGAGCTGA         | 2220 |
| Db | 2161 | GTAACAGACCAATATGAACAGACAGTAAGAAAGATGATATCTTTCCAGAGCTGA         | 2220 |
| QY | 2221 | AGTTAAACAAAGCAGCTGGTCTTTTACTTAAGTGTCAAAATACGAGAACTTAAGAAAT     | 2280 |
| Db | 2221 | AGTTAAACAAAGCAGCTGGTCTTTTACTTAAGTGTCAAAATACGAGAACTTAAGAAAT     | 2280 |
| QY | 2281 | TTGTCAATCTAGGCTTCCAGAGAGAAAAAGAAAGAACTTAAGAACTTAAATGT          | 2340 |
| Db | 2281 | TTGTCAATCTAGGCTTCCAGAGAGAAAAAGAAAGAACTTAAGAACTTAAATGT          | 2340 |
| QY | 2341 | CTAATTAATGCTGAAGAACCCCAAGATCTCATGTTAAGTGAAGAAAGGTTTTCGAACTG    | 2400 |
| Db | 2341 | CTAATTAATGCTGAAGAACCCCAAGATCTCATGTTAAGTGAAGAAAGGTTTTCGAACTG    | 2400 |
| QY | 2401 | AAAGATCTGTAGAGTAGCAGTATTTTCACTGCTGATACCTGGATATGATTAAGGCACTAGG  | 2460 |
| Db | 2401 | AAAGATCTGTAGAGTAGCAGTATTTTCACTGCTGATACCTGGATATGATTAAGGCACTAGG  | 2460 |
| QY | 2461 | AAAGATCTGTAGAGTAGCAGTATTTTCACTGCTGATACCTGGATATGATTAAGGCACTAGG  | 2520 |
| Db | 2461 | AAAGATCTGTAGAGTAGCAGTATTTTCACTGCTGATACCTGGATATGATTAAGGCACTAGG  | 2520 |
| QY | 2521 | GTGTGAGTCAATGAGGAGCACTTAAGAAACCCCAAGGACCTTAATTAAGTGTTCGAAAG    | 2580 |
| Db | 2521 | GTGTGAGTCAATGAGGAGCACTTAAGAAACCCCAAGGACCTTAATTAAGTGTTCGAAAG    | 2580 |
| QY | 2581 | ATTAATAGAAATAGACACAGAAAGCTTTAAGTATTCATTTGGGACATGAAGTTAACCAAGTC | 2640 |
| Db | 2581 | ATTAATAGAAATAGACACAGAAAGCTTTAAGTATTCATTTGGGACATGAAGTTAACCAAGTC | 2640 |
| QY | 2641 | GGGAAACAGAGATAGAAATGGAAGAAAGTGAACCTTGATGCTCAGATTTTGCAGATATCAT  | 2700 |
| Db | 2641 | GGGAAACAGAGATAGAAATGGAAGAAAGTGAACCTTGATGCTCAGATTTTGCAGATATCAT  | 2700 |

|    |      |   |      |
|----|------|---|------|
| QY | 2701 | TCAAAGTTTCAAAGGCCAGCATTTGCTCGTTTTCAAATCCAGAAATCAGAAAGG        | 2760 |
| Db | 2701 | TCAGGTTTCAAAGGCCAGATCTATTTGCTCCGTTTCAAATCCAGAAATCAGAAAGG      | 2760 |
| QY | 2761 | AATGTCAACATTTCTCTGCCACTCTCGGGTCTTTAAAGAAACAAAGTCCAAAGTCATT    | 2820 |
| Db | 2761 | AATGTCAACATTTCTCTGCCACTCTCGGGTCTTTAAAGAAACAAAGTCCAAAGTCATT    | 2820 |
| QY | 2821 | TTGAATGTGAACAAAGAGAAAGAAATCAAGAAAGAAATGAAGTCTAATTCAGGCTGTAC   | 2880 |
| Db | 2821 | TTGAATGTGAACAAAGAGAAAGAAATCAAGAAAGAAATGAAGTCTAATTCAGGCTGTAC   | 2880 |
| QY | 2881 | AGACAGTTAATATCATCTGACAGGCTTCTCGTGTGGTGGCAAAAGATTAAGCAGTTGATA  | 2940 |
| Db | 2881 | AGACAGTTAATATCATCTGACAGGCTTCTCGTGTGGTGGCAAAAGATTAAGCAGTTGATA  | 2940 |
| QY | 2941 | ATGCCAAATGTAGTATCAAGAGAGGCTCTAGGTTTTGTCTATCATCTCAGTTCAGAGCA   | 3000 |
| Db | 2941 | ATGCCAAATGTAGTATCAAGAGAGGCTCTAGGTTTTGTCTATCATCTCAGTTCAGAGCA   | 3000 |
| QY | 3001 | ACGAAACTGGACTCATTTCTCCAAATAAACATGGACTTTTACAAACCCATATCGTATAC   | 3060 |
| Db | 3001 | ACGAAACTGGACTCATTTCTCCAAATAAACATGGACTTTTACAAACCCATATCGTATAC   | 3060 |
| QY | 3061 | CACCACTTTTCCCATCAAGTCATTTGTTAATACTAATGTAGAAAAATTCGTAGAGG      | 3120 |
| Db | 3061 | CACCACTTTTCCCATCAAGTCATTTGTTAATACTAATGTAGAAAAATTCGTAGAGG      | 3120 |
| QY | 3121 | AAAACTTGAAGAAACATTCATATGTCACTGTAAGAGAAATGGAAATGAGAACATTCGA    | 3180 |
| Db | 3121 | AAAACTTGAAGAAACATTCATATGTCACTGTAAGAGAAATGGAAATGAGAACATTCGA    | 3180 |
| QY | 3181 | GTACAGTGAGCAATTAAGCCGTAAATACATTTAGAGAAATGTTTTAAAGAGCCAGCT     | 3240 |
| Db | 3181 | GTACAGTGAGCAATTAAGCCGTAAATACATTTAGAGAAATGTTTTAAAGAGCCAGCT     | 3240 |
| QY | 3241 | CAAGCAATTAATGAAGTAGTTCCTCGATATAAGAGTGGGCTCCAGTATTAATGA        | 3300 |
| Db | 3241 | CAAGCAATTAATGAAGTAGTTCCTCGATATAAGAGTGGGCTCCAGTATTAATGA        | 3300 |
| QY | 3301 | TAGGTTCCAGTAGAATAAAACATTCAGCAGAACTAGGTAGAAACAGAGGCCCAAAATTTGA | 3360 |
| Db | 3301 | TAGGTTCCAGTAGAATAAAACATTCAGCAGAACTAGGTAGAAACAGAGGCCCAAAATTTGA | 3360 |
| QY | 3361 | ATGCTATGCTTAGATTAGGGGTTTTGCACCTGAGGCTATTAACAAAGTCTTCTGGAA     | 3420 |
| Db | 3361 | ATGCTATGCTTAGATTAGGGGTTTTGCACCTGAGGCTATTAACAAAGTCTTCTGGAA     | 3420 |
| QY | 3421 | GTAATTTAGACATCTCGAAATTAAGAAAGCAAGATTAAGAAAGTGTTCAGACTGTA      | 3480 |
| Db | 3421 | GTAATTTAGACATCTCGAAATTAAGAAAGCAAGATTAAGAAAGTGTTCAGACTGTA      | 3480 |
| QY | 3481 | ATACAGATTTCTCCATATCTGATTTCAATACTTAGAAACAGCCATATGGGAATGTC      | 3540 |
| Db | 3481 | ATACAGATTTCTCCATATCTGATTTCAATACTTAGAAACAGCCATATGGGAATGTC      | 3540 |
| QY | 3541 | ATGCATCTCAGAGTTGTTCTGAGACACCTGATGACTGTTAGATGATGCTGAATAAAG     | 3600 |
| Db | 3541 | ATGCATCTCAGAGTTGTTCTGAGACACCTGATGACTGTTAGATGATGCTGAATAAAG     | 3600 |
| QY | 3601 | AAGATTAAGTGTTCGTAAGAAATGATTAAGAAAGTTCTGCTGTTTTAGCAAAAGCG      | 3660 |
| Db | 3601 | AAGATTAAGTGTTCGTAAGAAATGATTAAGAAAGTTCTGCTGTTTTAGCAAAAGCG      | 3660 |
| QY | 3661 | TCCAGAGAGGAGACTTAGCAGAGAGTCTAGACCTTTTACCCATACATTTGGCTAGG      | 3720 |
| Db | 3661 | TCCAGAGAGGAGACTTAGCAGAGAGTCTAGACCTTTTACCCATACATTTGGCTAGG      | 3720 |
| QY | 3721 | GTTACCGAAGAGGGCCCAAGAAATTAAGTCTTCAGAAAGAACTTATCTAGAGAGATG     | 3780 |
| Db | 3721 | GTTACCGAAGAGGGCCCAAGAAATTAAGTCTTCAGAAAGAACTTATCTAGAGAGATG     | 3780 |
| QY | 3781 | AAGAGCTTCCCTGCTTCCAAACCTGTTATTTGGTAAAGTAAACATATATCTTCTCAGT    | 3840 |

|    |      |           |           |          |            |            |                   |                 |           |          |         |      |
|----|------|-----------|-----------|----------|------------|------------|-------------------|-----------------|-----------|----------|---------|------|
| Db | 3781 | AAGAGCTTC | CGCTTCC   | CAACCTGT | TTTGGTAA   | GTAAACAAT  | TACTTCTCAGT       | 3844            |           |          |         |      |
| Qy | 3841 | CTACTAGG  | CATAGCA   | CCGTTG   | CTACCGAGT  | GTCTGTCT   | TAAGAACACAGAGAA   | TTTAT           | 3900      |          |         |      |
| Db | 3841 | CTACTAGG  | CATAGCA   | CCGTTG   | CTACCGAGT  | GTCTGTCT   | TAAGAACACAGAGAGAA | TTTAT           | 3900      |          |         |      |
| Qy | 3901 | TATCATTT  | GAAGATAG  | CTTAAAT  | TGACTG     | AGTACAGGTA | TATTTGGCAAGGCA    | CTTC            | 3966      |          |         |      |
| Db | 3901 | TATCATTT  | GAAGATAG  | CTTAAAT  | TGACTG     | AGTACAGGTA | TATTTGGCAAGGCA    | CTTC            | 3966      |          |         |      |
| Qy | 3961 | AGGAACAT  | CACTT     | AGTAGS   | AGAAACAAAT | TGTTTGCT   | AGCTGTGTTTCTT     | CACAGTGA        | 4020      |          |         |      |
| Db | 3961 | AGGAACAT  | CACTT     | AGTAGS   | AGAAACAAAT | TGTTTGCT   | AGCTGTGTTTCTT     | CACAGTGA        | 4020      |          |         |      |
| Qy | 4021 | GTGAATTG  | GAAGACTT  | GA       | CTGCAAA    | TACAAACACC | CAGAGTCC          | TTTGTGATTGGTCTT | 4086      |          |         |      |
| Db | 4021 | GTGAATTG  | GAAGACTT  | GA       | CTGCAAA    | TACAAACACC | CAGAGTCC          | TTTGTGATTGGTCTT | 4086      |          |         |      |
| Qy | 4081 | CCAAACA   | ANTAGGCAT | CAGTCT   | GTAAAGC    | CAGGAGT    | TGGTGTG           | AGTCAAGAA       | TTGG      | 4146     |         |      |
| Db | 4081 | CCAAACA   | ANTAGGCAT | CAGTCT   | GTAAAGC    | CAGGAGT    | TGGTGTG           | AGTCAAGAA       | TTGG      | 4146     |         |      |
| Qy | 4141 | TTTCAGAT  | GATGAAGAA | GAGAA    | GGGGCTT    | GGAA       | GAATATAT          | CAAGAA          | GCAACGA   | 4200     |         |      |
| Db | 4141 | TTTCAGAT  | GATGAAGAA | GAGAA    | GGGGCTT    | GGAA       | GAATATAT          | CAAGAA          | GCAACGA   | 4200     |         |      |
| Qy | 4201 | TGGATTCA  | ACTT      | AGTG     | AGCAGCAT   | CTGGGTGT   | GAGAGTGA          | CAAGCGTCT       | CTGAG     | 4266     |         |      |
| Db | 4201 | TGGATTCA  | ACTT      | AGTG     | AGCAGCAT   | CTGGGTGT   | GAGAGTGA          | CAAGCGTCT       | CTGAG     | 4266     |         |      |
| Qy | 4261 | ACTGCTC   | AGGGCTAT  | CTCTC    | TGAGATG    | ACATTTT    | TAACCACT          | TACAGAGG        | ATACATGC  | 4322     |         |      |
| Db | 4261 | ACTGCTC   | AGGGCTAT  | CTCTC    | TGAGATG    | ACATTTT    | TAACCACT          | TACAGAGG        | ATACATGC  | 4322     |         |      |
| Qy | 4321 | AACATA    | ACTGATTA  | AGCTCC   | GCAGS      | AAATGGCT   | GAATAGAA          | CTGTGT          | TAGAACACG | 4380     |         |      |
| Db | 4321 | AACATA    | ACTGATTA  | AGCTCC   | GCAGS      | AAATGGCT   | GAATAGAA          | CTGTGT          | TAGAACACG | 4380     |         |      |
| Qy | 4381 | ATGGAG    | CCAGCCTT  | CTAACAG  | CTACCC     | TCATAT     | AGTAGT            | CTCTTG          | CCCTTGAAG | 4440     |         |      |
| Db | 4381 | ATGGAG    | CCAGCCTT  | CTAACAG  | CTACCC     | TCATAT     | AGTAGT            | CTCTTG          | CCCTTGAAG | 4440     |         |      |
| Qy | 4441 | ACCTGCG   | AAATTC    | CAGAAC   | CACACAT    | CAGAAA     | AAAGCAGT          | ATTAACTT        | CACAGAA   | AGTA     | 4500    |      |
| Db | 4441 | ACCTGCG   | AAATTC    | CAGAAC   | CACACAT    | CAGAAA     | AAAGCAGT          | ATTAACTT        | CACAGAA   | AGTA     | 4500    |      |
| Qy | 4501 | GTGAAT    | ACCTCT    | TAAGCC   | AGATTC     | CAGAA      | GGCTTCTG          | CTGACAA         | GGTTTG    | GGTGTG   | 4566    |      |
| Db | 4501 | GTGAAT    | ACCTCT    | TAAGCC   | AGATTC     | CAGAA      | GGCTTCTG          | CTGACAA         | GGTTTG    | GGTGTG   | 4566    |      |
| Qy | 4561 | CAGATAGT  | CTTAC     | CAGTAA   | AAATTA     | AGAAC      | CAGAGT            | GAAGGAT         | CACTCC    | CTTTAAAT | 4620    |      |
| Db | 4561 | CAGATAGT  | CTTAC     | CAGTAA   | AAATTA     | AGAAC      | CAGAGT            | GAAGGAT         | CACTCC    | CTTTAAAT | 4620    |      |
| Qy | 4621 | GCCCAT    | CAATT     | AGATAT   | AGTGTGT    | ATGACAT    | GCATG             | CAAGTTC         | TTCAGAA   | TAGAA    | 4680    |      |
| Db | 4621 | GCCCAT    | CAATT     | AGATAT   | AGTGTGT    | ATGACAT    | GCATG             | CAAGTTC         | TTCAGAA   | TAGAA    | 4680    |      |
| Qy | 4681 | ACTACCA   | CTCT      | CAAGAG   | AGCTCAT    | TTAAAGT    | GTGTG             | TGAGAG          | CAACAG    | CTGGAAG  | 4746    |      |
| Db | 4681 | ACTACCA   | CTCT      | CAAGAG   | AGCTCAT    | TTAAAGT    | GTGTG             | TGAGAG          | CAACAG    | CTGGAAG  | 4746    |      |
| Qy | 4741 | AGTCTG    | GGCCAC    | ACAGAT   | TTTGA      | CGAAAC     | ATCTT             | ACCTTG          | CAAGGCA   | AGATCT   | AGAGGGA | 4800 |
| Db | 4741 | AGTCTG    | GGCCAC    | ACAGAT   | TTTGA      | CGAAAC     | ATCTT             | ACCTTG          | CAAGGCA   | AGATCT   | AGAGGGA | 4800 |
| Qy | 4801 | CCCTTAC   | CTGGAAT   | CTGGAAT  | CAGCTCTT   | CTCTG      | ATGAC             | CACTGAA         | CTGAT     | CTCTTG   | 4866    |      |
| Db | 4801 | CCCTTAC   | CTGGAAT   | CTGGAAT  | CAGCTCTT   | CTCTG      | ATGAC             | CACTGAA         | CTGAT     | CTCTTG   | 4866    |      |
| Qy | 4861 | AAGACAG   | AGCCCA    | AGTACAGT | CTGTG      | TTGGCA     | ATACAT            | CTTCA           | ACTCTG    | ATGGA    | 4920    |      |
| Db | 4861 | AAGACAG   | AGCCCA    | AGTACAGT | CTGTG      | TTGGCA     | ATACAT            | CTTCA           | ACTCTG    | ATGGA    | 4920    |      |

|    |      |  |      |
|----|------|--|------|
| Db | 4861 | AAGCAGAGCCCCAGAGTCACTGTGTGGCAATACCATCTTCAACCTCTGATTGA          | 4920 |
| Qy | 4921 | AAAGTTCCCCAATTGAAGTTGCAGATTCGCCAGGGTCCAGCTGTCTCATACTACTG       | 4980 |
| Db | 4921 | AAAGTTCCCCAATTGAAGTTGCAGATTCGCCAGAGTCCAGCTGTCTCATACTACTG       | 4980 |
| Qy | 4981 | ATACTGCTGGGATATATATSCAATGGAAGAAATGTGAGCAGAGGAAGACCAATTTGACAG   | 5040 |
| Db | 4981 | ATACTGCTGGGATATATATSCAATGGAAGAAATGTGAGCAGAGGAAGACCAATTTGACAG   | 5040 |
| Qy | 5041 | CTTCAACGAAAGGGTCAACAAAAGATGTCATGTGTGTCTGGCCTGACCCCAAG          | 5100 |
| Db | 5041 | CTTCAACGAAAGGGTCAACAAAAGATGTCATGTGTGTCTGGCCTGACCCCAAG          | 5100 |
| Qy | 5101 | AATTTATGCTGTATACAAAGTTGCCGAAACCCACATCTACTTAACTATCTAATTA        | 5160 |
| Db | 5101 | AATTTATGCTGTATACAAAGTTGCCGAAACCCACATCTACTTAACTATCTAATTA        | 5160 |
| Qy | 5161 | CTGAAGACTACTCATGTTGTTATGAAAACAGATGCTGAGTTGTGTGTGAACGACAC       | 5220 |
| Db | 5161 | CTGAAGACTACTCATGTTGTTATGAAAACAGATGCTGAGTTGTGTGTGAACGACAC       | 5220 |
| Qy | 5221 | TGAAATATTTTCTTAGGAAATTCGGGAGAGAAATGGTATGTTAGCTATTTCTGGGTGACCC  | 5280 |
| Db | 5221 | TGAAATATTTTCTTAGGAAATTCGGGAGAGAAATGGTATGTTAGCTATTTCTGGGTGACCC  | 5280 |
| Qy | 5281 | AGCTATTAAAGAAAGAAAATATGCTGAAATGACATGATTTTGAAGTCAAGAGAGATGTGG   | 5340 |
| Db | 5281 | AGCTATTAAAGAAAGAAAATATGCTGAAATGACATGATTTTGAAGTCAAGAGAGATGTGG   | 5340 |
| Qy | 5341 | TCATATGAAAGAACCCACAGAGTCCAAAGCAGACAGAGAAATCCAGACAGAAAGATCT     | 5400 |
| Db | 5341 | TCATATGAAAGAACCCACAGAGTCCAAAGCAGACAGAGAAATCCAGACAGAAAGATCT     | 5400 |
| Qy | 5401 | TCAGGGGCTTGAAGATCTGTTGCATGTGGGCCCTTACCAACAATGCCACAGATGAACCTGG  | 5460 |
| Db | 5401 | TCAGGGGCTTGAAGATCTGTTGCATGTGGGCCCTTACCAACAATGCCACAGATGAACCTGG  | 5460 |
| Qy | 5461 | AATGATATGTAACAGCTGTGTGTGCTTCTGTGTGAAGAGCTTTCAATTCACCCCTTG      | 5520 |
| Db | 5461 | AATGATATGTAACAGCTGTGTGTGCTTCTGTGTGAAGAGCTTTCAATTCACCCCTTG      | 5520 |
| Qy | 5521 | GCAACAGGTGTCAACCCCAATTGTGGTTGTGACGCCAGATGCTGTGACAGAGACATATGGCT | 5580 |
| Db | 5521 | GCAACAGGTGTCAACCCCAATTGTGGTTGTGACGCCAGATGCTGTGACAGAGACATATGGCT | 5580 |
| Qy | 5581 | TCCATATGCAATTTGGGAGATGTGTAGAGCACTGTGTGTGACCCGAGAGTGGGTGTTGGACA | 5640 |
| Db | 5581 | TCCATATGCAATTTGGGAGATGTGTAGAGCACTGTGTGTGACCCGAGAGTGGGTGTTGGACA | 5640 |
| Qy | 5641 | GTGTAGCACTTACCAAGTCCAGAGAGCTGACACCTTACTGTATACCCAGATCCCCCAACA   | 5700 |
| Db | 5641 | GTGTAGCACTTACCAAGTCCAGAGAGCTGACACCTTACTGTATACCCAGATCCCCCAACA   | 5700 |
| Qy | 5701 | GCCACTACTGA 5711   |      |
| Db | 5701 | GCCACTACTGA 5711   |      |

RESULT 12  
US-08-603-753D-1  
Sequence 1, Application US/08603753D  
Patent No. 5891857  
GENERAL INFORMATION:  
APPLICANT: HOLT, JEFFREY T.  
APPLICANT: JENSEN, ROY A.  
APPLICANT: PAGE, DAVID L.  
APPLICANT: KING, MARY-CLAIRE  
APPLICANT: SZABO, CSILLA I.  
APPLICANT: JETTON, THOMAS L.  
APPLICANT: ROBINSON-BENION, CHERYL L.  
APPLICANT: THOMPSON, MARILYN E.  
TITLE OF INVENTION: CHARACTERIZED BRCA1 AND BRCA2

TITLE OF INVENTION: PROTEINS AND SCREENING AND THERAPEUTIC METHODS BASED ON  
NUMBER OF INVENTION: CHARACTERIZED BRCA1 AND BRCA2 PROTEINS.  
NUMBER OF SEQUENCES: 29  
CORRESPONDENCE ADDRESS: 29  
ADDRESSEE: ARLES A. TAYLOR, JR.  
STREET: SUITE 1401, UNIVERSITY TOWER, 3100 TOWER  
CITY: DURHAM  
STATE: NORTH CAROLINA  
COUNTRY: USA  
ZIP: 27707  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 800 KB storage  
COMPUTER: IBM PC/XT/AT compatible  
OPERATING SYSTEM: Windows 3.1 and ASCII  
SOFTWARE: WORD PERFECT 6.1 and ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/603,753D  
FILING DATE: 20 FEB 1996  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: U.S. 08/373,799  
FILING DATE: 17 JAN 1995  
ATTORNEY/AGENT INFORMATION:  
NAME: ARLES A. TAYLOR, JR.  
REGISTRATION NUMBER: 39,395  
REFERENCE/DOCKET NUMBER: 1242/2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919) 493-8000  
TELEFAX: (919) 419-0383  
TELEX:  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5712  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
HYPOTHETICAL: no  
ANTI-SENSE: no  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
INDIVIDUAL ISOLATE:  
DEVELOPMENTAL STAGE: adult  
TISSUE TYPE: female breast  
CELL TYPE: ductal carcinoma in situ, invasive  
CELL TYPE: breast cancer and normal breast tissue  
CELL LINE: not derived from a cell line  
ORGANELLE: no  
IMMEDIATE SOURCE:  
LIBRARY: cDNA library derived from human  
CLONE: obtained using published sequence  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: unknown  
MAP POSITION: unknown  
UNITS: unknown  
FEATURE:  
NAME/KEY: BRCA1  
LOCATION: GenBank accession no. U14680  
IDENTIFICATION METHOD: microscopically directed  
IDENTIFICATION METHOD: sampling and nuclease protection assay  
OTHER INFORMATION: gene encoding BRCA1 protein  
PUBLICATION INFORMATION:  
AUTHORS: Miki, Y., et. al.  
TITLE: A strong candidate gene for the breast and  
TITLE: ovarian cancer susceptibility gene BRCA1.  
JOURNAL: Science  
VOLUME: 266  
PAGES: 66-71  
DATE: 1994  
RELEVANT RESIDUES IN SEQ ID NO: 1:  
US-08-603-753D-1

Query Match 99.8%; Score 5699.8; DB 2; Length 5712;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 5704; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
QY 1 AGCTGGCTGAGACTTCTGAGACCCGACACAGGCTGTGGGTTTCTCAGATTAAGTGGCC 60  
DB 1 AGCTGGCTGAGACTTCTGAGACCCGACACAGGCTGTGGGTTTCTCAGATTAAGTGGCC 60  
QY 61 CCTGGGCTGAGAGGCTTCACTCTGCTGCTGGGTAAGTTCATTGGAACGAAAGAA 120  
DB 61 CCTGGGCTGAGAGGCTTCACTCTGCTGCTGGGTAAGTTCATTGGAACGAAAGAA 120  
QY 121 TGGATTATCTCTCTCTGCTGCTGCTGGAAGATCAAAATGCTAATATGCTATGAGAAA 180  
DB 121 TGGATTATCTCTCTCTGCTGCTGCTGGAAGATCAAAATGCTAATATGCTATGAGAAA 180  
QY 181 TCTTAGAGTGTCCCATCTGTCTGAGATTGATCAAGAACTGTCTTCAAAAGTGACC 240  
DB 181 TCTTAGAGTGTCCCATCTGTCTGAGATTGATCAAGAACTGTCTTCAAAAGTGACC 240  
QY 241 ACAATATTTGCAATTTGCAATGCTGAACCTCTCAACGAGAAAGGCTTCAAGT 300  
DB 241 ACAATATTTGCAATTTGCAATGCTGAACCTCTCTCAACGAGAAAGGCTTCAAGT 300  
QY 301 GTCTTTATGTAAGATGATATTAACCAAAAGAGCTTCAAGAAAGTACGAGATTAGTC 360  
DB 301 GTCTTTATGTAAGATGATATTAACCAAAAGAGCTTCAAGAAAGTACGAGATTAGTC 360  
QY 361 AACTGTTGAAGAGCTATGTAATATCTTGTGCTTTTCAAGCTTGAACAGAGTTGGAGT 420  
DB 361 AACTGTTGAAGAGCTATGTAATATCTTGTGCTTTTCAAGCTTGAACAGAGTTGGAGT 420  
QY 421 ATGCAAAAGCTATATTTTGAAGAAAGAAATTAAGTCTCTGTAACCTTAAAGAG 480  
DB 421 ATGCAAAAGCTATATTTTGAAGAAAGAAATTAAGTCTCTGTAACCTTAAAGAG 480  
QY 481 AAGTTTCTATCAATCCAAAGATATGGCTACAGAAACCGTCCAAAGACTTCTACAGAGT 540  
DB 481 AAGTTTCTATCAATCCAAAGATATGGCTACAGAAACCGTCCAAAGACTTCTACAGAGT 540  
QY 541 AACCCGAAATCTCTCTCTGAGAAACCAAGTCTCAAGTCTCAACTCTTAACTTTGAA 600  
DB 541 AACCCGAAATCTCTCTCTGAGAAACCAAGTCTCAAGTCTCAACTCTTAACTTTGAA 600  
QY 601 CTGTGGAAGCTGTGAGAAAGCAAGCGGATCAACCTGTAAGAGCTGTCTACATG 660  
DB 601 CTGTGGAAGCTGTGAGAAAGCAAGCGGATCAACCTGTAAGAGCTGTCTACATG 660  
QY 661 AATTGGATCTGATCTTCTGAAAGATACCGTAAATAGGCAACTTATTCAGTGTGGAG 720  
DB 661 AATTGGATCTGATCTTCTGAAAGATACCGTAAATAGGCAACTTATTCAGTGTGGAG 720  
QY 721 ATCAAGAAATGTTACCAATCACCCCTCAAGGAACCGGATGATAAATCACTTTGGATTCTG 780  
DB 721 ATCAAGAAATGTTACCAATCACCCCTCAAGGAACCGGATGATAAATCACTTTGGATTCTG 780  
QY 781 CAAAAAAGGCTGCTGTAATTTTCTGAGACGAGTATCAAAATATGTAACATCAATCAAC 840  
DB 781 CAAAAAAGGCTGCTGTAATTTTCTGAGACGAGTATCAAAATATGTAACATCAATCAAC 840  
QY 841 CCAATATATATGTTGAAACCAACCTGAGAGAGCTGAGAGGATCCAGAAAGT 900  
DB 841 CCAATATATATGTTGAAACCAACCTGAGAGAGCTGAGAGGATCCAGAAAGT 900  
QY 901 ATCAGGGTATGTTCTGTTTCAAACTTGCAATGAGAGCAGTGTGCAATATCTATGCA 960  
DB 901 ATCAGGGTATGTTCTGTTTCAAACTTGCAATGAGAGCAGTGTGCAATATCTATGCA 960  
QY 961 GGTATTAAGAGTGAACAGAGTTTATCTCACTAAGACAGAAATGATAGAA 1020  
DB 961 GGTATTAAGAGTGAACAGAGTTTATCTCACTAAGACAGAAATGATAGAA 1020  
QY 1021 AGGCTGAATTTCTGATATTAAGCAACAGCTGCTTACAGAGAGCCAACTAACAGAT 1080

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Db 1021 AGCGTGAATTCGTATTAAGAGAAACAGCTGGCTTAGAGAGACCAATTAACGAT 1080
Qy 1081 GGGCTGGAAAGTAAGAGAAACATGTAATGATAGCGGAGCTCCAGCACAGAAAAAGGTAG 1140
Db 1081 GGGCTGGAAAGTAAGAGAAACATGTAATGATAGCGGAGCTCCAGCACAGAAAAAGGTAG 1140
Qy 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAAAGATGGAATTAAGCAAAAACTGCCATGCT 1200
Db 1141 ATCTGAATGCTGATCCCTGTGTGAGAGAAAAAGATGGAATTAAGCAAAAACTGCCATGCT 1200
Qy 1201 CAGAGAAATCTAGAGATGTAAGATGTTCTTGTGATTAACACTAAATAGCAGATTGAGA 1260
Db 1201 CAGAGAAATCTAGAGATGTAAGATGTTCTTGTGATTAACACTAAATAGCAGATTGAGA 1260
Qy 1261 AAGTTAATGATGAGTTTTCAGAGAGATGGAATCTGTTAGGTTCTGATGACTCATGATG 1320
Db 1261 AAGTTAATGATGAGTTTTCAGAGAGATGGAATCTGTTAGGTTCTGATGACTCATGATG 1320
Qy 1321 GGGAGCTGTAATCAAAATGCGCAAGTAGTGTATTTGACGTTCTAAATGAGGTAGATG 1380
Db 1321 GGGAGCTGTAATCAAAATGCGCAAGTAGTGTATTTGACGTTCTAAATGAGGTAGATG 1380
Qy 1381 AATATTTCTGTTCTTCAGAGAAAAATAGACTTACCTGACAGTGAATCTCATGAGGCTTTAA 1440
Db 1381 AATATTTCTGTTCTTCAGAGAAAAATAGACTTACCTGACAGTGAATCTCATGAGGCTTTAA 1440
Qy 1441 TATGTAAAAAGTAAAGAGTTCACTCCAAATCACTAGAGAGTAATATTGAAGACAAATAT 1500
Db 1441 TATGTAAAAAGTAAAGAGTTCACTCCAAATCACTAGAGAGTAATATTGAAGACAAATAT 1500
Qy 1501 TTGGGAAAACTATCGAGAGAAAGGCAAGGCTCCCAACTTAAGCCATGTAATCGAANAATC 1560
Db 1501 TTGGGAAAACTATCGAGAGAAAGGCAAGGCTCCCAACTTAAGCCATGTAATCGAANAATC 1560
Qy 1561 TAAATTATAGAGACATTTGTTACTGAGCCAAGATTAACAGAGACCTCCCTCACAAATA 1620
Db 1561 TAAATTATAGAGACATTTGTTACTGAGCCAAGATTAACAGAGACCTCCCTCACAAATA 1620
Qy 1621 AATTAAGCGTAAAGAGAGAACTACATCAAGGCTTATCTGAGAGTTTATCAAGAAAG 1680
Db 1621 AATTAAGCGTAAAGAGAGAACTACATCAAGGCTTATCTGAGAGTTTATCAAGAAAG 1680
Qy 1681 CAGATTTGGCAGTTCAAAAAGACTCTCGAATGATTAATCAAGGAACTTAACCAAGGAGC 1740
Db 1681 CAGATTTGGCAGTTCAAAAAGACTCTCGAATGATTAATCAAGGAACTTAACCAAGGAGC 1740
Qy 1741 AGAATGCTCAAGTGAATGAATTAATTAATAGTGTCTATGAGAAATTAACAAAAAGGTGAT 1800
Db 1741 AGAATGCTCAAGTGAATGAATTAATTAATAGTGTCTATGAGAAATTAACAAAAAGGTGAT 1800
Qy 1801 CTATTCAGAAATGAGAAAAATCTTAACCCAAATGAAATCACTCGAAAAAGAAATCTGCTTTA 1860
Db 1801 CTATTCAGAAATGAGAAAAATCTTAACCCAAATGAAATCACTCGAAAAAGAAATCTGCTTTA 1860
Qy 1861 AAACGAAAGCTGAACCTTAATAGCAGAGATATAGCAATATGGAATCGAATTAATATCC 1920
Db 1861 AAACGAAAGCTGAACCTTAATAGCAGAGATATAGCAATATGGAATCGAATTAATATCC 1920
Qy 1921 ACAATTTCAAAAGCACTTAAGAAATAGGCTGAGAGGAAATCTTCTACCAAGCATAATTC 1980
Db 1921 ACAATTTCAAAAGCACTTAAGAAATAGGCTGAGAGGAAATCTTCTACCAAGCATAATTC 1980
Qy 1981 ATGGCCTTGAATCTAGTCACTAGAGAAATCTTAAGCCCACTAATGTACTGATTTGCCAA 2040
Db 1981 ATGGCCTTGAATCTAGTCACTAGAGAAATCTTAAGCCCACTAATGTACTGATTTGCCAA 2040
Qy 2041 TTGATAGTTGTTCTAGCAGTGAAGATTAAGAAAAAAGTACAAACCAATGCCAGTCA 2100
Db 2041 TTGATAGTTGTTCTAGCAGTGAAGATTAAGAAAAAAGTACAAACCAATGCCAGTCA 2100
Qy 2101 GGCACAGAGAAACCTTACACTCATGAGAAAGGTAAAGAACTGAGCCAAAGAGA 2160
Db 2101 GGCACAGAGAAACCTTACACTCATGAGAAAGGTAAAGAACTGAGCCAAAGAGA 2160

Db 2101 GGCACAGAGAAACCTTACACTCATGAGAAAGGTAAAGAACTGAGCCAAAGAGA 2160
Qy 2161 GTTACAGGCCAAATGAAAGACAGCACTAATAAGACATGACGTATCTTTCCAGAGCTGA 2220
Db 2161 GTTACAGGCCAAATGAAAGACAGCACTAATAAGACATGACGTATCTTTCCAGAGCTGA 2220
Qy 2221 AGTTAAACAAATGACCTGCTTTCTTAAGTGTTCAAATTAACAGAGAACTTAAAGAT 2280
Db 2221 AGTTAAACAAATGACCTGCTTTCTTAAGTGTTCAAATTAACAGAGAACTTAAAGAT 2280
Qy 2281 TTGTCAATCTTACGCTTCCAGAGAGAAAAAGAAAGAACTGAAACAGTTAAAGTGT 2340
Db 2281 TTGTCAATCTTACGCTTCCAGAGAGAAAAAGAAAGAACTGAAACAGTTAAAGTGT 2340
Qy 2341 CTAAATTAATGCTGAAGAACCCCAAGATCTCATGTTTAAGTGAAGAAAGGTTTGCAAACTG 2400
Db 2341 CTAAATTAATGCTGAAGAACCCCAAGATCTCATGTTTAAGTGAAGAAAGGTTTGCAAACTG 2400
Qy 2401 AAAAGATCTGTAGAGATGACAGTATTTCACTGCTGATACCTGATGATTAATGCACTCAGG 2460
Db 2401 AAAAGATCTGTAGAGATGACAGTATTTCACTGCTGATGATTAATGCACTCAGG 2460
Qy 2461 AAAGTATCTGTTACTGGAAGTTAGCACTTAGGGAAGCAAAAAAGAAACCAATTAAT 2520
Db 2461 AAAGTATCTGTTACTGGAAGTTAGCACTTAGGGAAGCAAAAAAGAAACCAATTAAT 2520
Qy 2521 GTGTGATGCTAGTGTGACAGATTTTGAAGAAACCCCAAGGACTAATGCTGTTGCCAAG 2580
Db 2521 GTGTGATGCTAGTGTGACAGATTTTGAAGAAACCCCAAGGACTAATGCTGTTGCCAAG 2580
Qy 2581 ATAAATAGAAATGACACAGAGGCTTTAATGATTCATGTTGGGACATGAAGTTAACACAGTC 2640
Db 2581 ATAAATAGAAATGACACAGAGGCTTTAATGATTCATGTTGGGACATGAAGTTAACACAGTC 2640
Qy 2641 GGGAAACAGCATAGAAAAATGGAAGAAAGTGAATGCTCACTATTTGCAAAATCAT 2700
Db 2641 GGGAAACAGCATAGAAAAATGGAAGAAAGTGAATGCTCACTATTTGCAAAATCAT 2700
Qy 2701 TCAAGTTTCAAAAGGCCAGTCATTTGCTGTTTCAATCCAGAAATGCAAGAAAGG 2760
Db 2701 TCAAGTTTCAAAAGGCCAGTCATTTGCTGTTTCAATCCAGAAATGCAAGAAAGG 2760
Qy 2761 AATGTGCAACATTTCTGCTGCACTCTGAGGTCCTTAAGAAACCAAGTCCAAAGTCACTT 2820
Db 2761 AATGTGCAACATTTCTGCTGCACTCTGAGGTCCTTAAGAAACCAAGTCCAAAGTCACTT 2820
Qy 2821 TTGAATGTGAACAAAAGGAGAAATCAAGGAAAGAAATGAGTCAATATCAAGCTGTAC 2880
Db 2821 TTGAATGTGAACAAAAGGAGAAATCAAGGAAAGAAATGAGTCAATATCAAGCTGTAC 2880
Qy 2881 AGACAGTTAATATCACTGCAAGGCTTCTGTTGTTGTCAGAAAGATTAACCCAGTTGATA 2940
Db 2881 AGACAGTTAATATCACTGCAAGGCTTCTGTTGTTGTCAGAAAGATTAACCCAGTTGATA 2940
Qy 2941 ATGCCAAATGTAGTATCAAGAGAGGCTCTAGGTTTGTCTATCATCTCACTTCAAGAGCA 3000
Db 2941 ATGCCAAATGTAGTATCAAGAGAGGCTCTAGGTTTGTCTATCATCTCACTTCAAGAGCA 3000
Qy 3001 ACAGAACTGCACTATTAATCTCAAAATGAATGAATGAGAAATGAGAAATGAGAAATGAGAA 3060
Db 3001 ACAGAACTGCACTATTAATCTCAAAATGAATGAATGAGAAATGAGAAATGAGAAATGAGAA 3060
Qy 3061 CACCACTTTTCCATCAAGTCAATTTGTAAATTAATGAATGAATGAATGAATGAATGAATGA 3120
Db 3061 CACCACTTTTCCATCAAGTCAATTTGTAAATTAATGAATGAATGAATGAATGAATGAATGA 3120
Qy 3121 AAAACTTTGAGAGACATTTCAATGTCACTGAAAGAGAAATGAGAAATGAGAAATGAGAA 3180
Db 3121 AAAACTTTGAGAGACATTTCAATGTCACTGAAAGAGAAATGAGAAATGAGAAATGAGAA 3180
Qy 3181 GTACAGTGAAGCAATTAAGCCGTATTAACATTAAGAGAAATGTTTAAAGAGCCAGCT 3240
Db 3181 GTACAGTGAAGCAATTAAGCCGTATTAACATTAAGAGAAATGTTTAAAGAGCCAGCT 3240
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|    |  |      |   |      |
|----|--|------|---|------|
| OY |  | 3241 | CANGCAATTAATAAGACATGAGTCTCCACTACTAATGAAGTGCGCCTCCAGTTATTAAGA  | 3300 |
| Dd |  | 3241 | CAGCAATTATTAATGAAGTAGGTTCAGACTAAAGAAAGTGGCTCCAGATTATGA        | 3300 |
| OY |  | 3301 | TAGGTTCCAGCATGAAAAACAATTCAAGAGAACCTAGTAGAAAACAGAGGCCCAAATTTGA | 3360 |
| Dd |  | 3301 | TAGGTTCCAGTGTATBAAAACATTCAAGAGAACTAGTAGAAAACAGAGGCCCAAATTTGA  | 3360 |
| OY |  | 3361 | ATGCTATGCTTAGATTAGTAGGGTTTTGCACCTGAGGCTATATAACAAGTCTTCCTGGA   | 3420 |
| Dd |  | 3361 | ATGCTATGCTTAGATTAGTAGGGTTTTGCACCTGAGGCTATATAACAAGTCTTCCTGGA   | 3420 |
| OY |  | 3421 | GTAATTGTAAAGCATCCTGCAAAATATAAAAAGCAGAAATATGAAGAAAGTACTGACCTGT | 3480 |
| Dd |  | 3421 | GTAATTGTAAAGCATCCTGCAAAATATAAAAAGCAGAAATATGAAGAAAGTACTGACCTGT | 3480 |
| OY |  | 3481 | ATACAGATTTCTCTCCATATCTGATTGAGATTAAGAACAGCTATGGGAAGTATGC       | 3540 |
| Dd |  | 3481 | ATACAGATTTCTCTCCATATCTGATTGAGATTAAGAACAGCTATGGGAAGTATGC       | 3540 |
| OY |  | 3541 | ATGCACTCACGGTTGTTCTGAGACCTGATGACCTTGATAGATGCTAAATTAAGG        | 3600 |
| Dd |  | 3541 | ATGCACTCACGGTTGTTCTGAGACCTGATGACCTTGATAGATGCTAAATTAAGG        | 3600 |
| OY |  | 3601 | AAGATACTAGTTTGTCTGAAAAATGACATTAAGSAAAGTTCTGCTTTTTCAGCAAAACG   | 3660 |
| Dd |  | 3601 | AAGATACTAGTTTGTCTGAAAAATGACATTAAGSAAAGTTCTGCTTTTTCAGCAAAACG   | 3660 |
| OY |  | 3661 | TCCAGAGAGAGAGACTTAGCACAGAGTCTAGACCCTTCAACCATACACATTGGCTCAG    | 3720 |
| Dd |  | 3661 | TCCAGAGAGAGAGACTTAGCACAGAGTCTAGACCCTTCAACCATACACATTGGCTCAG    | 3720 |
| OY |  | 3721 | GTTACCGAAGAGGGGCCCAAGAAATATAGAGTCTCAGAAAGAACCTTATCTGTAGAGATG  | 3780 |
| Dd |  | 3721 | GTTACCGAAGAGGGGCCCAAGAAATATAGAGTCTCAGAAAGAACCTTATCTGTAGAGATG  | 3780 |
| OY |  | 3781 | AAGAGCTTCCCCTGCTTCCAACAATTGTAATTTGGTAAGTAAACAAATATACCTTCTCAGT | 3840 |
| Dd |  | 3781 | AAGAGCTTCCCCTGCTTCCAACAATTGTAATTTGGTAAGTAAACAAATATACCTTCTCAGT | 3840 |
| OY |  | 3841 | CTACTAGGCATATAGACACCGGTGTCACCGAGTCTGTCTAABAACAACAGAGAGAATTTAT | 3900 |
| Dd |  | 3841 | CTACTAGGCATATAGACACCGGTGTCACCGAGTCTGTCTAABAACAACAGAGAGAATTTAT | 3900 |
| OY |  | 3901 | TATCATTTAAGAAATAGCTTAATATGCTGACAGTAAACAGTATATTTGGCAAGGCATCTC  | 3960 |
| Dd |  | 3901 | TATCATTTAAGAAATAGCTTAATATGCTGACAGTAAACAGTATATTTGGCAAGGCATCTC  | 3960 |
| OY |  | 3961 | AGGAACATCACCTTAGTAGAGAAAACMAAATGTTCTGCTAGCTGTGTTTTCTTCAAGTGA  | 4020 |
| Dd |  | 3961 | AGGAACATCACCTTAGTAGAGAAAACMAAATGTTCTGCTAGCTGTGTTTTCTTCAAGTGA  | 4020 |
| OY |  | 4021 | GTAATTGTGAAGACTTGAAGTCAAAATACAAACACCCAGAGATCCCTTCTGATAGGTTCTT | 4080 |
| Dd |  | 4021 | GTAATTGTGAAGACTTGAAGTCAAAATACAAACACCCAGAGATCCCTTCTGATAGGTTCTT | 4080 |
| OY |  | 4081 | CCAAACAATAGAGCATCAGTCTGAAAGCCAGGAGTTGGTCTGAGTGACACAGGAATTGG   | 4140 |
| Dd |  | 4081 | CCAAACAATAGAGCATCAGTCTGAAAGCCAGGAGTTGGTCTGAGTGACACAGGAATTGG   | 4140 |
| OY |  | 4141 | TTTCAGATGATGAAGAAAGAGAAACGGGCTTGAAAGAAATATATCAGAAAGAGAAAGCA   | 4200 |
| Dd |  | 4141 | TTTCAGATGATGAAGAAAGAGAAACGGGCTTGAAAGAAATATATCAGAAAGAGAAAGCA   | 4200 |
| OY |  | 4201 | TGGATTCAAACTTAGGTGAGCAGCATCTGGGTGTGAGAGTGAACAAGCTCTCTGAG      | 4260 |
| Dd |  | 4201 | TGGATTCAAACTTAGGTGAGCAGCATCTGGGTGTGAGAGTGAACAAGCTCTCTGAG      | 4260 |
| OY |  | 4261 | ACTGCTCAGGGCTATCCTCTCTAGATGACATTTTAAACCTCAGCAGAGGATACATGC     | 4320 |
| Dd |  | 4261 | ACTGCTCAGGGCTATCCTCTCTAGATGACATTTTAAACCTCAGCAGAGGATACATGC     | 4320 |

|    |      |  |      |
|----|------|--|------|
| QY | 4321 | AAACATACCTGATTAAGCTCCAGAGAGGAAATGGCTGAACCTAGAAGCTGTGTTAACACACG   | 4380 |
| Db | 4321 | AACATTAACCTATTAAGCTCCAGAGAGGAAATGGCTGAACCTAGAAGCTGTGTTAACACACG   | 4380 |
| QY | 4381 | ATGGGAGCCACGCTTCTTAACAGCTAACCTTCCATCATTAAGTACCTCTGCCCCCTGAGG     | 4440 |
| Db | 4381 | ATGGGAGCCACGCTTCTTAACAGCTAACCTTCCATCATTAAGTACCTCTGCCCCCTGAGG     | 4440 |
| QY | 4441 | ACCTGCGAATCCAGAACAAAGCAATCAGAAAAAGCATTTAACTTACAGAAAAAGTA         | 4500 |
| Db | 4441 | ACCTGCGAATCCAGAACAAAGCAATCAGAAAAAGCATTTAACTTACAGAAAAAGTA         | 4500 |
| QY | 4501 | GTTGAATACCCCTATTAAGCCAGAAATCCAGAGGCCCTTCTGCGTGAAGATTTGAGAGTCTG   | 4560 |
| Db | 4501 | GTTGAATACCCCTATTAAGCCAGAAATCCAGAGGCCCTTCTGCGTGAAGATTTGAGAGTCTG   | 4560 |
| QY | 4561 | CAGATAGTTCCTACCAAGTAAATAATGAACCAAGAGTGAAGAGTCAATCCCTCTTAAT       | 4620 |
| Db | 4561 | CAGATAGTTCCTACCAAGTAAATAATGAACCAAGAGTGAAGAGTCAATCCCTCTTAAT       | 4620 |
| QY | 4621 | GCCCATCTTAAGATGATAGTGTGTAATGACACAGTGTCTTGAGAGTCTTCAGAAATAGAA     | 4680 |
| Db | 4621 | GCCCATCTTAAGATGATAGTGTGTAATGACACAGTGTCTTGAGAGTCTTCAGAAATAGAA     | 4680 |
| QY | 4681 | ACTACCCATCTCAAGAGAGCTCATTTAAGTGTGTTGATGTGGAGAGCAACAGCTGGAAG      | 4740 |
| Db | 4681 | ACTACCCATCTCAAGAGAGCTCATTTAAGTGTGTTGATGTGGAGAGCAACAGCTGGAAG      | 4740 |
| QY | 4741 | AGTCTGGGCCCAAGATTTGAACGGAAACATTTTACTTGGCCAAAGGCAAGATTTAAGAGGAA   | 4800 |
| Db | 4741 | AGTCTGGGCCCAAGATTTGAACGGAAACATTTTACTTGGCCAAAGGCAAGATTTAAGAGGAA   | 4800 |
| QY | 4801 | CCCCCTTACCTGGAATCTGGAATCAGCCTCTTCTCTGATGACCCCTGAATCTGATCCTTCTG   | 4860 |
| Db | 4801 | CCCCCTTACCTGGAATCTGGAATCAGCCTCTTCTCTGATGACCCCTGAATCTGATCCTTCTG   | 4860 |
| QY | 4861 | AAAGACAGAGCCCCAGAGTCAAGTCTGTGTGGCAATATCCATCTTCAACCTCTGCATTTGA    | 4920 |
| Db | 4861 | AAAGACAGAGCCCCAGAGTCAAGTCTGTGTGGCAATATCCATCTTCAACCTCTGCATTTGA    | 4920 |
| QY | 4921 | AAAGTTCGCCAATTTAAAGTTGCAAAATCTGCCCCAGAGTCAAGCTGCTGTCTATATCTACTG  | 4980 |
| Db | 4921 | AAAGTTCGCCAATTTAAAGTTGCAAAATCTGCCCCAGAGTCAAGCTGCTGTCTATATCTACTG  | 4980 |
| QY | 4981 | ATACTGCTGGGTATATATGCAATGGAAGAAGTGTGACAGAGGAGAAAGCCAGAAATTTGACAG  | 5040 |
| Db | 4981 | ATACTGCTGGGTATATATGCAATGGAAGAAGTGTGACAGAGGAGAAAGCCAGAAATTTGACAG  | 5040 |
| QY | 5041 | CTTCAACAGAAAGGGTCAACAAAAGAAATGTTCATGTGTGTGTCTGCGCTTGACCCACAGAG   | 5100 |
| Db | 5041 | CTTCAACAGAAAGGGTCAACAAAAGAAATGTTCATGTGTGTGTCTGCGCGCTTGACCCACAGAG | 5100 |
| QY | 5101 | AAATTATGCTGTGTATACAGTTTGGCCGAAAAAGCAACCATCATTAACTTAATCTTAATTA    | 5160 |
| Db | 5101 | AAATTATGCTGTGTATACAGTTTGGCCGAAAAAGCAACCATCATTAACTTAATCTTAATTA    | 5160 |
| QY | 5161 | CTGAAGAGACTACTCATGTTGTTTATGAAAAAGATGCTGAATTTGTGTGTGAACGAGACAC    | 5220 |
| Db | 5161 | CTGAAGAGACTACTCATGTTGTTTATGAAAAAGATGCTGAATTTGTGTGTGAACGAGACAC    | 5220 |
| QY | 5221 | TGAAATATTTTCTAGGAATTCGGGAGGAAAAATGGGTAGTTAGCTATTTCTGGGTGACC      | 5280 |
| Db | 5221 | TGAAATATTTTCTAGGAATTCGGGAGGAAAAATGGGTAGTTAGCTATTTCTGGGTGACC      | 5280 |
| QY | 5281 | AGTCTATTTAAAGAAAGAAAAATGCTGATAGCAATGATTTTGAAGTGAAGAGAGATGTGG     | 5340 |
| Db | 5281 | AGTCTATTTAAAGAAAGAAAAATGCTGATAGCAATGATTTTGAAGTGAAGAGAGATGTGG     | 5340 |
| QY | 5341 | TCAATGGAAGAAACCAACCAAGGTCCAAGCGAGACAAAGATCCCAAGACAGAAAAAGTCT     | 5400 |
| Db | 5341 | TCAATGGAAGAAACCAACCAAGGTCCAAGCGAGACAAAGATCCCAAGACAGAAAAAGTCT     | 5400 |
| QY | 5401 | TCAAGGGGCTAGAAATCTGTGTCTATAGGGCCCTTCAACCAATGCCCCACAGATCAACTGG    | 5460 |

Db 5401 TCAGGGGCTGAAATCTGTTCTATGCGCCCTTACCAAACTGCCACAGATCAACTGG 5460  
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Db 5701 GCCACTACTGA 5711

RESULT 13  
US-09-099-753-1  
Sequence 1, Application US/09099753  
Patent No. 6149903  
GENERAL INFORMATION:  
APPLICANT: HOLT, JEFFREY T.  
APPLICANT: JENSEN, ROY A.  
APPLICANT: PAGE, DAVID L.  
APPLICANT: KING, MARY-CLAIRE  
APPLICANT: SZABO, CSILLA I.  
APPLICANT: JETTON, THOMAS L.  
APPLICANT: ROBINSON-BENION, CHERYL L.  
APPLICANT: THOMPSON, MARILYN E.  
TITLE OF INVENTION: CHARACTERIZED BRCA1 AND BRCA2  
TITLE OF INVENTION: PROTEINS AND SCREENING AND THERAPEUTIC METHODS BASED ON  
TITLE OF INVENTION: CHARACTERIZED BRCA1 AND BRCA2 PROTEINS.  
NUMBER OF SEQUENCES: 29  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ARLES A. TAYLOR, JR.  
STREET: SUITE 1401, UNIVERSITY TOWER, 3100 TOWER  
CITY: DURHAM  
STATE: NORTH CAROLINA  
COUNTRY: USA  
ZIP: 27707  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 800 KB storage  
COMPUTER: IBM PC/XT/AT compatible  
OPERATING SYSTEM: Windows 3.11  
SOFTWARE: WORD PERFECT 6.1 and ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/099,753  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/603,753  
FILING DATE: 20 FEB 1996  
APPLICATION NUMBER: U.S. 08/373,799  
FILING DATE: 17 JAN 1995  
ATTORNEY/AGENT INFORMATION:  
NAME: ARLES A. TAYLOR, JR.  
REGISTRATION NUMBER: 39,395  
REFERENCE/DOCKET NUMBER: 1242/2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919) 493-8000  
TELEFAX: (919) 419-0383  
TELEX:  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:

LENGTH: 5712  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA to mRNA  
HYPOTHETICAL: no  
ANTI-SENSE: no  
ORIGINAL SOURCE:  
ORGANISM: Homo sapiens  
INDIVIDUAL ISOLATE:  
DEVELOPMENTAL STAGE: adult  
TISSUE TYPE: female breast  
CELL TYPE: ductal carcinoma in situ, invasive  
CELL LINE: breast cancer and normal breast tissue  
CELL LINE: not derived from a cell line  
ORGANELLE: no  
IMMEDIATE SOURCE:  
LIBRARY: CDNA library derived from human  
CLONE: obtained using published sequence  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: unknown  
MAP POSITION: unknown  
UNITS: unknown  
FEATURE:  
NAME/KEY: BRCA1  
LOCATION: Genbank accession no. U14680  
IDENTIFICATION METHOD: microscopically directed  
IDENTIFICATION METHOD: sampling and nuclease protection assay  
OTHER INFORMATION: gene encoding BRCA1 protein  
AUTHORS: Miki, Y., et. al.  
TITLE: A strong candidate gene for the breast and  
TITLE: ovarian cancer susceptibility gene BRCA1.  
JOURNAL: Science  
VOLUME: 266  
PAGES: 66-71  
DATE: 1994  
RELEVANT RESIDUES IN SEQ ID NO: 1:  
US-09-099-753-1  
Query Match 99.8%; Score 5699.8; DB 3; Length 5712;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 5704; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
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```

1 APPLICANT: ROBINSON-BENION, CHERYL L.
2 APPLICANT: THOMPSON, MARTIN E
3 TITLE OF INVENTION: THERAPEUTIC METHODS FOR
4 TITLE OF INVENTION: PROSTATE CANCER
5 NUMBER OF SEQUENCES: 26
6 CORRESPONDENCE ADDRESS:
7 ADDRESSEE: ARLES A. TAYLOR, JR.
8 STREET: SUITE 1401, UNIVERSITY TOWER, 3100 TOWER
9 STREET: BOULEVARD
10 CITY: DURHAM
11 STATE: NORTH CAROLINA
12 COUNTRY: USA
13 ZIP: 27707
14
15 COMPUTER READABLE FORM:
16 MEDIUM TYPE: Diskette, 3.50 inch, 1.44MB storage
17 COMPUTER: IBM PC/XT/AT compatible
18 OPERATING SYSTEM: Windows 3.1
19 SOFTWARE: WORD PERFECT 6.1 and ASCII
20 CURRENT APPLICATION DATA:
21 APPLICATION NUMBER: US/08/986,106
22 FILING DATE:
23 CLASSIFICATION:
24 PRIOR APPLICATION DATA:
25 APPLICATION NUMBER: 08/603,753
26 FILING DATE: 20 FEB 1996
27 ATTORNEY/AGENT INFORMATION:
28 NAME: ARLES A. TAYLOR, JR.
29 REGISTRATION NUMBER: 39,395
30 REFERENCE/DOCKET NUMBER: 1242/3
31 TELECOMMUNICATION INFORMATION:
32 TELEPHONE: (919) 493-8000
33 TELEFAX: (919) 419-0383
34 INFORMATION FOR SEQ ID NO: 1:
35 SEQUENCE CHARACTERISTICS:
36 LENGTH: 5712
37 TYPE: nucleic acid
38 STRANDEDNESS: double
39 TOPOLOGY: linear
40 FEATURE:
41 NAME/KEY: BRCA1
42 LOCATION: Genbank accession no. U14680
43 PUBLICATION INFORMATION:
44 AUTHORS: Miki, Y., et. al.
45 TITLE: A strong candidate gene for the breast and
46 TITLE: ovarian cancer susceptibility gene BRCA1.
47 JOURNAL: Science
48 VOLUME: 266
49 PAGES: 66-71
50 DATE: 1994
51
52 US-08-966-106-1
53
54 Query Match 99.8%; Score 5699.8; DB 4; Length 5712;
55 Best Local Similarity 99.9%; Pred. No. 0;
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4621 GCCCATCATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4680

|    |      |  |      |
|----|------|--|------|
| Db | 4621 | GGCCATCAATTAGATGATAGTGSTGCATGTCACAGATGGCTCTGGAGTCTTCAGATTAGA | 4688 |
| Oy | 4661 | ACTACCATCTCAAGAGAGCTCATTAAAGTGTGTAATGTGGAGGACACAGCTGGAA      | 4740 |
| Db | 4661 | ACTACCACATCTCAAGAGAGCTCATTAAAGTGTGTAATGTGGAGGACACAGCTGGAA    | 4740 |
| Oy | 4741 | AGTCTGGGCGACACGATTTGACGAAACATCTTACTTGGCAAGGCAAGATCTAGAGGAA   | 4800 |
| Db | 4741 | AGTCTGGGCGACACGATTTGACGAAACATCTTACTTGGCAAGGCAAGATCTAGAGGAA   | 4800 |
| Oy | 4801 | CCCCTTACCTGGAAATCTGGAAATCAGCTCTTCTCTGATGACCTGAAATCTGATCTCTG  | 4866 |
| Db | 4801 | CCCCTTACCTGGAAATCTGGAAATCAGCTCTTCTCTGATGACCTGAAATCTGATCTCTG  | 4866 |
| Oy | 4861 | AAGACAGAGCCCCAGAGTCACTCGTGGTGGCAATACATCTTCAACTCTGATCTGA      | 4920 |
| Db | 4861 | AAGACAGAGCCCCAGAGTCACTCGTGGTGGCAATACATCTTCAACTCTGATCTGA      | 4920 |
| Oy | 4921 | AAATTCGCCCAATTGAAAGTTGAGAAATCTGCCAGAGTCTCAGCTGCTCATACTACTG   | 4980 |
| Db | 4921 | AAATTCGCCCAATTGAAAGTTGAGAAATCTGCCAGAGTCTCAGCTGCTCATACTACTG   | 4980 |
| Oy | 4961 | ATACGTCTGGGTATATATGCAATGGAAGAAAGTGTGACAGAGGAGAAAGCAATATGACAG | 5040 |
| Db | 4961 | ATACGTCTGGGTATATATGCAATGGAAGAAAGTGTGACAGAGGAGAAAGCAATATGACAG | 5040 |
| Oy | 5041 | CTTCAACGAAAGGGGTCAACAAAGAAATGTCATGATGGTGTCTGGCTGACCCAGAG     | 5100 |
| Db | 5041 | CTTCAACGAAAGGGGTCAACAAAGAAATGTCATGATGGTGTCTGGCTGACCCAGAG     | 5100 |
| Oy | 5101 | AATTATATCTGCTGTACAAAGTTTGGCAGAAAACACACATCATCTTAACTAATTA      | 5160 |
| Db | 5101 | AATTATATCTGCTGTACAAAGTTTGGCAGAAAACACACATCATCTTAACTAATTA      | 5160 |
| Oy | 5161 | CTGAAGAGACTACTATGTTGTTATGAAAAACAGTGTGAGTTTGTGTGAACGGAAC      | 5220 |
| Db | 5161 | CTGAAGAGACTACTATGTTGTTATGAAAAACAGTGTGAGTTTGTGTGAACGGAAC      | 5220 |
| Oy | 5221 | TGAAATATTTTCTAGGAATTCGGGAGGAAAAATGGGTAGTTAGTATTTCTGGGTGACC   | 5280 |
| Db | 5221 | TGAAATATTTTCTAGGAATTCGGGAGGAAAAATGGGTAGTTAGTATTTCTGGGTGACC   | 5280 |
| Oy | 5281 | AGCTAATTAAGAAAGAAAAAGCTGAAATGAGCATGATTTGAAATCAGAGAGATGTGG    | 5340 |
| Db | 5281 | AGCTAATTAAGAAAGAAAAAGCTGAAATGAGCATGATTTGAAATCAGAGAGATGTGG    | 5340 |
| Oy | 5341 | TCAATGAGAAAGAACCAACAGGTCCAAAGCGAACAGAAATCCAGAGACAGAAAGATCT   | 5400 |
| Db | 5341 | TCAATGAGAAAGAACCAACAGGTCCAAAGCGAACAGAAATCCAGAGACAGAAAGATCT   | 5400 |
| Oy | 5401 | TCAGGGGGCTTGAATCTGTGCTATGAGCCCTTACCAATGGCCCAATCAACTGG        | 5460 |
| Db | 5401 | TCAGGGGGCTTGAATCTGTGCTATGAGCCCTTACCAATGGCCCAATCAACTGG        | 5460 |
| Oy | 5461 | AATGATGATGATCAGCTGTGTGTGCTTGTGTGTGAAGAGCTTTCATCATTCACCTTG    | 5520 |
| Db | 5461 | AATGATGATGATCAGCTGTGTGTGCTTGTGTGTGAAGAGCTTTCATCATTCACCTTG    | 5520 |
| Oy | 5521 | GCACAGGTGTCCACCAATTTGTGTGTGTGACACCGATGCTGTGACAGAGACATGGCT    | 5580 |
| Db | 5521 | GCACAGGTGTCCACCAATTTGTGTGTGTGACACCGATGCTGTGACAGAGACATGGCT    | 5580 |
| Oy | 5581 | TCATGACATTTGGGAGATGTGTGAGGACCTGTGTGTACCCGAGTGGGTGTGAC        | 5640 |
| Db | 5581 | TCATGACATTTGGGAGATGTGTGAGGACCTGTGTGTACCCGAGTGGGTGTGAC        | 5640 |
| Oy | 5641 | GTGTAGCACTCTACCAAGTCCAGAGCTGACACCTTACTGATACCCAGATCCCCACA     | 5700 |
| Db | 5641 | GTGTAGCACTCTACCAAGTCCAGAGCTGACACCTTACTGATACCCAGATCCCCACA     | 5700 |
| Oy | 5701 | GCACACTACTGA 5711  |      |
| Db | 5701 | GCACACTACTGA 5711  |      |

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RESULT 15
US-09-007-678B-47
Sequence 47, Application US/0907678B
Patent No. 6342483
GENERAL INFORMATION:
APPLICANT: HOLT, JEFFREY T.
APPLICANT: JENSEN, ROY A.
APPLICANT: PAGE, DAVID L.
APPLICANT: OBERMILLER, PATRICE S.
APPLICANT: ROBINSON-BENION, CHERYL L.
APPLICANT: THOMPSON, MARILYN E.
TITLE OF INVENTION: METHOD FOR DETECTION AND TREATMENT OF BREAST CANCER
FILE REFERENCE: Attorney Docket No. 6342483 1242-1-2-2
CURRENT FILING DATE: 1998-01-15
PRIOR APPLICATION NUMBER: 08/373,799
PRIOR FILING DATE: 1995-01-17
PRIOR APPLICATION NUMBER: 08/182,961
PRIOR FILING DATE: 1994-01-14
NUMBER OF SEO ID NOS: 61
SOFTWARE: Microsoft Wordpad
SEO ID NO 47
LENGTH: 5712
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (120)..(5708)
NAME/KEY: misc feature
LOCATION: (4532)..(4535)
OTHER INFORMATION: Xaa=any amino acid
US-09-007-678B-47

Query Match          99.8%; Score 5699.8; DB 4; Length 5712;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 5704; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY      1  AGCTGCTGAGACTCTCTCGAAGCCCGACAGGCTGTGGGGTTCTCATGATACTGGGCC 60
DB      1  AGCTGCTGAGACTCTCTCGAAGCCCGACAGGCTGTGGGGTTCTCATGATACTGGGCC 60

QY      61  CCTGGGCTCAGGAGGAGCCCTTACCCCTGCTCTGGGTTAAAGTTCAATGGAAACAGAAAGAA 120
DB      61  CCTGGGCTCAGGAGGAGCCCTTACCCCTGCTCTGGGTTAAAGTTCAATGGAAACAGAAAGAA 120

QY      121  TGGATTTATCTGCTCTTCGCGGTGGAAGATACAAAATGTCATTAAATGCTATGACAGAAA 180
DB      121  TGGATTTATCTGCTCTTCGCGGTGGAAGATACAAAATGTCATTAAATGCTATGACAGAAA 180

QY      181  TCTTAGAGTGTCCATCTGCTGTGGAGTTGATCAAGAGAACTGTCTCCACAAAGTGTACC 240
DB      181  TCTTAGAGTGTCCATCTGCTGTGGAGTTGATCAAGAGAACTGTCTCCACAAAGTGTACC 240

QY      241  ACATATTTTGGAAATTTTGGCATGCTGAAACTTCTCAACAGAGAAAGAGGCTTCACAGT 300
DB      241  ACATATTTTGGAAATTTTGGCATGCTGAAACTTCTCAACAGAGAAAGAGGCTTCACAGT 300

QY      301  GTCTTTATGTGAAGATGATATAACCAAAAAGAGCCTTACAGAAAGTACAGATTTAGTC 360
DB      301  GTCTTTATGTGAAGATGATATAACCAAAAAGAGCCTTACAGAAAGTACAGATTTAGTC 360

QY      361  AACTGTGTGAAGACTATTTGAAATCAATTTGTGCTTTACGTTGACACAGAGTTTGAAGT 420
DB      361  AACTGTGTGAAGACTATTTGAAATCAATTTGTGCTTTACGTTGACACAGAGTTTGAAGT 420

QY      421  ATGCAAAAGCTATATAATTTTGCAGAAAAGGAAATAATCTCTCGAATCATTAATAAGATG 480
DB      421  ATGCAAAAGCTATATAATTTTGCAGAAAAGGAAATAATCTCTCGAATCATTAATAAGATG 480

QY      481  AAGTTTCTATCATCAAAAGTATGGGCTACAGAAACGCTGCCAAAAGACTTTCACAGATG 540
DB      481  AAGTTTCTATCATCAAAAGTATGGGCTACAGAAACGCTGCCAAAAGACTTTCACAGATG 540

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Db 481 AAGTTCTATCATCCAAAGTATGGGCTACAGAAACCGTCCMAAAGACTTCTACAGAGTG 540  
 QY 541 AACCCGAAATCCTCTCTGAGAGAAACAGCTCAGTGTCCAACTCTTACCTTGAA 600  
 Db 541 AACCCGAAATCCTCTCTGAGAGAAACAGCTCAGTGTCCAACTCTTACCTTGAA 600  
 QY 601 CTGTGAACTCTGAGACAAAGCAGGATACAACTCAAAAGAGCTGTCTACATTTG 660  
 Db 601 CTGTGAACTCTGAGACAAAGCAGGATACAACTCAAAAGAGCTGTCTACATTTG 660  
 QY 661 AATTGGATCTGATCTTCTGAAAGATACCTTAATAAGCACTTATGTGAGTGGAG 720  
 Db 661 AATTGGATCTGATCTTCTGAAAGATACCTTAATAAGCACTTATGTGAGTGGAG 720  
 QY 721 ATCAGAAATGTTACAAATCACCCCTCAAGAAACAGGATGAATCAGTTGGATTCTG 780  
 Db 721 ATCAGAAATGTTACAAATCACCCCTCAAGAAACAGGATGAATCAGTTGGATTCTG 780  
 QY 781 CAAAAAAGGCTGCTTGTGAATTTTCTGAGCGGATGTAACTGAACTATCAAC 840  
 Db 781 CAAAAAAGGCTGCTTGTGAATTTTCTGAGCGGATGTAACTGAACTATCAAC 840  
 QY 841 CCGATATATATGATTTTGAACACCACTGAGAAAGCTGAGAGGCACTCCAGAAAGT 900  
 Db 841 CCGATATATATGATTTTGAACACCACTGAGAAAGCTGAGAGGCACTCCAGAAAGT 900  
 QY 901 ATCAGGATGTTGTTTCAACTGTGAGTGTGAGGCACTGAGCAAAATCTCATGCA 960  
 Db 901 ATCAGGATGTTGTTTCAACTGTGAGTGTGAGGCACTGAGCAAAATCTCATGCA 960  
 QY 961 GCTCATTAACAGATGAGAAACAGAGTTTATCTCACTAAGACAGATGATGAGAA 1020  
 Db 961 GCTCATTAACAGATGAGAAACAGAGTTTATCTCACTAAGACAGATGATGAGAA 1020  
 QY 1021 AGGCTGATCTGATTAATAAGCAACAGCTGCTTGTGAGAGGCACTCATACAT 1080  
 Db 1021 AGGCTGATCTGATTAATAAGCAACAGCTGCTTGTGAGAGGCACTCATACAT 1080  
 QY 1081 GGGCTGGAAGTGAAGAAACATGATGATGAGGCGGACTCCAGACAGAAAGAGTGA 1140  
 Db 1081 GGGCTGGAAGTGAAGAAACATGATGATGAGGCGGACTCCAGACAGAAAGAGTGA 1140  
 QY 1141 ATCTGATGCTGATCCCTGTGTGAGAGAAAGATGAAATGAGCAAACTGCTGCT 1200  
 Db 1141 ATCTGATGCTGATCCCTGTGTGAGAGAAAGATGAAATGAGCAAACTGCTGCT 1200  
 QY 1201 CAGAGATCTGAGATGATGAGATGCTTGTGATTAACCTAATAGACAGATTGAGA 1260  
 Db 1201 CAGAGATCTGAGATGATGAGATGCTTGTGATTAACCTAATAGACAGATTGAGA 1260  
 QY 1261 AAGTTATGAGTGTCTTCCAGAGTGAAGTGAAGTGTGATGATGATGATGATG 1320  
 Db 1261 AAGTTATGAGTGTCTTCCAGAGTGAAGTGAAGTGTGATGATGATGATGATG 1320  
 QY 1321 GGGAGTCTGATCAAAATGCAAGTGTGATGATGATGATGATGATGATGATGATG 1380  
 Db 1321 GGGAGTCTGATCAAAATGCAAGTGTGATGATGATGATGATGATGATGATGATG 1380  
 QY 1381 AATATCTGATCTTCCAGAGAAATGACTTACCTGAGTGTGATGATGATGATGATG 1440  
 Db 1381 AATATCTGATCTTCCAGAGAAATGACTTACCTGAGTGTGATGATGATGATGATG 1440  
 QY 1441 TATGTAAGTGAAGTGTCTCCAAATCAGTGAAGTGAATGTAAGTGAAGTGAATG 1500  
 Db 1441 TATGTAAGTGAAGTGTCTCCAAATCAGTGAAGTGAATGTAAGTGAAGTGAATG 1500  
 QY 1501 TTGGGAAACCTATCGGAAAGCAAGCTCCCACTTAAGGCACTGTAAGTGAATG 1560  
 Db 1501 TTGGGAAACCTATCGGAAAGCAAGCTCCCACTTAAGGCACTGTAAGTGAATG 1560  
 QY 1561 TAAATTAAGAGATTTGTTACTGAGCCACAGATTAATACAGAGGCTCCCTCACAATA 1620  
 Db 1561 TAAATTAAGAGATTTGTTACTGAGCCACAGATTAATACAGAGGCTCCCTCACAATA 1620

QY 1621 AATTAAGGTAAGAGAGACCTACATCAGGCTTCACTGAGATTTTATCAAGAAAG 1680  
 Db 1621 AATTAAGGTAAGAGAGACCTACATCAGGCTTCACTGAGATTTTATCAAGAAAG 1680  
 QY 1681 CAGATTTGGCAGTTCAAAAGACTCTGAAATGATTAATAGGAACTAAACAGGAGC 1740  
 Db 1681 CAGATTTGGCAGTTCAAAAGACTCTGAAATGATTAATAGGAACTAAACAGGAGC 1740  
 QY 1741 AGAATGCTCAATGATGAATTTACTTAATAGTGTATGAAATTAACAAAGTGAAT 1800  
 Db 1741 AGAATGCTCAATGATGAATTTACTTAATAGTGTATGAAATTAACAAAGTGAAT 1800  
 QY 1801 CTATTGAGAAATGAGAAATTCCTAACCCATGAAATCACTCGAAAAAGATCTGCTTCA 1860  
 Db 1801 CTATTGAGAAATGAGAAATTCCTAACCCATGAAATCACTCGAAAAAGATCTGCTTCA 1860  
 QY 1861 AAACGAAAGCTGAACCTATTAAGCAGATTAAGCAATTAAGAACTGAAATTAATATCC 1920  
 Db 1861 AAACGAAAGCTGAACCTATTAAGCAGATTAAGCAATTAAGAACTGAAATTAATATCC 1920  
 QY 1921 ACAATTCAAAGACCTTAATAAGATAGGCTGAGAGAGAGTCTTACAGGCAATATTC 1980  
 Db 1921 ACAATTCAAAGACCTTAATAAGATAGGCTGAGAGAGAGTCTTACAGGCAATATTC 1980  
 QY 1981 ATGCGCTGAATAGTACATGATGATGAAATCTAAGCCCACTAATGTACTGAATGCAAA 2040  
 Db 1981 ATGCGCTGAATAGTACATGATGATGAAATCTAAGCCCACTAATGTACTGAATGCAAA 2040  
 QY 2041 TTGATAGTGTCTTACAGTGAAGATTAAGAAAAAAGTAAACCAATGCGAGTCA 2100  
 Db 2041 TTGATAGTGTCTTACAGTGAAGATTAAGAAAAAAGTAAACCAATGCGAGTCA 2100  
 QY 2101 GGCACAGCAAAACCTTAACATCAGAGAGTAAAGAACTGCACTGAGGCAAGAGA 2160  
 Db 2101 GGCACAGCAAAACCTTAACATCAGAGAGTAAAGAACTGCACTGAGGCAAGAGA 2160  
 QY 2161 GTTACAGCAAAATGAACAGACAGTAAAGACATGACAGTATCTTCCAGAGCTGA 2220  
 Db 2161 GTTACAGCAAAATGAACAGACAGTAAAGACATGACAGTATCTTCCAGAGCTGA 2220  
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 Db 2221 AGTTAAACAATGACCTGCTTCTTAACTAAGTGTCAATACAGTGAATCTTAAGAT 2280  
 QY 2281 TTGTCAATCTTACCTTCCAGAGAAAGAAAGAGAACTTGAACAGTTAAAGTGT 2340  
 Db 2281 TTGTCAATCTTACCTTCCAGAGAAAGAAAGAGAACTTGAACAGTTAAAGTGT 2340  
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 Db 2341 CTAATTAAGCTGAAGACCCCAAGATCTCATGTAAGTGAAGAGGTTTGCACAACTG 2400  
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 QY 2521 GTGTAGTCAAGTGTGACAGATTTGAAACCCCAAGGACTAATTAAGTGTGTTCCAAAG 2580  
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 Db 2581 ATTAATGAATGACACAGAGGCTTTAAGTATCAATTGGACATGAAGTTAACACAGTGC 2640  
 QY 2641 GGGAAACAGATTAAGAAATGGAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 2700  
 Db 2641 GGGAAACAGATTAAGAAATGGAAGAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 2700





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